



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 197086

TO: Ginny Portner
Location: REM/3B02/3C18
Art Unit: 1645
Monday, August 07, 2006
Case Serial Number: 09/732091

From: Vira David
Location: Biotech-Chem Library
REM-1A41
Phone: (571)272-1972

Virajita.David@uspto.gov

Search Notes

Examiner Portner,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Vira David
Intern
STIC Biotech/Chem Library
(571)272-1972

STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact **the searcher or contact:**

Mary Hale, Information Branch Supervisor
571-272-2507 Remsen E01 D86

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library Remsen Bldg.

STIC-Biotech/ChemLib

197086

From: Portner, Ginny
Sent: Monday, July 31, 2006 1:04 PM
To: STIC-Biotech/ChemLib
Subject: 09/732,091

please interference search SEQ ID No 3 and 4. thanks!

Ginny Portner
Remsen Building
Art Unit 1645
Room E03, B02; Mail Box 3C18
(571) 272-0862

7/31/2006

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 3, 2006, 09:12:51 ; Search time 202 Seconds
(without alignments)
7030.552 Million cell updates/sec

Title: US-09-732-091-3

Perfect score: 759

Sequence: 1 atggcatacaaatatgatag.....cgttgcaaatagaatccatt 759

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 93554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents NA:**

- 1: /EMC Celerra_SIDS3/ptodata/2/ina/1 COMB.seq.*
- 2: /EMC Celerra_SIDS3/ptodata/2/ina/5 COMB.seq.*
- 3: /EMC Celerra_SIDS3/ptodata/2/ina/6A COMB.seq.*
- 4: /EMC Celerra_SIDS3/ptodata/2/ina/6B COMB.seq.*
- 5: /EMC Celerra_SIDS3/ptodata/2/ina/7 COMB.seq.*
- 6: /EMC Celerra_SIDS3/ptodata/2/ina/H COMB.seq.*
- 7: /EMC Celerra_SIDS3/ptodata/2/ina/PCTUS COMB.seq.*
- 8: /EMC Celerra_SIDS3/ptodata/2/ina/PP COMB.seq.*
- 9: /EMC Celerra_SIDS3/ptodata/2/ina/RE COMB.seq.*
- 10: /EMC Celerra_SIDS3/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
C 1	68.2	9.0	7218	2	US-08-232-463-14
2	58.8	7.7	966	3	US-09-252-991A-13269
3	43.4	5.7	822	3	US-09-252-991A-13270
4	41.4	5.5	183	3	US-09-134-001C-1310
5	41.4	5.5	3666	3	US-09-710-279-3543
6	41.2	5.4	612	3	US-09-902-540-1357
7	40.8	5.4	19124	2	US-08-487-826B-13
8	40.2	5.3	5852	2	US-07-867-106-2
9	40.2	5.3	640681	3	US-09-790-988-1
10	40.2	5.3	1664976	3	US-08-916-421B-1
11	40.2	5.3	1664976	3	US-09-692-570-1
12	40	5.3	1305	3	US-09-854-326-65
13	39.8	5.2	795	3	US-09-248-796A-878
14	39.2	5.2	525	3	US-09-513-999C-14352
15	39.2	5.2	601	3	US-09-949-016-17780
16	39.2	5.2	601	3	US-09-949-016-88247
17	39.2	5.2	612	3	US-09-222-575-75
18	39.2	5.2	612	3	US-09-389-681-75
19	39.2	5.2	612	3	US-09-620-405B-75
20	39.2	5.2	612	3	US-09-339-338-75
21	39.2	5.2	612	3	US-09-433-826B-75
22	39.2	5.2	612	3	US-09-604-287A-75
23	39.2	5.2	612	3	US-09-285-480-75

24 39.2 5.2 612 3 US-09-834-759-75 Sequence 75, Appl
25 39.2 5.2 612 3 US-09-590-751A-75 Sequence 75, Appl
26 39.2 5.2 612 3 US-09-551-621-75 Sequence 75, Appl
27 39.2 5.2 612 3 US-09-551-621A-75 Sequence 75, Appl
28 39.2 5.2 612 3 US-10-076-622-75 Sequence 75, Appl
29 39.2 5.2 612 4 US-10-124-805-75 Sequence 25, Appl
30 39.2 5.2 1141 3 US-09-806-708B-22 Sequence 2477, Ap
31 39.2 5.2 5418 3 US-09-949-016-12477 Sequence 11753, A
32 39.2 5.2 40315 3 US-09-949-016-11753 Sequence 14219, A
33 39.2 5.2 40649 3 US-09-949-016-14219 Sequence 3928, Ap
34 38.8 5.1 3332 3 US-09-710-279-3928 Sequence 3752, Ap
35 38.8 5.1 3532 3 US-09-710-279-3752 Sequence 12848, A
36 38.4 5.1 51621 3 US-09-949-016-12848 Sequence 16503, A
37 38.4 5.1 263693 3 US-09-949-016-16503 Sequence 12386, A
38 38.4 5.1 263694 3 US-09-949-016-16915 Sequence 16915, A
39 38.2 5.0 1956 3 US-08-559-896B-1 Sequence 1, Appli
40 38.2 5.0 1956 3 US-09-351-794A-1 Sequence 1, Appli
41 38.2 5.0 2823 3 US-10-104-047-169 Sequence 169, App
42 38.2 5.0 3958 4 US-10-094-749-944 Sequence 944, App
43 38.2 5.0 1039 3 US-09-902-540-1280 Sequence 1280, Ap
44 38 5.0 6124 3 US-08-213-419B-3 Sequence 3, Appli
45 38

ALIGNMENTS

RESULT 1
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:

Db 65 ATTGAGAACAACTTATGAACAAACGCAACAAAGAGAAACATTTCTCTCAAGAAG 124
Qy 407 TATCCATAAAACACGACCAATTTAAACACAGCAA 441
Db 125 TATCTCAATGATTAAAGATCGTTTAGCTAGAAA 159

RESULT 5

US-09-710-279-3543
; Sequence 3543, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3543
; LENGTH: 3666
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-3543

Query Match 5.5%; Score 41.4; DB 3; Length 3666;
Best Local Similarity 54.2%; Pred. No. 0.25; Indels 0; Gaps 0;
Matches 84; Conservative 0; Mismatches 71; Indels 0; Gaps 0;
Qy 287 AGGTCAATTACAAACAGAAACTGAAACGACTTTAAATTGAACAAACATGCTTTCTAAAA 346
Db 2728 AGGTATATCTCATGAGAACCAATCAAAAGTAAATTAATGAGAAACGAAACACAATGATA 2787
Qy 347 TCTTAGAAGAGTTTGAAGAAATGGATGATGAAGAAGTGAAGAAATGTCGATGAAT 406
Db 2788 ATTGAGAACAACTTATGAACAAACGCAACAAAGAGAAACATTTCTCAAGAAGAA 2847
Qy 407 TATCCATAAAACACGACCAATTTAAACACGCAA 441
Db 2848 TATCTCAATGATTAAAGATCGTTTAGCTAGAAA 2882

RESULT 6

US-09-902-540-1357
; Sequence 1357, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1357
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(612)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1357

Query Match 5.4%; Score 41.2; DB 3; Length 612;
Best Local Similarity 44.6%; Pred. No. 0.15;
Matches 157; Conservative 0; Mismatches 195; Indels 0; Gaps 0;
Qy 90 TAAAGACGCGGAAAGAACACCAATGAAGAACTGACAGCTCCATAGATAACAAAAGCA 149
Db 151 TAAAAAATAAAATTTAAAAAATAAAATTAATAAAATTAATAAAATTAATAAA 210
Qy 150 TGGCGATGATTACGCTTAAATACGCAGAAAGAAATCGCTGAAGAGTTGCAATCTATGGAG 209
Db 211 AAAAAAATAAAATTAATAAAATTAATAAAATTAATAAAATTAATAAAATTAATAAA 270
Qy 210 CAATAGTTTGGCGAGTTTCATTAAGCGGAAGAGTCTTATACAAAGAGATTTATGCGA 269
Db 271 TAAAAAATAAAATTTAAAAAATAAAATTAATAAAATTAATAAAATTAATAAA 330
Qy 270 TGTGTCGATTAATTAAGTCAATTAACACAGAAACTGAAACGACTTTAAATTGACA 329
Db 331 AAAAAAATAAAATTAATAAAATTAATAAAATTAATAAAATTAATAAAATTAATAAA 390
Qy 330 AAACATGCTTTCTTAAATCTTAGAAGAGAGTTTGGAGAAATGATGATGAAGAGTCAA 389
Db 391 TAAAAAATAAAATTAATAAAATTAATAAAATTAATAAAATTAATAAAATTAATAAA 450
Qy 390 AGAAATGTGCGATGATTAATTCATATAAAACACGCAATTTTAAACAGACAA 441
Db 451 TTAATAAATAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAA 502

RESULT 7

US-08-487-826B-13
; Sequence 13, Application US/08487826B
; Patent No. 5933827
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellens, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CPI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19124 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

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; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-487-826B-13

Query Match 5.4%; Score 40.8; DB 2; Length 19124;
Best Local Similarity 53.0%; Pred. No. 0.68; 77; Indels 0; Gaps 0;
Matches 87; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 278 ATAAATTTAAAGTGCAATTACAACAAGAAAACCTGAAACGACTTTAATTGAAACAAACATGC 337
Db 15575 AAAAAATGAAAAGAGATTATCAAAAAAAATTAACAAAAAATTTTATATAAAAAAATGA 15634

QY 338 TTTCTAAAATCTTAGAAAAGAGTTTGGAGAAATGATGATGAAGAAGTGAAGAAATGT 397
Db 15635 TTATAAAAAAATAAAAAACAAGAGAAAAAACAATTTAAAAAATAAAAAATATAT 15694

QY 398 GCGATGAATTATCCATAAAAAACACGGACAATTTAAACAGACAA 441
Db 15695 ATCATAAAAACAAAAAAGAAAAAATAATATATATAAATAANA 15738

RESULT 8
US-07-867-106-2/c
; Sequence 2, Application US/07867106
; Patent No. 5389526
; GENERAL INFORMATION:
; APPLICANT: Slade, Martin B
; APPLICANT: Chang, Andy C M
; APPLICANT: Williams, Keith L
; TITLE OF INVENTION: Improved plasmid Vectors for Cellular
; TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/867,106
; FILING DATE: 19920625
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PJ 7187
; APPLICATION NUMBER: PCT/AU90/00530
; FILING DATE: 02-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Feeney, Joanne Longo
; REGISTRATION NUMBER: 35,134
; REFERENCE/DOCKET NUMBER: RICE-0002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5852 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2378..5038
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2378..5038
; US-07-867-106-2

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Qy 373 GATGATGAAGAGTGAAGAATGTGGCATGAA 405
|||||
Db 623802 GATTACAATCCATTGATTATTTTATAATCAA 623770

RESULT 10
US-08-916-421B-1/c
; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
; Patent No. 6503729
; FILE REFERENCE: PB275
; CURRENT APPLICATION NUMBER: US/08/916,421B
; CURRENT FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1664976
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (28222)..(28222)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (28257)..(28258)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (84773)..(84773)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (84808)..(84808)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (84812)..(84812)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98120)..(98120)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98159)..(98159)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98239)..(98239)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98266)..(98266)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98343)..(98343)
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; LOCATION: (103998)..(103998)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (148948)..(148948)
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; LOCATION: (163385)..(163385)
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; NAME/KEY: misc feature
; LOCATION: (191989)..(191989)
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; LOCATION: (191995)..(191995)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (231980)..(231980)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (234187)..(234187)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (234220)..(234220)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (234814)..(234814)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (309398)..(309398)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (309418)..(309418)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (312837)..(312837)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (312993)..(312993)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (319226)..(319226)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (559167)..(559167)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (559241)..(559241)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (600992)..(600992)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (622708)..(622708)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (657081)..(657081)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (657203)..(657203)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (674435)..(674435)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (682442)..(682442)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (713652)..(713652)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (741684)..(741684)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (779455)..(779455)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (779676)..(779676)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (855539)..(855539)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (871619)..(871619)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1084830)..(1084830)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1096846)..(1096846)
; OTHER INFORMATION: n equals a, t, c, or g

;; TITLE OF INVENTION: OF PITUITARY TUMOR TRANSFORMING GENE (PTTG)1 USING PTTG2
;; FILE REFERENCE: 18810-81401
;; CURRENT APPLICATION NUMBER: US/09/854,326
;; CURRENT FILING DATE: 2001-05-11
;; PRIOR APPLICATION NUMBER: US09/730,469
;; PRIOR FILING DATE: 2000-12-04
;; PRIOR APPLICATION NUMBER: US 09/687,911
;; PRIOR FILING DATE: 2000-10-13
;; PRIOR APPLICATION NUMBER: US 09/569,956
;; PRIOR FILING DATE: 2000-05-12
;; PRIOR APPLICATION NUMBER: US 08/894,251
;; PRIOR FILING DATE: 1999-07-23
;; PRIOR APPLICATION NUMBER: PCT/US86/21463
;; PRIOR FILING DATE: 1997-11-21
;; PRIOR APPLICATION NUMBER: US 60/031,338
;; PRIOR FILING DATE: 1996-11-21
;; NUMBER OF SEQ ID NOS: 68
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 65
;; LENGTH: 1305
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-854-326-65

Query Match 5.3%; Score 40; DB 3; Length 1305;
Best Local Similarity 53.1%; Pred. No. 0.41; Mismatches 0; Indels 75; Gaps 0;
Matches 85; Conservative 0;
QY 246 CTTATACAAAGAGATTTTATCGCATGTGTCGATAAATAAAGTCAATTAACAACAGAA 305
DB 929 CTCGACATAGATTTAAATTTCTTAGTGCTTTAGAGTTTGTGTATATTTCTTAATA 988
QY 306 AACTGAAACGACTTTAATTGAACAAAACATGCTTTCTTAAATCTTAGAAGAGTTTGGGA 365
DB 989 AAGCATTTATTTGTTAAACAGAAAAAGATATATATCTTAATCTCTTAAATAAATAACCA 1048
QY 366 AGAATCGATGATCAAGAGTGAAGAAATCTGCGATGAA 405
DB 1049 TTAAGGAAAAACAGGAGTTATTAACATAAAGGAACAA 1088

RESULT 13
US-09-248-796A-878
; Sequence 878, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 878
; LENGTH: 795
; TYPE: DNA
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (28)
; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unknown
US-09-248-796A-878

Query Match 5.2%; Score 39.8; DB 3; Length 795;
Best Local Similarity 47.2%; Pred. No. 0.39;
Matches 159; Conservative 0; Mismatches 172; Indels 6; Gaps 1;
QY 41 AATTGGAATCTAGCATTTATTTGATTTGTTGAGTCTGCTTTTGTGTAAGACGGCG 100

DB 254 AAGTTTATTATCTGATTTGATATTGTTATTAGAACCTGTTGAATCACAATCGAAGCAT 313
QY 101 AAAAAAGACACAATGAAAACTGACCCAGCTCCATAGATAAAGAGCATGCGGATGATT 160
DB 314 TAGCAAGATTGAATCTCTAAACCTTGAGAAAAAGAAAGAGGTGATGATGATGATA 373
QY 161 ACGCTAAATACGCAGAAAAAGAAATCGCTGAAGAGTTGCAATATCTATGGGAGCAATAGTTTGG 220
DB 374 ACAATAAAATGGTATACCAACCATGAAGAATTAATTAATAAATCACTAATGTTGTT 433
QY 221 CGAGTTTCATTAAGCGGAGGAGGAGTCTTATACAAAGAGATTTTATCGCATGTGTGGGATA 280
DB 434 CGATTTTAAATTAATGATATAACAAATTTGATGATATATATCACTAACTA-----GAGAAG 487
QY 281 AATTAAAGTCAATTACAAACAGAAACTGAAACGACTTTAATTGACAAACACATGCTTTT 340
DB 488 AATTGACGAGGAAATTTTCAACAACTGACAAAGTTTAAATGTTGAACGAGGTCTTA 547
QY 341 CTAATAATCTTAGAAAAAGAGTTTGGAAAGAAATCGATGA 377
DB 548 AACGATCAAGAGAGAAAGTGTGATGACGAGAGATGATGA 584

RESULT 14
US-09-513-999C-14352/c
; Sequence 14352, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 14352
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 392
; OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-14352

Query Match 5.2%; Score 39.2; DB 3; Length 525;
Best Local Similarity 55.0%; Pred. No. 0.49;
Matches 77; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 8 ACAATATCATAGAGACTTGGAAATTTTAAACCAATTTGAAATCTAGTGTATTATCGATT 67
DB 258 AAAAAAGAGAGAGAAATGGCAAGAGAAAGTTTTTCAAAATTTCTTTCTTTTAAAT 199
QY 68 TGTGAGTGCTGTTGTTTGTGTAAGACGCGGAAAAAGACACAAATGAAAACTGACCA 127
DB 198 TAGATTGAGTTTCATTTATTGAAACAGACTGGCCCAATCTCCACAAGAAATTCCTGTCA 139
QY 128 GCTCCATAGATACAAAAGG 147
DB 138 GCACCACCGATGTCACAAAGG 119

RESULT 15
US-09-949-016-17780/c
; Sequence 17780, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17780
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17780

Query Match 5.2%; Score 39.2; DB 3; Length 601;
Best Local Similarity 55.0%; Pred. No. 0.52;
Matches 77; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
Qy 8 ACAATATGATAGACACTTGGAAATTTTAAAGCAATTTGGAATCTAGTGAATTTATTGGATT 67
Db 181 AAAAAGAGAGAGAGAAATGGCAAGAGAGAAAGTTTTTCAAATTTCTTTCTTTTAAAT 122
Qy 68 TGTGTGAGTCTGTTGTTTGTGTAAGACGGCGAAAGACACAAATGNAAACTGACCA 127
Db 121 TAGATTGAGTTCAATTTATTGAAACAGACTGGGCCAATGTCCACAAAGAAATTCCTGGTCA 62
Qy 128 GCTCCATAGAAATACAAAAGG 147
Db 61 GCACCCCGATGTCCAAAGG 42

Search completed: August 3, 2006, 09:18:19
Job time : 207 secs

GenCore version 5.1.9

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OM nucleic - nucleic search, using sw model

Run on: August 3, 2006, 09:18:35 ; Search time 1473 Seconds
(without alignments)

6331.511 Million cell updates/sec

Title: US-09-732-091-3

Perfect score: 759

Sequence: 1 atggcatcaaatatgatag.....cgttgcaaatagaatccatt 759

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA Main:

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	759	100.0	759	3	US-09-732-091-3
2	759	100.0	759	8	US-10-433-970-3
3	759	100.0	795	3	US-09-732-091-43
4	759	100.0	795	8	US-10-433-970-43
5	727	95.8	762	8	US-10-335-977-4400
6	727	95.8	762	8	US-10-335-977-4401
7	727	95.8	768	8	US-10-335-977-4402
8	717.4	94.5	762	8	US-10-433-970-47
9	717.4	94.5	798	8	US-10-433-970-45
10	365.8	48.2	744	8	US-10-335-977-2937
11	359.4	47.4	714	8	US-10-335-977-2936
12	271.4	35.8	547	3	US-09-882-227-413
13	153	20.2	153	3	US-09-732-091-36
14	153	20.2	153	8	US-10-433-970-36
15	114	15.0	114	3	US-09-732-091-33
16	114	15.0	114	8	US-10-433-970-33
17	108	14.2	108	3	US-09-732-091-35

18	108	14.2	108	8	US-10-433-970-35	Sequence 35, Appl
19	90	11.9	90	3	US-09-732-091-32	Sequence 32, Appl
20	90	11.9	90	3	US-09-732-091-34	Sequence 34, Appl
21	90	11.9	90	8	US-10-433-970-32	Sequence 32, Appl
22	90	11.9	90	8	US-10-433-970-34	Sequence 34, Appl
23	47.6	6.3	1214	8	US-10-424-599-102083	Sequence 102083,
24	47.6	6.3	1243	9	US-10-425-115-17217	Sequence 17217,
c	25	47	627	8	US-10-021-323-9336	Sequence 9336, Ap
26	46.2	6.1	476	9	US-10-425-115-50533	Sequence 50533, A
27	46.2	6.1	3588	8	US-10-282-122A-16553	Sequence 16553, A
c	28	45.4	547	4	US-09-925-065A-115849	Sequence 115849,
c	29	45.4	547	5	US-09-925-065A-115849	Sequence 115849,
c	30	45.4	548	12	US-10-301-480-214754	Sequence 214754,
c	31	45.4	548	12	US-10-301-480-828163	Sequence 828163,
c	32	45.4	1062	9	US-10-425-115-120013	Sequence 120013,
33	45.2	6.0	564	4	US-09-925-065A-109807	Sequence 109807,
34	45.2	6.0	564	4	US-09-925-065A-109808	Sequence 109808,
35	45.2	6.0	564	4	US-09-925-065A-109809	Sequence 109809,
36	45.2	6.0	564	5	US-09-925-065A-109807	Sequence 109807,
37	45.2	6.0	564	5	US-09-925-065A-109808	Sequence 109808,
38	45.2	6.0	564	5	US-09-925-065A-109809	Sequence 109809,
39	45.2	6.0	587	12	US-10-301-480-209418	Sequence 209418,
40	45.2	6.0	587	12	US-10-301-480-209419	Sequence 209419,
41	45.2	6.0	587	12	US-10-301-480-209420	Sequence 209420,
42	45.2	6.0	587	12	US-10-301-480-822827	Sequence 822827,
43	45.2	6.0	587	12	US-10-301-480-822828	Sequence 822828,
44	45.2	6.0	587	12	US-10-301-480-822829	Sequence 822829,
45	45.2	6.0	3272	10	US-10-750-185-62663	Sequence 62663, A

ALIGNMENTS

RESULT 1

US-09-732-091-3
 ; Sequence 3, Application US/09732091
 ; Patent No. US20020107368A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tian, Jing-Hui
 ; APPLICANT: Walker, Richard I.
 ; APPLICANT: Jackson, W. James
 ; TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses
 ; TITLE OF INVENTION: thereof
 ; FILE REFERENCE: 7969-088
 ; CURRENT APPLICATION NUMBER: US/09/732,091
 ; CURRENT FILING DATE: 2000-12-07
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 759
 ; TYPE: DNA
 ; ORGANISM: Helicobacter sp.
 US-09-732-091-3

Query Match	100.0%;	Score	759;	DB	3;	Length	759;
Best Local Similarity	100.0%;	Pred. No.	7.8e-179;	Mismatches	0;	Indels	0;
Matches	759;	Conservative	0;	Mismatches	0;	Indels	0;
QY	1	ATGGCATACAAATATGATAGAGACTTTGGAATTTTAAAGCAATTTGGAATCTAGTGATT	60				
Db	1	ATGGCATACAAATATGATAGAGACTTTGGAATTTTAAAGCAATTTGGAATCTAGTGATT	60				
QY	61	TTGGATTTTGTTCAGTGTCTTTTGGTAAAGACGGCGAAAAAGACACAAATGAAAAA	120				
Db	61	TTGGATTTTGTTCAGTGTCTTTTGGTAAAGACGGCGAAAAAGACACAAATGAAAAA	120				
QY	121	CTGACCAAGTCCATAGAAATACAAAGCGATGCGCATGATTACGCTAAATACGCAGAAAGA	180				
Db	121	CTGACCAAGTCCATAGAAATACAAAGCGATGCGCATGATTACGCTAAATACGCAGAAAGA	180				
QY	181	ATCGCTGAAGAGTTGCAATCTACTATGGAGCAATAGTTTTTCGAGTTTCATTAAAGCGAA	240				
Db	181	ATCGCTGAAGAGTTGCAATCTACTATGGAGCAATAGTTTTTCGAGTTTCATTAAAGCGAA	240				

QY 241 GGAGTCTTATACAAAGAGATTTTATGCGATGTCGCGATGATTAAGGTCATTAACAAC 300
DB 241 GGAGTCTTATACAAAGAGATTTTATGCGATGTCGCGATGATTAAGGTCATTAACAAC 300
QY 301 AAGAAACTGAAACGACTTTAAATGGAACAAACATGCTTTCTAAATCTTAGAAGAAAGT 360
DB 301 AAGAAACTGAAACGACTTTAAATGGAACAAACATGCTTTCTAAATCTTAGAAGAAAGT 360
QY 361 TTGGAAGAAATGGAATGATGAAGAAAGTGAAGAAATGTCGATGAATATCCATAAAAAC 420
DB 361 TTGGAAGAAATGGAATGATGAAGAAAGTGAAGAAATGTCGATGAATATCCATAAAAAC 420
QY 421 ACGGACAAATTTAAACAGACAGCCTTTAAGCGCGGAGCTTTAAACGCTGTTTAAATGGG 480
DB 421 ACGGACAAATTTAAACAGACAGCCTTTAAGCGCGGAGCTTTAAACGCTGTTTAAATGGG 480
QY 481 GGTTTTAAATCTTATCAATTAAGTCTGTCATTTGCGAATGCGGTGCGAAACCAATCTTA 540
DB 481 GGTTTTAAATCTTATCAATTAAGTCTGTCATTTGCGAATGCGGTGCGAAACCAATCTTA 540
QY 541 GGGCGTGGTTTATCGTTGCGGCAATCAGGTGCTTACAAGAACTCTGAGCTTTTAAACA 600
DB 541 GGGCGTGGTTTATCGTTGCGGCAATCAGGTGCTTACAAGAACTCTGAGCTTTTAAACA 600
QY 601 GGTCTGTTGGTGGATCATTAACGCGTATGACGAGGATGATATGACGGCGCGCT 660
DB 601 GGTCTGTTGGTGGATCATTAACGCGTATGACGAGGATGATATGACGGCGCGCT 660
QY 661 TATAGGTAACCATACCGGCAATCAGGTGCTTACAAGAACTCTGAGCTTTTAAACA 720
DB 661 TATAGGTAACCATACCGGCAATCAGGTGCTTACAAGAACTCTGAGCTTTTAAACA 720
QY 721 GCCAATGGAGATAAGAAAGTCTGTTGCAAAATAGAATCCATT 759
DB 721 GCCAATGGAGATAAGAAAGTCTGTTGCAAAATAGAATCCATT 759

RESULT 2

US-10-433-970-3

; Sequence 3, Application US/10433970
; Publication No. US20040138415A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Jing-Hui
; APPLICANT: Walker, Richard
; APPLICANT: Jackson, James
; TITLE OF INVENTION: HELICOBACTER PROTEINS, GENE SEQUENCES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 7969-091-999
; CURRENT APPLICATION NUMBER: US/10/433,970
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 09/732,091
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 759
; TYPE: DNA
; ORGANISM: Helicobacter sp.
US-10-433-970-3

Query Match 100.0%; Score 759; DB 8; Length 759;
Best Local Similarity 100.0%; Pred. No. 7.8e-179;
Matches 759; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCATACAATATGATAGAGACTTGGAAATTTTAAAGCAATGGAATCTAGTATTTA 60
DB 1 ATGGCATACAATATGATAGAGACTTGGAAATTTTAAAGCAATGGAATCTAGTATTTA 60
QY 61 TTGGATTGTTTGGAGTCTGTTGTTTGGTAAAGACGGGAAAAAGACAAATGAAAAA 120
DB 61 TTGGATTGTTTGGAGTCTGTTGTTTGGTAAAGACGGGAAAAAGACAAATGAAAAA 120

QY 121 CTGACGAGCTCCATAGAAATCAAAAGGCGATGCGGATGATTAAGCTAAATACGACAGAA 180
DB 121 CTGACGAGCTCCATAGAAATCAAAAGGCGATGCGGATGATTAAGCTAAATACGACAGAA 180
QY 181 ATCGCTGAAGAGTTGCAATACTATGCGGCAATAGTTTTGCGAGTTTCAATTAAGGCGAA 240
DB 181 ATCGCTGAAGAGTTGCAATACTATGCGGCAATAGTTTTGCGAGTTTCAATTAAGGCGAA 240
QY 241 GGAGTCTTATCAAAAGAGATTTTATGCGATGTCGCGATGATTAAGCTCAATTAACAAC 300
DB 241 GGAGTCTTATCAAAAGAGATTTTATGCGATGTCGCGATGATTAAGCTCAATTAACAAC 300
QY 301 AAGAAACTGAAACGACTTTAAATGGAACAAACATGCTTTCTAAATCTTAGAAGAAAGT 360
DB 301 AAGAAACTGAAACGACTTTAAATGGAACAAACATGCTTTCTAAATCTTAGAAGAAAGT 360
QY 361 TTGGAAGAAATGGAATGATGAAGAAAGTGAAGAAATGTCGATGAATATCCATAAAAAC 420
DB 361 TTGGAAGAAATGGAATGATGAAGAAAGTGAAGAAATGTCGATGAATATCCATAAAAAC 420
QY 421 ACGGACAAATTTAAACAGACAGCCTTTAAGCGCGGAGCTTTAAACGCTGTTTAAATGGG 480
DB 421 ACGGACAAATTTAAACAGACAGCCTTTAAGCGCGGAGCTTTAAACGCTGTTTAAATGGG 480
QY 481 GGTTTTAAATCTTATCAATTAAGTCTGTCATTTGCGAATGCGGTGCGAAACCAATCTTA 540
DB 481 GGTTTTAAATCTTATCAATTAAGTCTGTCATTTGCGAATGCGGTGCGAAACCAATCTTA 540
QY 541 GGGCGTGGTTTATCGCTTTCGCGGCAATCAGGTGCTTACAAGAACTCTGAGCTTTTAAACA 600
DB 541 GGGCGTGGTTTATCGCTTTCGCGGCAATCAGGTGCTTACAAGAACTCTGAGCTTTTAAACA 600
QY 601 GGTCTGTTGGTGGATCATTAACGCGTATGACGAGGATGATATGACGGCGCGCT 660
DB 601 GGTCTGTTGGTGGATCATTAACGCGTATGACGAGGATGATATGACGGCGCGCT 660
QY 661 TATAGGTAACCATACCGGCAATCAGGTGCTTACAAGAACTCTGAGCTTTTAAACA 720
DB 661 TATAGGTAACCATACCGGCAATCAGGTGCTTACAAGAACTCTGAGCTTTTAAACA 720
QY 721 GCCAATGGAGATAAGAAAGTCTGTTGCAAAATAGAATCCATT 759
DB 721 GCCAATGGAGATAAGAAAGTCTGTTGCAAAATAGAATCCATT 759

RESULT 3

US-09-732-091-43
; Sequence 43, Application US/09732091
; Patent No. US20020107368A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Jing-Hui
; APPLICANT: Walker, Richard I.
; APPLICANT: Jackson, W. James
; TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses
; TITLE OF INVENTION: thereof
; FILE REFERENCE: 7969-088
; CURRENT APPLICATION NUMBER: US/09/732,091
; CURRENT FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 43
; LENGTH: 795
; TYPE: DNA
; ORGANISM: Helicobacter sp.
US-09-732-091-43

Query Match 100.0%; Score 759; DB 3; Length 795;
Best Local Similarity 100.0%; Pred. No. 8e-179;
Matches 759; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCATACAATATGATAGAGACTTGGAAATTTTAAAGCAATGGAATCTAGTATTTA 60
DB 37 ATGGCATACAATATGATAGAGACTTGGAAATTTTAAAGCAATGGAATCTAGTATTTA 96

Qy 61 TTGATTTGTTGAGTCTGTTGTTTGGTAAAGACGGCGGAAAAAGACAAATGAAAAA 120
Db 97 TTGATTTGTTGAGTCTGTTGTTTGGTAAAGACGGCGGAAAAAGACAAATGAAAAA 156
Qy 121 CTGACGAGCTCCATAGATAAAGAGGATGCGGATGATTAGCTTAATACGCAAGAA 180
Db 157 CTGACGAGCTCCATAGATAAAGAGGATGCGGATGATTAGCTTAATACGCAAGAA 216
Qy 181 ATCCCTGAAGAGTTGCAATCTATGCGAGCAATAGTTTGGAGTTTCATTAAGGCGAA 240
Db 217 ATCCCTGAAGAGTTGCAATCTATGCGAGCAATAGTTTGGAGTTTCATTAAGGCGAA 276
Qy 241 GGAGTCTTATACAAAGAGATTTTATGCGATGTGCGGATAAATTAAGGTCATTAACAC 300
Db 277 GGAGTCTTATACAAAGAGATTTTATGCGATGTGCGGATAAATTAAGGTCATTAACAC 336
Qy 301 AAGAAACTGAAACGACCTTTAATTAAGCAAAACATGCTTTCTAAATCTTAGAAAGAGT 360
Db 337 AAGAAACTGAAACGACCTTTAATTAAGCAAAACATGCTTTCTAAATCTTAGAAAGAGT 396
Qy 361 TTGGAAGAAATGGATGATGAAGAGTGAAGAAATGTCGGATGAATTAATCCATAAAAC 420
Db 397 TTGGAAGAAATGGATGATGAAGAGTGAAGAAATGTCGGATGAATTAATCCATAAAAC 456
Qy 421 ACGGACAAATTTAAACAGACAGCTTAAAGCGCGGACCTTTAAACGCTGTTTAAATGGG 480
Db 457 ACGGACAAATTTAAACAGACAGCTTAAAGCGCGGACCTTTAAACGCTGTTTAAATGGG 516
Qy 481 GGTCTTAAATCTTATCAATAGCTGTCAATGTTGCGAATGCGGTGCGCAAAACCAATCTTA 540
Db 517 GGTCTTAAATCTTATCAATAGCTGTCAATGTTGCGAATGCGGTGCGCAAAACCAATCTTA 576
Qy 541 GGGCGTGTGTTATCGCTTGGCGCAATCAGTGTCTTACAGAACTCTGAGCTTTTAAACA 600
Db 577 GGGCGTGTGTTATCGCTTGGCGCAATCAGTGTCTTACAGAACTCTGAGCTTTTAAACA 636
Qy 601 GGTCTGTGCTGGATCAATACAGGCTATGAGCGGATGAGATGATTAATGCGGCGGCT 660
Db 637 GGTCTGTGCTGGATCAATACAGGCTATGAGCGGATGAGATGATTAATGCGGCGGCT 696
Qy 721 GCCAATGGAGATAAGAGTCTGTTGCAATAGAAATCCATT 759
Db 757 GCCAATGGAGATAAGAGTCTGTTGCAATAGAAATCCATT 795

RESULT 4

US-10-433-970-43
; Sequence 43, Application US/10433970
; Publication No. US20040138415A1
; GENERAL INFORMATION:

; APPLICANT: Tian, Jing-Hui
; APPLICANT: Walker, Richard
; APPLICANT: Jackson, James

; TITLE OF INVENTION: HELICOBACTER PROTEINS, GENE SEQUENCES AND USES
; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 7969-091-999

; CURRENT APPLICATION NUMBER: US/10/433,970

; PRIOR FILING DATE: 2003-06-06

; PRIOR APPLICATION NUMBER: 09/732,091

; PRIOR FILING DATE: 2000-12-07

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: PatentIn ver. 2.1

; SEQ ID NO 43

; LENGTH: 795

; TYPE: DNA

; ORGANISM: Helicobacter sp.

US-10-433-970-43

Query Match 100.0%; Score 759; DB 8; Length 795;
Best Local Similarity 100.0%; Pred. No. 8e-179;
Matches 759; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCATACAAATATGATAGACACTTTGGAAATTTTAAAGCAATTTGAATCTAGTGATTTA 60
Db 37 ATGGCATACAAATATGATAGACACTTTGGAAATTTTAAAGCAATTTGAATCTAGTGATTTA 96
Qy 61 TTGGATTTTGTGGAGTGTCTTGTGTTTGGTAAAGACGGCGGAAAAAGACAAATGAAAAA 120
Db 97 TTGGATTTTGTGGAGTGTCTTGTGTTTGGTAAAGACGGCGGAAAAAGACAAATGAAAAA 156
Qy 121 CTGACGAGCTCCATAGATAAAGAGGATGCGGATGATTACGCTTAATACGCAAGAA 180
Db 157 CTGACGAGCTCCATAGATAAAGAGGATGCGGATGATTACGCTTAATACGCAAGAA 216
Qy 181 ATCCCTGAAGAGTTGCAATCTATGCGAGCAATAGTTTGGAGTTTCATTAAGGCGAA 240
Db 217 ATCCCTGAAGAGTTGCAATCTATGCGAGCAATAGTTTGGAGTTTCATTAAGGCGAA 276
Qy 241 GGAGTCTTATACAAAGAGATTTTATGCGATGTGCGGATAAATTAAGGTCATTAACAC 300
Db 277 GGAGTCTTATACAAAGAGATTTTATGCGATGTGCGGATAAATTAAGGTCATTAACAC 336
Qy 301 AAGAAACTGAAACGACCTTTAATTAAGCAAAACATGCTTTCTAAATCTTAGAAAGAGT 360
Db 337 AAGAAACTGAAACGACCTTTAATTAAGCAAAACATGCTTTCTAAATCTTAGAAAGAGT 396
Qy 361 TTGGAAGAAATGGATGATGAAGAGTGAAGAAATGTCGGATGAATTAATCCATAAAAC 420
Db 397 TTGGAAGAAATGGATGATGAAGAGTGAAGAAATGTCGGATGAATTAATCCATAAAAC 456
Qy 421 ACGGACAAATTTAAACAGACAGCTTAAAGCGCGGACCTTTAAACGCTGTTTAAATGGG 480
Db 457 ACGGACAAATTTAAACAGACAGCTTAAAGCGCGGACCTTTAAACGCTGTTTAAATGGG 516
Qy 481 GGTCTTAAATCTTATCAATAGCTGTCAATGTTGCGAATGCGGTGCGCAAAACCAATCTTA 540
Db 517 GGTCTTAAATCTTATCAATAGCTGTCAATGTTGCGAATGCGGTGCGCAAAACCAATCTTA 576
Qy 541 GGGCGTGTGTTATCGCTTGGCGCAATCAGTGTCTTACAGAACTCTGAGCTTTTAAACA 600
Db 577 GGGCGTGTGTTATCGCTTGGCGCAATCAGTGTCTTACAGAACTCTGAGCTTTTAAACA 636
Qy 601 GGTCTGTGCTGGATCAATACAGGCTATGAGCGGATGAGATGATTAATGCGGCGGCT 660
Db 637 GGTCTGTGCTGGATCAATACAGGCTATGAGCGGATGAGATGATTAATGCGGCGGCT 696
Qy 661 TATAGGATAACCATACCGGATGCAATGTTGGTTGCCACTTTACGCTTAAACACAGCAA 720
Db 697 TATAGGATAACCATACCGGATGCAATGTTGGTTGCCACTTTACGCTTAAACACAGCAA 756

RESULT 5

US-10-335-977-4400

; Sequence 4400, Application US/10335977

; Publication No. US20040052799A1

; GENERAL INFORMATION:

; APPLICANT: DOUGLAS SMITH et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES

; RELATING TO HELICOBACTER PYLORI FOR

; DIAGNOSTICS AND THERAPEUTICS

; NUMBER OF SEQUENCES: 10031

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 28 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

Best Local Similarity 97.4%; Pred. No. 7.6e-171;			
Matches 739; Conservative 0; Mismatches 20; Indels 0; Gaps 0;			
Qy	1	ATGGCATCAAAATATGATAGAGACTTGGAAATTTTAAAGCAATTTGGAATCTAGTGATT	60
Db	1	ATGGCATCAAAATATGATAGAGACTTGGAAATTTTAAAGCAATTTGGAATCTAGTGATT	60
Qy	61	TTGATTTGTTTGAGGTGCTTTGTTTGGTAAAGACGGCGAAAAAGACACAATGAAAAA	120
Db	61	TTGATTTGTTTGAGGTGCTTTGTTTGGTAAAGACGGCGAAAAAGACACAATGAAAAA	120
Qy	121	CTGACAGCTCCATAGAAATCAAAAGCATGGCGATGATTCGCTAAATACGCGAAGA	180
Db	121	CTCAAGCTCCATAGAAATCAAAAGCATGGCGATGATTCGCTAAATACGCGAAGA	180
Qy	181	ATCGCTGAAGATTGGCAATACTATGGGAGCAATAGTTTGGGAGTTTCATTTAAAGCGCA	240
Db	181	ATCGCTGAAGATTGGCAATACTATGGGAGCAATAGTTTGGGAGTTTCATTTAAAGGTGAA	240
Qy	241	GGAGTCTTTATCAAAAGAGATTTTATGCGATGTGTGCGATAAAATTAAGGTCAATTAACA	300
Db	241	GGAGTCTTTATCAAAAGAGATTTTATGCGATGTGTGCGATAAAATTAAGGTCAATTAACA	300
Qy	301	AAGAAATCTGAACGACTTTAAATTGAACAAAAATGCTTTCTAAAAATCTTAGAAGAAGT	360
Db	301	AAGAAATCTGAACGACTTTAAATTGAACAAAAATGCTTTCTAAAAATCTTAGAAGAAGT	360
Qy	361	TTGGAAGAAATGGATGATGAAGAGTCAAGAAATGTGCGATGAATTCATATAAAAAAC	420
Db	361	CTAGAAGAAATGGATGATGAAGAGTCAAGAAATGTGCGATGAATTCATATAAAAAAC	420
Qy	421	ACGACAAATTTAAACAGACAAAGCTTAAAGCGCGCGACTTTAAACGCTGTTTAAAAATGGG	480
Db	421	ACGACAAATTTGAACAGACAAAGCTTAAAGCGCGCGACTTTAAACGCTGTTTAAAAATGGG	480
Qy	481	GGTTTTAAATCTTTATCAATTAGCTGTCATTTGTTGCGAATCGGTCGCAAAACCATTTCTA	540
Db	481	GGCTTTAAATCTTTATCAATTAGCTGTCATTTGTTGCGAATCGGTCGCAAAACCATTTCTA	540
Qy	541	GGGCGTGTTTATCGCTTGGCGGCAATCAGGTGCTTACAGAACTCTGAGCTTTTAAACA	600
Db	541	GGGCGTGTTTATCGCTTGGCGGCAATCAGGTGCTTACAGAACTCTGAGCTTTTAAACA	600
Qy	601	GGTCTGTTGCGTGGATCAATTAACGGCGTATGGAACGCGATTGATATTGACAGGCGCGGT	660
Db	601	GGCCCTGTTGGCTGGATCAATTAACGGCGTATGGAACGCGATTGATATTGACAGGCGCGGT	660
Qy	661	TATAGGTTAACCATACCGGATGTCATTTGTTGGTTGCCACTTTTACGCCCTAAAAACACAGCAA	720
Db	661	TATAGGTTAACCATACCGGATGTCATTTGTTGGTTGCCACTTTTACGCCCTAAAAACACAGCAA	720
Qy	721	GCCAAATGGAGATGAAGATCGTTGCAAAATAGAAATCCATT	759
Db	721	GCCAAATGAAGATGAAGATCGTTGCAAAATAGAAATCCGTT	759

```

RESULT 7
US-10-335-977-4402
; Sequence 4402, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
;
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875

```

COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 4402:
SEQUENCE CHARACTERISTICS:
LENGTH: 768 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...768
SEQUENCE DESCRIPTION: SEQ ID NO: 4402:
US-10-335-977-4402

Query Match	95.8%	Score 727;	DB 8;	Length 768;
Best Local Similarity	97.4%;	Pred. No. 7.6e-171;		
Matches 739;	Conservative 0;	Mismatches 20;	Indels 0;	Gaps 0;
Qy	1	ATGGCATACAAATATGATAGACGACTTGGAAATTTTAAAGCAATTTGGAATCTAGTGATTTA	60	
Db	10	ATGGCATACAAATATGATAGACGACTTGGAAATTTTAAAGCAATCTAGTGATTTA	69	
Qy	61	TTGGATTTGTTTGAGGTGCTGTGTTTGTGTAAAGACGGCGAAAAAGACACAATGAAAAA	120	
Db	70	TTGGATTTGTTTGAGGTGCTGTGTTTGTGTAAAGACGGCGAAAAAGACACAATGAAAAA	129	
Qy	121	CTGACGAGCTCCATAGAAATACAAAAGCGCATGGCGATGATTACGCTAAATACGCAGAAAGA	180	
Db	130	CTCACAAGCTCCATAGAAATACAAAAGCGCATGGCGATGATTACGCTAAATACGCAGAAAGA	189	
Qy	181	ATCGCTGAAGAGTTGCAATATCATGGAGCAATAGTTTTTGGCGAGTTTTCATTAAAGCGCAA	240	
Db	190	ATCGCTGAAGAGTTGCAATATCATGGAGCAATAGTTTTTGGCGAGTTTTCATTAAAGCGTGA	249	
Qy	241	GGAGTCTTATACAAAGAGATTTTATGCGATGTGTGGATAAATTAAGGTCAATTACAAC	300	
Db	250	GGAGTCTTATACAAAGAGATTTTATGCGATGTGTGGATAAATTAAGGTCAATTACAAC	309	
Qy	301	AGAAAACTGMAACGACTTTAATTGGAACAAAAACATCGTTCTTAAATCTTTAGAAAGAGT	360	
Db	310	AGAAAACTGMAACGACTTTAATTGGAACAAAAACATCGTTCTTAAATCTTTAGAAAGAGC	369	
Qy	361	TTGGAAAGAAATGGATGATCAAGAGGTGAAAGAAATGTGCGATGAAATATTCATTAATAAAC	420	
Db	370	CTAGAAGAAATGGATGATGAGAGGTGAAAGAAATGTGCGATGAAATATTCATTAATAAAC	429	
Qy	421	ACGGAACAATTTAAACAGACAAGCTTTAAGCGGGCGACTTTTAACCGTGTTTAAAAATGGGG	480	
Db	430	ACGGAACAATTTGAACAGACAAGCTTTAAGCGGGCGACTTTTAACCGTGTTTAAAAATGGGA	489	
Qy	481	GGTTTTAAATCTTATCAATTAGCTGTGTCATGTTGGAAATGGCGTCCGAAAAACCATTTCTA	540	

Db 490 GGCTTTAAATCTTATCAATAGCTGTCAATGTTGCGAATCGGTGTCAGAAACCAATTTCTA 549
Qy 541 GCGCGTGGTTATCGCTTGGCGCAATCAGTGTCTTACAGAACTCTGAGCTTTTAAACA 600
Db 550 GCGCGTGGTTATCGCTTGGCGCAATCAAGTGTCTTACAGAACTCTGAGCTTTTAAACA 609
Qy 601 GGTCTCTGTTGGCTGGATCAATACAGGCGTATGACAGCGATTGATATTGAGGCGCGGCT 660
Db 610 GCGCGTGGCTGGATCAATACAGGCGTATGACAGCGATTGATATTGAGGCGCGGCT 669
Qy 661 TATAGGTAACCATACCGGCATGCAATGTGTGTCCTTTACGCCCTTAAACACACAGCAA 720
Db 670 TATAGGTAACCATACCGGCATGCAATGTGTGTCCTTTACGCCCTTAAACACACAGCAA 729
Qy 721 GCCAATGGAGATAGAAAGTGTGTCGAATAGAAATCCATT 759
Db 730 GCCAATGAAGATAAGAAAGTGTGTCGAATAGAAATCCGTT 768

RESULT 8

US-10-433-970-47
; Sequence 47, Application US/10433970
; Publication No. US20040138415A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Jing-Hui
; APPLICANT: Walker, Richard
; APPLICANT: Jackson, James
; TITLE OF INVENTION: HELICOBACTER PROTEINS, GENE SEQUENCES AND USES
; FILE REFERENCE: 7969-091-999
; CURRENT APPLICATION NUMBER: US/10/433,970
; PRIOR FILING DATE: 2003-06-06
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 762
; TYPE: DNA
; ORGANISM: Helicobacter sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(762)
US-10-433-970-47

Query Match 94.5%; Score 717.4; DB 8; Length 762;
Best Local Similarity 96.6%; Pred. No. 1.9e-168;
Matches 733; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 1 ATGGCATACAAATATGATAGAGACTTGGAAATTTTAAAGCAATTGGAAATCTAGTGATTTA 60
Db 1 ATGGCATACAAATATGATAGAGACTTGGAAATTTTAAAGCAATTGGAAATCTAGTGATTTA 60
Qy 61 TTGGATTTGTTGAGGTGCTTTTGGTAAAGCGCGGAAAGACACAAATGAAAA 120
Db 61 TTGGATTTGTTGAGGTGCTTTTGGTAAAGCGCGGAAAGACACAAATGAAAA 120
Qy 121 CTGACAGCTCCATAGATAACAAAGGCATGGCGATGATTACGTTAAATACCGAGAAAGA 180
Db 121 CTGACAGCTCCATAGATAACAAAGGCATGGCGATGATTACGTTAAATACCGAGAAAG 180
Qy 181 ATCGCTGAAGATTGCAATCTATGGGAGCAATAGTTTGGAGTTTCATTTAAAGGCGAA 240
Db 181 ATCGCTGAAGATTGCAATCTATGGGAGCAATAGTTTGGAGTTTCATTTAAAGGCGAA 240
Qy 241 GGAGTCTTATCAAGAGATTTTATGCGATGTGCGGTAATTTAAAGTCAATTTACAC 300
Db 241 GGAGTCTTATCAAGAGATTTTATGCGATGTGCGGTAATTTAAAGTCAATTTACAC 300
Qy 301 AAGAAACTGAAACGACTTTAATTAAGCAACATGCTTTCTTAAATCTTAAAGAAAGT 360
Db 301 AAGAAACTGAAACGACTTTAATTAAGCAACATGCTTTCTTAAATCTTAAAGAAAGT 360

Qy 361 TTGGAAGAAATGGATGATGAAGAACTGAAAGAAATGTGCGATGAATATCCATAAAAAAC 420
Db 361 TTGGAAGAAATGGATGATGAAGAACTGAAAGAAATGTGCGATGAATATCCATAAAAAAC 420
Qy 421 ACAGCAATTTAAACAGACAAAGCCTTAAAGCGCGGCGACCTTTAAACGCTGTTTAAATGGGG 480
Db 421 ACTGACAAATTTGAAACAGACAAAGCCTTAAAGCGCGGCGACCTTTAAACGCTGTTTAAATGGGA 480
Qy 481 GGTTTTAAATCTTATCAATTAGCTGTCAATGTTGCGAATGCGGTGTCGCAAAACCAATTTCTA 540
Db 481 GGTTTTAAATCTTATCAATTAGCTGTCAATGTTGCGAATGCGGTGTCGCAAAACCAATTTCTA 540
Qy 541 GGGCGTGGTTTATCGCTTGGCGCAATCAGTGTCTTCAAGAACTCTGAGCTTTTAAACA 600
Db 541 GGGCGTGGTTTATCGCTTGGCGCAATCAGTGTCTTCAAGAACTCTGAGCTTTTAAACA 600
Qy 601 GGTCTGTGTGGCTGGATCAATACAGGCGTATGGAACAGCGATTGATATGAGGCGCGGCT 660
Db 601 GGTCTGTGTGGCTGGATCAATACAGGCGTATGGAACAGCGATTGATATGAGGCGCGGCT 660
Qy 661 TATAGGTAACCATACCGGCATGCAATGTGTGCGAATGCGGTGTCGCAAAACCAATTTCTA 720
Db 661 TATAGGTAACCATACCGGCATGCAATGTGTGCGAATGCGGTGTCGCAAAACCAATTTCTA 720
Qy 721 GCCAATGGAGATAAGAAAGTGTGTCGAATAGAAATCCATT 759
Db 721 GCCAATGAAGATAAGAAAGTGTGTCGAATAGAAATCCATT 759

RESULT 9

US-10-433-970-45
; Sequence 45, Application US/10433970
; Publication No. US20040138415A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Jing-Hui
; APPLICANT: Walker, Richard
; APPLICANT: Jackson, James
; TITLE OF INVENTION: HELICOBACTER PROTEINS, GENE SEQUENCES AND USES
; FILE REFERENCE: 7969-091-999
; CURRENT APPLICATION NUMBER: US/10/433,970
; PRIOR FILING DATE: 2003-06-06
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 798
; TYPE: DNA
; ORGANISM: Helicobacter sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(798)
US-10-433-970-45

Query Match 94.5%; Score 717.4; DB 8; Length 798;
Best Local Similarity 96.6%; Pred. No. 1.9e-168;
Matches 733; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 1 ATGGCATACAAATATGATAGAGACTTGGAAATTTTAAAGCAATTGGAAATCTAGTGATTTA 60
Db 37 ATGGCATACAAATATGATAGAGACTTGGAAATTTTAAAGCAATTGGAAATCTAGTGATTTA 96
Qy 61 TTGGATTTGTTGAGGTGCTTTTGGTAAAGCGCGGAAAGACACAAATGAAAA 120
Db 97 TTGGATTTGTTGAGGTGCTTTTGGTAAAGCGCGGAAAGACACAAATGAAAA 156
Qy 121 CTGACAGCTCCATAGATAACAAAGGCATGGCGATGATTACGTTAAATACCGAGAAAGA 180
Db 157 CTGACAGCTCCATAGATAACAAAGGCATGGCGATGATTACGTTAAATACCGAGAAAG 216
Qy 181 ATCGCTGAGAGATTCGAATCTATGGGCAATAGTTTTCGAGTTTCTATTAAAGCGAA 240

Db 217 ATCGCTGAAGAGTTGCCAATCTATCGGAGCAATAGTTTTGCGAGTTTCATTAAAGCGGAA 276
Qy 241 GGAGTCTTATACAAAGAGATTTTATGCGATGTGCGATATAAATTAAGGTCAATTACAAAC 300
Db 277 GGGGTCTTATACAAAGAGATCTATGCGATGTGCGATATAAATTAAGGTCAATTACAAAC 336
Qy 301 AAGAAACTGAAACGACTTTTAAATGAAACAAACATGCTTTCTAAATCTTAAAGAGAGT 360
Db 337 AAGAAACTGAAACGACTTTGATTGAAACAAACATGCTTTCTAAATCTTAAAGAGAGT 396
Qy 361 TTGGAAGAAATGCGATGATGAAGAGTGAAGAAATGCGGATGAATTCATTAATAAAC 420
Db 397 TTAGAGGAAATGCGATGATGAAGAGTGAAGAAATGCGGATGAATTCATTAATAAAC 456
Qy 421 ACGGCAATTTAAACAGACAAAGCCTTAAAGCGCGGCGACTTTAAAGCTGTTTAAATGGG 480
Db 457 ACTGACAAATTTGAACAGACAGCTTTAAAGCGCGGCGACTTTAAAGCTGTTTAAATGGG 516
Qy 481 GGTTTTAAATCTTATCAATTAAGCTGTCTATGTTGCGAATGCGGTGCGAAACCAATTTCTA 540
Db 517 GGCTTTAAATCTTATCAATTAAGCTGTCTATGTTGCGAATGCGGTGCGAAACCAATTTCTA 576
Qy 541 GGGCGTGTGTTATGCTGCGGCGCAATCAGGTGCTTTACAGAACTCTGAGCTTTTAAACA 600
Db 577 GGGCGTGTGTTATGCTGCGGCGCAATCAGGTGCTTTACAGAACTCTGAGCTTTTAAACA 636
Qy 601 GGTCTGTGTGCTGATCATTTACAGGCGGTATGAGCGAGTGTGATTTGCGAGGCGCGCT 660
Db 637 GGCCCTGTGTGCTGATCATTTACAGGCGGTATGAGCGAGTGTGATTTGCGAGGCGCGCT 696
Qy 661 TATAGGGTAAACATACCGGCGATGATTGTGTTGCGCACTTTACGCTTAAACACAGCAA 720
Db 697 TATAGGGTAAACATACCGGCGATGATTGTGTTGCGCACTTTACGCTTAAACACAGCAA 756
Qy 721 GCCAATGAGATAGAAGTCTGTTGCAATAGAAATCCATT 759
Db 757 GCCAATGAGATAGAAGTCTGTTGCAATAGAAATCCATT 795

RESULT 10

US-10-335-977-2937
; Sequence 2937, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335,977
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400

TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 2937:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 744 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...744
; SEQUENCE DESCRIPTION: SEQ ID NO: 2937:
US-10-335-977-2937

Query Match 48.2%; Score 365.8; DB 8; Length 744;
Best Local Similarity 71.5%; Pred. No. 1.1e-80;
Matches 513; Conservative 0; Mismatches 192; Indels 12; Gaps 2;

Qy 17 ATAGAGACTTGGAAATTTTAAAGCAATTTGGAATCTAGTGAATTTATTTGGATTTTTCAGG 76
Db 26 ATAGCGACTTGGAAATTTTAAAGCGATTAAAGCTCTAGCGATTTTGAAGATTTGTTGATG 85
Qy 77 TCCTTGTGTTTGTAAAGACGCGGAAAAAGACACAAATGAAAACTGACCAGCTCCATAG 136
Db 86 CCGCTGTCTATGATGAAGATGGCACACTAAGAAATGAATGAAGATTTGCAAGTTTAAACAG 145
Qy 137 AATACAAAAGGATGGCGATGATTACGCTAAATATACGACAGAAAGATTCGCTGAAGAGTTGC 196
Db 146 AATACAAAAGGATGGCGATGATTACGCTAAATATACGACAGAAAGATTCGCTGAAGAGTTGC 205
Qy 197 AATATATGGGAGCAATAGTTTTGCGAGTTTCATTAAGCGGAGAGTCTTTATACAAAG 256
Db 206 AGCGTTATGGGCGCAATAGTTTTTGGCAATTTTTTAGAGATGAAGGGGTCTTTATACAAAG 265
Qy 257 AGATTTTATGCGATGTGCGGATTAATTAAGTCAATTAACAACAGAAATCTGAAACGA 316
Db 266 AGATTTTGTGCGATGCGTGGATCAATTTGGATTAATTAACAATGAAGATCTGCAACCT 325
Qy 317 CTTTAAATGAACAAACACATGCTTTCTAAATCTTAGAAGAAAGTTCGGAAGAAATGAGTG 376
Db 326 CTTTCAATGAGCAAAACATGCTTTCTAACTTTTGAAGATAGTTTAGAAGAAATGAGTG 385
Qy 377 ATGAAGAGTGAAGAAATGTCGATGAATATCCATAAAAAACACGACAA----- 428
Db 386 GGAGAGAGATTAAAGAACTCTCGGATGGATTGGGCATGCCAAATATTGATAAAGTGATTG 445
Qy 429 -TTTAAACAGACAAAGCCTTAAGCGCGGCGACTTTTAACGCTGTTTAAATGCGGGGTTTA 487
Db 446 GTGAAAAACAAACAGTCTCTAATCGCATCTGTTTAAACGCTGTTTAAAGCGCGGCTCTC 505
Qy 488 AATCTTATCAATTAGCTGTCATTGTTGCGAATGCGGTGCGCAAAACCAATCTCTAGGGCGTG 547
Db 506 ATTCTTATGCGTTGGCTGTAGCTGTGAGATGCAATGTTAGCAAACTCTAGGGCGATG 565
Qy 548 GTTTATCG---CTTGGCGGCAATCAGGTGCTTTACAGAACTCTGAGCTTTTAAACAGGTC 604
Db 566 GTTTATCGTCTGTGGTGAAGTAGCGCTTTAAAAAACTCTAGACATTTTAACTAGTGGCC 625
Qy 605 CTGTTGGCTGGATCATTTACAGCGGTATGGACAGGATTTGATATTGACGGGCGGCTTATA 664
Db 626 CTATTGTTGGGTCAATTACGGGCGGCTTAGTGAGCATCAATCTTGTGGGCGGCTTATA 685
Qy 665 GGTTAAACCATACCGGCTGCTGTTGGTGGCCACTTTAGCCCTTAAACACACAGCAAG 721
Db 686 GGGTGACCGTGCCTGCTGCGTTTGTAGTTGGCCACTTACGCAAAAAATTAAGAGCAG 742

RESULT 11
US-10-335-977-2936

; Sequence 2936, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335,977
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 2936:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 714 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...714
; SEQUENCE DESCRIPTION: SEQ ID NO: 2936:

Query Match 47.4%; Score 359.4; DB 8; Length 714;
Best Local Similarity 71.4%; Pred. No. 4.3e-79;
Matches 506; Conservative 0; Mismatches 191; Indels 12; Gaps 2;

QY 25 TTGGAATTTTAAAGCAATTCGAATCTAGTATTATTGGATTGTTTGGAGTCTTGT 84
DB 1 TTGGAATTTTAAAGCGATTAAAGTCTTAGCGATTGAAAGATTGTTTGGTGGTGC 60

QY 85 TTTCGTAAGACGGCGAAAAAGACACAAATGAAAACTGACAGCTCCATAGATACAAA 144
DB 61 TATGATGAGATGGCAGCACTAAGATGATGAGATTTGACAGTTTACAGATACCAA 120

QY 145 AGGATGCGCATGATTACGCTTAAATACGCAGAAAGAAATCGCTGAGAGTTTCAAT 204
DB 121 AGGTATGCCATGATTACGCCAAATACCCAAAGAGGATCGCTGAAGAAATTCAGCGTTAT 180

QY 205 GGGAGCAATAGTTTTCGAGTTTCATTAAGCGAGAGTCTTATACAAAGATTTTA 264
DB 181 GGGGGCAATAGTTTTCGGAATTTTTTTTAGAGATGAAGGGGCTTATACAAAGAGATT 240

QY 265 TGGCATGTGCGCAATTAAGTCAATTACAAAGAAAGAACTGAAACGACTTTAATT 324
DB 241 TGGCATGCGTCCGATCATTTGGATTAATTAACAATGAAGATCTGCAACCTCTTTGATT 300

QY 325 GAACAAAACATGCTTTCTAAAAATCTTAGAAAAGAACTTTGGAAGAAATGATGATGAAGAA 384
DB 301 GAGCAAAACATGCTTTCTAAACTTTTGAAGAGATAGTTTAGAAAATAATGATGGAGAGAG 360

QY 385 GTGAAAGAAATGTGCGATGAATATCCATAAAAAACACGGACAA-----TTTAAAC 435
DB 361 ATTAAGAAACTCTCGATGGATTGGGCATGCGCAAAATATTGATAAAGTATTGTTGGTGAAGAA 420

QY 436 AGACAAGCCTTAAGCGGGCGACCTTTAAGCTGTGTTTAAATGCGGGGTTTAAATCTTAT 495
DB 421 AAACAAGTCTTAATCGCATCTGTTTAAACGCTGTGTTTAAAGCGGGCGGCTCTCATCTTAT 480

QY 496 CAATTAGCTGTCATTTGTCGAATCGCGTTCGCAAAACCAATTCCTAGGCGGTGTTTATCG 555
DB 481 CGTTGGCTGTAGCTGTTCAGATGCAATGTTAAGACAACTCTAGGGCATGTTTATCG 540

QY 556 ---CTTGGGGCAATCAGGTGCTTCAAGAACTCTGAGCTTTTAAACAGTCTCTGTGGC 612
DB 541 TCTGTGGTGGCTAAAGTAGCGCTTAAAAAACTCTAGACATTTTAGCTGGCCCTATTGCT 600

QY 613 TGGATCATTACAGCGGTATGACAGCGATTGATTTGAGGGCGGCTTATAGGTAACC 672
DB 601 TGGGTCAATTACGGCGCGTGTAGTGAGCATCAATCTTGTGGCGCGCTTATAGGGTGACC 660

QY 673 ATACGGCATGCTTGTGTTGCGCACTTTACGCCCTAAAAAACACAGCAAG 721
DB 661 GTGCTGCATGCGTTTGTAGTTGCCACCTTACGCAAAAAATTAAGAGCAG 709

RESULT 12

US-09-882-227-413
; Sequence 413, Application US/09882227
; Publication No. US20030158396A1
; GENERAL INFORMATION:
; APPLICANT: Kleanthous, Harold
; APPLICANT: Al-Gatawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean-Francois
; APPLICANT: Oomen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding No. US20030158396A1
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 06132/047002
; CURRENT APPLICATION NUMBER: US/09/882,227
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 08/902,615
; PRIOR FILING DATE: 1997-07-29
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 413
; LENGTH: 547
; TYPE: DNA
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (34)...(498)
US-09-882-227-413

Query Match 35.8%; Score 271.4; DB 3; Length 547;
Best Local Similarity 71.6%; Pred. No. 3.6e-57;
Matches 389; Conservative 0; Mismatches 141; Indels 13; Gaps 2;

QY 84 TTTTGGTAAGACGGCGAAAAAGACACAAATGAAAACTGACAGCTCCATAGAAATCAA 143
DB 9 TTATGATGAAGATGCGCACCTAAGAAATGAATGAAGACTTGACAAATTCACAGAAATATA 68

QY 144 AAGCATGCGCATGATTAGCTTAATATACGCAAGAAAGAAATCGCTGAAGAGTTGCAATCTA 203
DB 69 AAGATATGCCATGATTAGCGCAAAATACCCAAAGAAAGAAATCGCTGAAGAAATTCGAACATTA 128

QY 204 TGGGAGCAATAGTTTTCGAGTTTTCATTAAGCGGAGGAGTCTTATACAAAGAGATTTT 263

Db 129 TGGGGCAATAGTTTGGCAATTTTTTGGAGATGAAGGGGTCTTATACAAAGAGATTTT 188
Qy 264 ATGCATGTGCGGATAAATTAAGGTCAATTAACAAGAAAGTGAAGCGACTTTAAT 323
Db 189 GTGCGATCGTGGGATCAATTAAGGTAAATTAACAAGAGATCTGCAACCTCTTTGAT 248
Qy 324 TGAACAAACATGCTTTCTAAATCTTAAAGAAAGTTTGAAGAAAGTGAATGAAGA 383
Db 249 TGAGCAAAACATGCTTTCTAACTCTTGAAGATAGTTTGAAGAAAGTGAAGAGAGA 308
Qy 384 AGTGAAGAAATGCGGATGAATTCATTAACAAACAGGACAA-----TTTAAA 434
Db 309 GATTAAAGAACTTTGCAATGAATGGGCATGCAAAATATGATAAAGTGAATGGTGA 368
Qy 435 CAGCAAGCCCTTAAGCGGGGACCTTTAAACGCTGTTTAAATATGGGGGTTTAAATCTTA 494
Db 369 CAACAAGTCTTAATCGCATCTACTTTAAAGCTGTTTAAAGCGGTGGCTCTCATCTTA 428
Qy 495 TCAATTAGCTGTCAATGTTGCGAATGCGGTGCGAAACCAATCTTAGGCGGTGTTTATC 554
Db 429 TGGCTTGGCTGTATCTGTTGAGATGCAATGTTAAAGCAAACTCTAGGCGATGTTAT-- 485
Qy 555 GCTTGGGGGAATCAGGTGCTTAAAGAACTCTGAGCTTTTAAAGAGTCTCTGTTGGCTG 614
Db 486 -GTGTTGGTAAAGTAGCACTTAAAGAACTTTGGGCGTTTGGCTGGCCCTATTGGTTG 544
Qy 615 GAT 617
Db 545 GGT 547

RESULT 13

US-09-732-091-36
; Sequence 36, Application US/09732091
; Patent No. US20020107368A1

; GENERAL INFORMATION:

; APPLICANT: Tian, Jing-Hui

; APPLICANT: Walker, Richard I.

; APPLICANT: Jackson, W. James

; TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses

; FILE REFERENCE: 7969-088

; CURRENT APPLICATION NUMBER: US/09/732,091

; CURRENT FILING DATE: 2000-12-07

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: Patent in Ver. 2.1

; SEQ ID NO 36

; LENGTH: 153

; TYPE: DNA

; ORGANISM: Helicobacter sp.

US-09-732-091-36

Query Match 20.2%; Score 153; DB 3; Length 153;

Best Local Similarity 100.0%; Pred. No. 7.3e-28;

Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 601 GGTCTGTGCTGGATCAATTAAGGCGTATGACAGCGATTTGATTTGAGGGCGCGCT 660

Db 1 GGTCTGTGCTGGATCAATTAAGGCGTATGACAGCGATTTGATTTGAGGGCGCGCT 60

Qy 661 TATAGGGTAAACCATACCGGCATGATTTGCTTCCACTTTACGCTTAAACACAGCAA 720

Db 61 TATAGGGTAAACCATACCGGCATGATTTGCTTCCACTTTACGCTTAAACACAGCAA 120

Qy 721 GCCAATGAGATAAGAGTCTGTTGCAATAGAA 753

Db 121 GCCAATGAGATAAGAGTCTGTTGCAATAGAA 153

RESULT 14

US-10-433-970-36

; Sequence 36, Application US/10433970

; Publication No. US20040138415A1

; GENERAL INFORMATION:

; APPLICANT: Tian, Jing-Hui

; APPLICANT: Walker, Richard

; APPLICANT: Jackson, James

; TITLE OF INVENTION: HELICOBACTER PROTEINS, GENE SEQUENCES AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 7969-091-999

; CURRENT APPLICATION NUMBER: US/10/433,970

; CURRENT FILING DATE: 2003-06-06

; PRIOR APPLICATION NUMBER: 09/732,091

; PRIOR FILING DATE: 2000-12-07

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: Patent in Ver. 2.1

; SEQ ID NO 36

; LENGTH: 153

; TYPE: DNA

; ORGANISM: Helicobacter sp.

US-10-433-970-36

Query Match

Best Local Similarity 100.0%; Pred. No. 7.3e-28;

Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 601 GGTCTGTGCTGGATCAATTAAGGCGTATGACAGCGATTTGATTTGAGGGCGCGCT 660

Db 1 GGTCTGTGCTGGATCAATTAAGGCGTATGACAGCGATTTGATTTGAGGGCGCGCT 60

Qy 661 TATAGGGTAAACCATACCGGCATGATTTGCTTCCACTTTACGCTTAAACACAGCAA 720

Db 61 TATAGGGTAAACCATACCGGCATGATTTGCTTCCACTTTACGCTTAAACACAGCAA 120

Qy 721 GCCAATGAGATAAGAGTCTGTTGCAATAGAA 753

Db 121 GCCAATGAGATAAGAGTCTGTTGCAATAGAA 153

RESULT 15

US-09-732-091-33

; Sequence 33, Application US/09732091

; Patent No. US20020107368A1

; GENERAL INFORMATION:

; APPLICANT: Tian, Jing-Hui

; APPLICANT: Walker, Richard I.

; APPLICANT: Jackson, W. James

; TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses

; TITLE OF INVENTION: thereof

; FILE REFERENCE: 7969-088

; CURRENT APPLICATION NUMBER: US/09/732,091

; CURRENT FILING DATE: 2000-12-07

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: Patent in Ver. 2.1

; SEQ ID NO 33

; LENGTH: 114

; TYPE: DNA

; ORGANISM: Helicobacter sp.

US-09-732-091-33

Query Match

Best Local Similarity 100.0%; Pred. No. 3.5e-18;

Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 157 GATTACGCTTAATACGCAAGAAATCGCTGAAGAGTTGCAATCTATCGGAGCAATAGT 216

Db 1 GATTACGCTTAATACGCAAGAAATCGCTGAAGAGTTGCAATCTATCGGAGCAATAGT 60

Qy 217 TTTGGAGTTTTCATTTAAAGCGAAGAGTCTTATACAAAGAGATTTTATGCGAT 270

Db 61 TTTGGAGTTTTCATTTAAAGCGAAGAGTCTTATACAAAGAGATTTTATGCGAT 114

Search completed: August 3, 2006, 10:42:35

Job time : 1475 secs

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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OM nucleic - nucleic search, using sw model

Run on: August 4, 2006, 20:14:32 ; Search time 164 Seconds
(without alignments)
7330.066 Million cell updates/sec

Title: US-09-732-091-3

Perfect score: 759

Sequence: 1 atggcacaataatgatag.....cggtgcaatagaatccatt 759

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2193277 seqs, 791917567 residues

Total number of hits satisfying chosen parameters: 4386554

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /EMC Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:
- 3: /EMC Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:
- 4: /EMC Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:
- 5: /EMC Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:
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- 7: /EMC Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:
- 8: /EMC Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:
- 9: /EMC Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	45.4	6.0	1738	US-10-449-902-5401	Sequence 5401, Ap
2	42.6	5.6	4009	US-11-218-305-3660	Sequence 3660, Ap
3	41	5.4	1110	US-11-266-748A-52434	Sequence 52434, A
4	40.4	5.3	1173	US-11-348-413-7111	Sequence 7111, Ap
5	40	5.3	780	US-11-359-953-20	Sequence 20, Appl
6	39.4	5.2	1826	US-11-216-545-774	Sequence 774, Appl
7	39.4	5.2	523643	US-10-540-898-308	Sequence 308, Appl
8	39.2	5.2	1000	US-11-266-748A-115072	Sequence 115072, A
9	39.2	5.2	1000	US-11-266-748A-157236	Sequence 157236, A
10	39.2	5.2	1000	US-11-266-748A-283572	Sequence 283572, A
11	39.2	5.2	1000	US-11-266-748A-335001	Sequence 335001, A
12	39.2	5.2	1000	US-11-266-748A-393321	Sequence 393321, A
13	39.2	5.2	1000	US-11-266-748A-464367	Sequence 464367, A
14	39.2	5.2	1815	US-11-266-748A-70584	Sequence 70584, A
15	39.2	5.2	1815	US-11-266-748A-106086	Sequence 106086, A
16	39.2	5.2	1815	US-11-266-748A-123395	Sequence 123395, A
17	39.2	5.2	2522	US-11-218-305-24510	Sequence 24510, A
18	39.2	5.2	6521	US-10-517-441-310	Sequence 310, Appl
19	39.2	5.2	6521	US-10-517-441-584	Sequence 584, Appl
20	38.8	5.1	11913	US-10-517-441-536	Sequence 536, Appl
21	38.6	5.1	3532	US-11-266-748A-28445	Sequence 28445, A
22	38.6	5.1	13286	US-10-517-441-472	Sequence 472, Appl
23	38.4	5.1	151052	US-10-540-898-503	Sequence 503, Appl
24	38	5.0	5087	US-10-517-441-320	Sequence 320, Appl

c 25	38	5.0	5087	6	US-10-517-441-380	Sequence 380, App
c 26	38	5.0	5087	6	US-10-517-441-594	Sequence 594, App
c 27	38	5.0	5087	6	US-10-517-441-654	Sequence 654, App
c 28	37.6	5.0	168	7	US-11-348-413-12181	Sequence 12181, A
c 29	37.6	5.0	2185	6	US-10-449-902-13623	Sequence 13623, A
c 30	37.6	5.0	5084	8	US-11-105-233-92	Sequence 92, Appl
c 31	37.6	5.0	14147	6	US-10-517-441-265	Sequence 265, App
c 32	37.4	4.9	3434	8	US-11-266-748A-27358	Sequence 27358, A
c 33	37.4	4.9	5493	6	US-10-517-441-691	Sequence 691, App
c 34	37.2	4.9	348	8	US-11-217-529-191030	Sequence 191030, A
c 35	37.2	4.9	4930	6	US-10-517-441-354	Sequence 354, App
c 36	37.2	4.9	4930	6	US-10-517-441-628	Sequence 628, App
c 37	37.2	4.9	6001	6	US-10-517-441-511	Sequence 511, App
c 38	37.2	4.9	6001	6	US-10-517-441-785	Sequence 785, App
c 39	37.2	4.9	7833	6	US-10-517-441-350	Sequence 350, App
c 40	37.2	4.9	7833	6	US-10-517-441-624	Sequence 624, App
c 41	37.2	4.9	8666	6	US-10-517-441-284	Sequence 284, App
c 42	37.2	4.9	8666	6	US-10-517-441-558	Sequence 558, App
c 43	37	4.9	1698	6	US-10-471-571A-919	Sequence 919, Appl
c 44	37	4.9	2126	1	US-09-949-925-49	Sequence 49, Appl
c 45	37	4.9	13286	6	US-10-517-441-746	Sequence 746, App

ALIGNMENTS

RESULT 1

US-10-449-902-5401
; Sequence 5401, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A02051-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5401
; LENGTH: 1738
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK062580
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-5401

Query Match

Best Local Similarity 6.0%; Score 45.4; DB 6; Length 1738;
Matches 85; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY	134	TAGATACAAAGGCATGCGATGATTACGCTAAATACGCAGAAAGATCGCTGAAGT	193
DB	1258	TTGAAACATACCGATATGAATGAATATGCTGTAATATAGCGCAATTGGATGAATTT	1317
QY	194	TGCAATATCTGGGAGCAATAGTTTGGAGTTTCATTAAGCGAAGAGTCTTATACA	253
DB	1318	TGTAATCTAGAGAAAGAAATCTTTGGAGTTTCCAATTAAGTGTCAGTTTATTGTTCA	1377
QY	254	AAGAGATTTTATGCGATGTGTCGATAAATT	284
DB	1378	TAGCCACATATTATTGTTTTCACAAATTTGTT	1408

RESULT 2

US-11-218-305-3660


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NAME/KEY: misc feature
LOCATION: (811)..(811)
OTHER INFORMATION: n is a, c, g, or t
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NAME/KEY: misc feature
LOCATION: (814)..(815)
OTHER INFORMATION: n is a, c, g, or t
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NAME/KEY: misc feature
LOCATION: (827)..(827)
OTHER INFORMATION: n is a, c, g, or t
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NAME/KEY: misc feature
LOCATION: (837)..(842)
OTHER INFORMATION: n is a, c, g, or t
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LOCATION: (933)..(937)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
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OTHER INFORMATION: n is a, c, g, or t
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NAME/KEY: misc feature
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NAME/KEY: misc feature
LOCATION: (1041)..(1041)
OTHER INFORMATION: n is a, c, g, or t
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NAME/KEY: misc feature
LOCATION: (1051)..(1052)
OTHER INFORMATION: n is a, c, g, or t
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NAME/KEY: misc feature
LOCATION: (1086)..(1086)
OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-52434
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Query Match 5.4%; Score 41; DB 8; Length 1110;
Best Local Similarity 37.6%; Pred. No. 0.51;
Matches 74; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

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QY 282 ATTAAGGTCAATTACAACAAGAAAGTTTGGAGAAATGGATGATGAAGAGTGAAGAAATGTGCGA 341
Db 748 ATCAAAAAAANNNNAAAAAANNNNAAAAAANNNNAAAAAANNNNAAAAAANNNNAAAAAANNNN 807
QY 342 TAAATCTTAGAAAGAAAGTTTGGAGAAATGGATGATGAAGAGTGAAGAAATGTGCGA 401
Db 808 AAANAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAA 867
QY 402 TGAATTATCCATAAAAAACACGACCAATTTAAACACAGACGCTTTAAGCCGCGGACTTT 461
Db 868 AAAAAAANNNNNAAAAAANNNNAAAAAANNNNAAAAAANNNNAAAAAANNNNAAAAA 927
QY 462 AACGCTGTTTAAATGG 478
Db 928 AAAAAANNNNAAAAAAGG 944
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RESULT 4

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US-11-348-413-7111
; Sequence 7111, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
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; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 7111
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Streptococcus agalactiae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1173)
; OTHER INFORMATION: WAN01ULX2; ORF: 00000011100000; Cluster contains WAN01PJ38
; OTHER INFORMATION: SAGI752::conserved hypothetical protein IIGR00275:2603:NC
; OTHER INFORMATION: _004116.1
US-11-348-413-7111

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Query Match      5.3%; Score 40.4; DB 7; Length 1173;
Best Local Similarity 45.1%; Pred. No. 0.75;
Matches 183; Conservative 2; Mismatches 218; Indels 3; Gaps 1;

QY 218 TTGCGAGTTTCATTAAAGCGGAGAGTCTTTATACAAAGAGATTTTATGCGATGTGTGCG 277
Db 725 TTTCYAGCTTTGTCAAGGGGAGAACTATATACCTAGATGTTTGGCCCAATATCTCTG 784
QY 278 ATAAATTAAGGTCAATTAACAAGAAACTGAAAGCATTTTAATTGAACAAAAACATGC 337
Db 785 TTAAGAATTTGGAAYACACTTC--CAAAATGAAGAGAGAAAAATCTTTGAAAAACGCTC 841
QY 338 TTCTCTAAATCTTAGAAGAGTTTGGAGAAATGATGATGAAGAGTGAAGAAATGT 397
Db 842 TTAATAATCTTCTTCTGAGCGTTTAGCTGAATTTTACGCTGAAGACTTACCMGAAAG 901
QY 398 GCATGAATTTATCATATAAAAAACACGACAAATTTAAACAGACAGCGCTTAAAGCGCGCGA 457
Db 902 TAAACAGATCTGTATAAGAGCTTAGAAYGTTAATTCAAAACTTAAAAAATCTCTTA 961
QY 458 CTTTAACGCTGTTTAAATAGGGGGTGTAAATCTTATCAATTAAGCTGTGCTATGTCGGA 517
Db 962 TTTTAGTAACCTGGAAGATCTCTAGCAAAATCTTTGTAACAAAAAGGKGAGTTGATC 1021
QY 518 ATCCGCTGCGAAAAACCTCTAGGCGGTGTTTATGCTTGGCGGCAATCAGTGTCTTA 577
Db 1022 TTAAGAATAAACCACCACTTGAAGTAAAGAGTGTGCTGTTTACATTTTCTGCTG 1081
QY 578 CAAGAACTCTGAGCTTTTAAACAGGTCTCTGCTGCTGATCAATAC 623
Db 1082 GTGAAGTCTAGACATCAATGCTCATACCGGAGGTTTAAATAC 1127

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RESULT 5
US-11-359-953-20
; Sequence 20, Application US/11359953
; Publication No. US20060141577A1
; GENERAL INFORMATION:
; APPLICANT: ChromaGenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kwaks, Theodorius H.J.
; APPLICANT: Sewalt, Richard G.A.B.
; APPLICANT: van Blokland, Rik
; TITLE OF INVENTION: Selection of host cells expressing protein at high levels
; FILE REFERENCE: 0117 A US P00 CIP
; CURRENT APPLICATION NUMBER: US/11/359,953
; CURRENT FILING DATE: 2006-02-21
; PRIOR APPLICATION NUMBER: US 11/269,525
; PRIOR FILING DATE: 2005-11-07
; PRIOR APPLICATION NUMBER: US 60/626,301
; PRIOR FILING DATE: 2004-11-08
; PRIOR APPLICATION NUMBER: US 60/696,610
; PRIOR FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: EP 04105593.0
; PRIOR FILING DATE: 2004-11-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
; LENGTH: 780
; TYPE: DNA

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: sequence of STAR20
US-11-359-953-20

Query Match      5.3%; Score 40; DB 7; Length 780;
Best Local Similarity 53.1%; Pred. No. 0.82;
Matches 85; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 246 CTTATACAAAGAGATTTTATGCGGATGTGTGCGATAAATAAAGTCAATTACAAAGAA 305
Db 479 CTCTGACATAGATATTTAAATTTCTTAGTGGCTTTGTGTATATTTCTTATTAATA 538
QY 306 AACTGAAACGACTTTAAATTGAACAAAAACATGCTTTCTAAAAATCTTAGAAAGAGTTTGA 365
Db 539 AGCAATTATTTGTTTAAACAGAAAAAAGATATATATCTTAAATCTTAAATAAATAACCA 598
QY 366 AGAAATGATGATGAAGAAGTGAAGAAGTGAAGAAGTGTGCGATGAA 405
Db 599 TTAAGAGGAAAAACAGGAGTTTAACTAAATAAGGGAACAA 638

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RESULT 6
US-11-216-545-774
; Sequence 774, Application US/11216545
; Publication No. US20060135758A1
; GENERAL INFORMATION:
; APPLICANT: MONSANTO Technology, LLC
; APPLICANT: McLaird, Paul L
; APPLICANT: Tao, Nengbing
; APPLICANT: Wu, Kunsheng
; TITLE OF INVENTION: Single Nucleotide Polymorphic Markers and Methods of Genotyping
; FILE REFERENCE: 38-21 (53659)B
; CURRENT APPLICATION NUMBER: US/11/216,545
; CURRENT FILING DATE: 2005-08-31
; PRIOR APPLICATION NUMBER: US 60/606,062
; PRIOR FILING DATE: 2004-08-31
; NUMBER OF SEQ ID NOS: 8783
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 774
; LENGTH: 1826
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15)..(16)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (33)..(39)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (42)..(43)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (45)..(46)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (51)..(53)
; OTHER INFORMATION: n is a, c, g, or t

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FEATURE:
NAME/KEY: misc feature
LOCATION: (58)..(61)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (73)..(73)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (75)..(80)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (97)..(97)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (100)..(103)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (106)..(109)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (112)..(113)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (118)..(121)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (125)..(125)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (133)..(133)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (136)..(141)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (148)..(152)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (156)..(158)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (171)..(172)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (175)..(175)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (190)..(192)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (196)..(198)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (214)..(218)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:

NAME/KEY: misc feature
LOCATION: (224)..(224)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (226)..(228)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (230)..(232)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (247)..(248)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (252)..(252)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (254)..(255)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (263)..(264)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (269)..(273)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (275)..(277)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (283)..(285)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (288)..(288)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (291)..(293)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (297)..(297)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (300)..(301)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (308)..(310)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (313)..(317)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (322)..(324)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (331)..(331)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature

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; LOCATION: (333)..(335)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (340)..(340)
; OTHER INFORMATION: n is a, c, g, or t

Query Match      5.2%; Score 39.4; DB 8; Length 1826;
Best Local Similarity 31.1%; Pred. No. 1.6; Indels 0; Gaps 0;
Matches 109; Conservative 0; Mismatches 242;

Qy 91 AAAGACGGCGAAAGACCAATGAAAGAACTGACCGCTCCATAGAAATACAAAAGGCAT 150
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 63

Qy 151 GCGCATGATTACGCTAAATACGCGAAGAAATCGCTGAAGAGTTGCGAATCTATGGGAGC 210
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 64 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 123

Qy 211 AATAGTTTTCGAGTTTCATTAAGGCGAAGGAGTCTTATACAAAGAGATTTTATGCGAT 270
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 124 ANAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 183

Qy 271 GTGTGCGATAAATTAAGGTCATTAACAAGAAAGAACTGAAACGACTTTAAATTGAACAA 330
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 184 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 243

Qy 331 AACATGCTTCTTAAATCTTAGAAGAAAGTTTGGGAAGAAATGGATGATGAAGAGTGAAA 390
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 244 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 303

Qy 391 GAATGTCGATGAATTCATCAATAAACAACGCGACATTTTAAACAGACAA 441
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 304 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 354

RESULT 7
US-10-540-898-308/c
; Sequence 308, Application US/10540898
; Publication No. US20060166213A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: CHIR0056-101 (PP023367.0003)
; CURRENT APPLICATION NUMBER: US/10/540.898
; CURRENT FILING DATE: 2005-06-27
; PRIOR APPLICATION NUMBER: US 10/330,773
; PRIOR FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 308
; LENGTH: 523643
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(523643)
; OTHER INFORMATION: n = A,T,C or G
US-10-540-898-308

Query Match      5.2%; Score 39.4; DB 6; Length 523643;
Best Local Similarity 59.3%; Pred. No. 12;
Matches 67; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 326 AACAAACATCTTCTAAATCTTAGAAGAGTTTGGAGAAATGGATGATGAAGAG 385
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 183741 AAGATAAAATACCTTAGAATAAATTAAGAGAAATGTGGAAGACCTTAATGAAGAAACT 183682
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 386 TGAAGAAATGCGCATGAAATTCATATAAAAAACACGCAAAATTTAAACAGA 438
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 183681 TTAAGTACTATGGATTAATTTTAAAGAGAAATTTGAATAATAATAATA 183629
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RESULT 8
US-11-266-748A-115072/c
; Sequence 115072, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 115072
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-115072

Query Match      5.2%; Score 39.2; DB 8; Length 1000;
Best Local Similarity 55.0%; Pred. No. 1.5;
Matches 77; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Qy 8 ACAAAATATGATAGACACTTGGAAATTTTAAAGCAATTTGGAATCTAGTGTATTGATT 67
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 235 AAAAAAGAGAGAGAAATGGCAAGAGAAATTTTCAAAATTTCTTTTAAATTT 176
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 68 TGTTTGAGGTGCTTGTGTTTTTGGTAAAGACGGCGAAAAAGACACAAATGAAACCA 127
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 175 TAGATTGAGTTTCATTTTATTTGAAACAGACTGGGCGCAATGTCCACAAAGAAATTCCTGTGCA 116
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 128 GCTCCATAGATACAAAAGG 147
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 115 GCACCACCGATGTCCAAAGG 96
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
US-11-266-748A-157236
; Sequence 157236, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4

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Query Match 5.2%; Score 39.2; DB 8; Length 1000;
Best Local Similarity 55.0%; Pred. No. 1.5;
Matches 77; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 157236
LENGTH: 1000
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-157236

Query Match 5.2%; Score 39.2; DB 8; Length 1000;
Best Local Similarity 55.0%; Pred. No. 1.5;
Matches 77; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 8 ACAATATGATAGACACTTGGAAATTTTAAAGCAATTTGAATCTAGTGAATTTATTTGGATT 67
DB 766 AAAAGAAGAAGAAATGGCAAGAGAAAGTTTTTCAAAATTTCTTTCTTTTAAATT 825
QY 68 TGTGAGGTGCTGTTGTTTGGTAAAGACGGCGGCAAAAGACACAAATGAAAACTGACCA 127
DB 826 TAGATTGAGTTTCATTTATTTGAAACAGACTGGGCCAATGTCCACAAAGAAATTCCTGGTCA 885
QY 128 GCTCCATAGATACAAAAGG 147
DB 886 GCACCACCGATGTCCAAAGG 905

RESULT 10
US-11-266-748A-283572/c
Sequence 283572, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 283572
LENGTH: 1000
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-283572

Query Match 5.2%; Score 39.2; DB 8; Length 1000;
Best Local Similarity 55.0%; Pred. No. 1.5;
Matches 77; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 8 ACAATATGATAGACACTTGGAAATTTTAAAGCAATTTGAATCTAGTGAATTTATTTGGATT 67
DB 235 AAAAGAAGAAGAAATGGCAAGAGAAAGTTTTTCAAAATTTCTTTCTTTTAAATT 176
QY 68 TGTGAGGTGCTGTTGTTTGGTAAAGACGGCGGCAAAAGACACAAATGAAAACTGACCA 127
DB 175 TAGATTGAGTTTCATTTATTTGAAACAGACTGGGCCAATGTCCACAAAGAAATTCCTGGTCA 116
QY 128 GCTCCATAGATACAAAAGG 147
DB 115 GCACCACCGATGTCCAAAGG 96

RESULT 11
US-11-266-748A-335001
Sequence 335001, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 335001
LENGTH: 1000
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-335001

Query Match 5.2%; Score 39.2; DB 8; Length 1000;
Best Local Similarity 55.0%; Pred. No. 1.5;
Matches 77; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 8 ACAATATGATAGACACTTGGAAATTTTAAAGCAATTTGAATCTAGTGAATTTATTTGGATT 67
DB 766 AAAAGAAGAAGAAATGGCAAGAGAAAGTTTTTCAAAATTTCTTTCTTTTAAATT 825
QY 68 TGTGAGGTGCTGTTGTTTGGTAAAGACGGCGGCAAAAGACACAAATGAAAACTGACCA 127
DB 826 TAGATTGAGTTTCATTTATTTGAAACAGACTGGGCCAATGTCCACAAAGAAATTCCTGGTCA 885
QY 128 GCTCCATAGATACAAAAGG 147
DB 886 GCACCACCGATGTCCAAAGG 905

RESULT 12
US-11-266-748A-393321/c

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; Sequence 393321, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 393321
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-11-266-748A-393321

Query Match      5.2%; Score 39.2; DB 8; Length 1000;
Best Local Similarity 55.0%; Pred. No. 1.5;
Matches 77; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Qy      8  ACAATATGATAGACACTTGGAAATTTTAAAGCAATTGGAATCTAGTATTGGATT 67
Db      235 AAAAAGAGAGAGAAAGAAATGCAAGAGAGAAAGTTTTCAAATTTCTTTTAAATT 176
Qy      68  TGTTTGAGTCTGTTTGTGTAAGACGCGGAAAGACACAAATGAAAACTGACCA 127
Db      175 TAGATTGAGTTCAATTATTTGAAACAGACTGGGCCAATGTCCACAAAGAAATTCCTGGTCA 116
Qy      128  GCTCCATAGATACAAAAGG 147
Db      115 GCACCACCGATGTCCAAAGG 96

RESULT 13
; Sequence 464367, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 464367
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-11-266-748A-464367

Query Match      5.2%; Score 39.2; DB 8; Length 1000;
Best Local Similarity 55.0%; Pred. No. 1.5;
Matches 77; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Qy      8  ACAATATGATAGACACTTGGAAATTTTAAAGCAATTGGAATCTAGTATTGGATT 67
Db      235 AAAAAGAGAGAGAAAGAAATGCAAGAGAGAAAGTTTTCAAATTTCTTTTAAATT 176
Qy      68  TGTTTGAGTCTGTTTGTGTAAGACGCGGAAAGACACAAATGAAAACTGACCA 127
Db      175 TAGATTGAGTTCAATTATTTGAAACAGACTGGGCCAATGTCCACAAAGAAATTCCTGGTCA 116
Qy      128  GCTCCATAGATACAAAAGG 147
Db      115 GCACCACCGATGTCCAAAGG 96

RESULT 14
; Sequence 70584, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 70584
; LENGTH: 1815
; TYPE: DNA
; ORGANISM: Homo Sapiens
; NAME/KEY: misc feature
; LOCATION: (1190)..(1198)
; OTHER INFORMATION: n is a, c, g, or t
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; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
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; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
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; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; METHODS OF USING THE SAME
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
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; NAME/KEY: misc feature
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US-11-266-748A-106086

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Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions **.rnpm** and **.rnpn**

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions **.rapm** and **.rapn**

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .

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OM nucleic - nucleic search, using sw model

Run on: August 3, 2006, 09:12:56 ; Search time 5922 Seconds
(without alignments)
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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SUMMARIES

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4	759	100.0	795	1	PCT-US01-48392-43	Sequence 43, Appl
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6	759	100.0	795	50	US-10-433-970-43	Sequence 43, Appl
7	727	95.8	762	3	PCT-US96-18542-91	Sequence 91, Appl
8	727	95.8	762	14	US-08-561-469A-971	Sequence 971, App
9	727	95.8	762	16	US-08-761-184-48	Sequence 48, Appl
10	727	95.8	762	16	US-08-761-184-649	Sequence 649, App
11	727	95.8	762	17	US-08-821-931-48	Sequence 4400, Ap
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17	727	95.8	768	16	US-08-761-184-393	Sequence 393, App
18	727	95.8	768	17	US-08-821-931-393	Sequence 393, App
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; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 268
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
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SOFTWARE:
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APPLICATION NUMBER: PCT/US96/18542
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/561,469
FILING DATE: 17-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-001CPPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 762 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
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DB 121 CTGACAGCTCCATAGAAATCAAAAAGGATGCGGATGATTACGCTAAATACGCAAGAA 180
QY 181 ATCGCTGAAGAGTTGCAATATCATGAGGAGCAATAGTTTTCGAGTTTCATTAAGCGGAA 240
DB 181 ATCGCTGAAGAGTTGCAATATCATGAGGAGCAATAGTTTTCGAGTTTCATTAAGCGGAA 240
QY 241 GGAGTCTTATCAAGAGATTTTATGCGATGTCGCGATGATAAATTAAGGTCAATTACAAC 300
DB 241 GGAGTCTTATCAAGAGATTTTATGCGATGTCGCGATGATAAATTAAGGTCAATTACAAC 300
QY 301 AAGAAATCTGAAACGACTTTAATTTGAAACAAACATGCTTTCTTAAATCTTAGAAAGAGT 360
DB 301 AAGAAATCTGAAACGACTTTAATTTGAAACAAACATGCTTTCTTAAATCTTAGAAAGAGT 360
QY 361 TTGGAAGAAATGGATGATGAAGAGTGAAGAAATGTGCGATGAATTTCCATAAAAAAC 420
DB 361 TTGGAAGAAATGGATGATGAAGAGTGAAGAAATGTGCGATGAATTTCCATAAAAAAC 420
QY 421 ACGGCAATTTAAACAGACAGCCCTTAAGCGGCGGCACTTTAAACGCTGTTTAAATGGG 480
DB 421 ACGGCAATTTAAACAGACAGCCCTTAAGCGGCGGCACTTTAAACGCTGTTTAAATGGG 480
QY 481 GGTTTTAAATCTTATCAATTAAGTCTGATTTGCGAATGCGGTGCGGTAACCAATCTA 540
```

Db 481 GGCTTTAAATCTTATCAATAGCTGCTCAATTTGCGAATGCGTTGCAAAACCAATCTTA 540
Qy 541 GGGCGTGTATCGCTTGGGGCAATCAGTGTCTTACAAGACTCTGAGCTTTTAAACA 600
Db 541 GGGCGTGTATCGCTTGGGGCAATCAGTGTCTTACAAGACTCTGAGCTTTTAAACA 600
Qy 601 GGTCTCTTGGCTGGATCATTTACAGGCGTATGGACAGATTTGATTTGACAGGCGCGCT 660
Db 601 GGGCTCTTGGCTGGATCATTTACAGGCGTATGGACAGATTTGATTTGACAGGCGCGCT 660
Qy 661 TATAGGTAAACCAATACCGGCGATGCTGTTGCGCACTTTACGCTTAAACACAGCAA 720
Db 661 TATAGGTAAACCAATACCGGCGATGCTGTTGCGCACTTTACGCTTAAACACAGCAA 720
Qy 721 GCCAATGAAGATAGAGTCTGCTCAATAGCAATCCATT 759
Db 721 GCCAATGAAGATAGAGTCTGCTCAATAGCAATCCGTT 759

RESULT 8

US-08-561-469A-971
; Sequence 971, Application US/08561469A
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 994
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,469A
; FILING DATE: 17-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,032
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-001CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 971:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 762 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
US-08-561-469A-971

Query Match 95.8%; Score 727; DB 14; Length 762;
Best Local Similarity 97.4%; Pred. No. 9.6e-212;
Matches 739; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
Qy 1 ATGGCATAACAATATGATAGAGACTTGGAAATTTTAAAGCAATCTGGAATCTAGTATT 60
Db 1 ATGGCATAACAATATGATAGAGACTTGGAAATTTTAAAGCAATCTGGAATCTAGTATT 60

Qy 61 TTGATTTGTTTGGAGTCTTGTGTTTAAAGACGCGGAAAAAGACACAAATGAAAA 120
Db 61 TTGATTTGTTTGGAGTCTTGTGTTTAAAGACGCGGAAAAAGACACAAATGAAAA 120
Qy 121 CTGACAGCTCATAGATAACAAAGGCGATGCGGATGATTACGCTAAATACGACAGAA 180
Db 121 CTGACAGCTCATAGATAACAAAGGCGATGCGGATGATTACGCTAAATACGACAGAA 180
Qy 181 ATCCGTGAAGAGTTGCAATATCTGGGAGCAATAGTTTTCGAGTTTCAATTAAGGCGAA 240
Db 181 ATCCGTGAAGAGTTGCAATATCTGGGAGCAATAGTTTTCGAGTTTCAATTAAGGCGAA 240
Qy 241 GGAGTCTTATACAAAGAGATTTTATGCGATGTTGCGATAAATTAAGGTCAATTAACA 300
Db 241 GGAGTCTTATACAAAGAGATTTTATGCGATGTTGCGATAAATTAAGGTCAATTAACA 300
Qy 301 AAGAAACTGAAACGACTTTAATTCGAAACAAACATGCTTTCTAATAATCTTAAAGAG 360
Db 301 AAGAAACTGAAACGACTTTAATTCGAAACAAACATGCTTTCTAATAATCTTAAAGAG 360
Qy 361 TTGGAAGAAATGGATGATGAAGAGTGAAGAAATGTCGATGAATTTATCCATAAAGAC 420
Db 361 TTGGAAGAAATGGATGATGAAGAGTGAAGAAATGTCGATGAATTTATCCATAAAGAC 420
Qy 421 ACGGACAAATTTAAACAGACAGCCCTTAAGCGCGGCGACTTTAAACGCTGTTTAAATGGGG 480
Db 421 ACGGACAAATTTAAACAGACAGCCCTTAAGCGCGGCGACTTTAAACGCTGTTTAAATGGGG 480
Qy 481 GGTTTTAAATCTTATCAATAGCTGCTCAATTTGTCGAATGCGGTGCAAAACCAATCTTA 540
Db 481 GGTTTTAAATCTTATCAATAGCTGCTCAATTTGTCGAATGCGGTGCAAAACCAATCTTA 540
Qy 541 GGGCGTGTGTTATCGCTTGGCGGCAATCAGTGTCTTACAAGAACTCTGAGCTTTTAAACA 600
Db 541 GGGCGTGTGTTATCGCTTGGCGGCAATCAGTGTCTTACAAGAACTCTGAGCTTTTAAACA 600
Qy 601 GGTCTGTGTTGCTGATCATTTACAGCGTATGACAGCGGATGATTTGACAGGCGCGCT 660
Db 601 GGTCTGTGTTGCTGATCATTTACAGCGTATGACAGCGGATGATTTGACAGGCGCGCT 660
Qy 661 TATAGGTTAAACCATACCGGCGATGCTGTTGTCGACCTTTACGCTTAAACACAGCAA 720
Db 661 TATAGGTTAAACCATACCGGCGATGCTGTTGTCGACCTTTACGCTTAAACACAGCAA 720
Qy 721 GCCAATGAAGATAGAGTCTGTTGCAATAGCAATCCATT 759
Db 721 GCCAATGAAGATAGAGTCTGTTGCAATAGCAATCCGTT 759

RESULT 9

US-08-761-184-48
; Sequence 48, Application US/08761184
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH ET AL
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 1810
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER:
; OPERATING SYSTEM:
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761,184

[illegible][illegible]

```

TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 649:
SEQUENCE CHARACTERISTICS:
LENGTH: 762 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: misc feature
LOCATION: 1...762
US-08-761-184-649

```

Query Match 95.8%; Score 727; DB 16; Length 762;
Best Local Similarity 97.4%; Pred. No. 9.6e-212;
Matches 739; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy	1	ATGCATACAAATATGATAGAGACTTGGAAATTTTAAAGCAATTTGGATCTAGTGATTTA	60
Db	1	ATGCATACAAATATGATAGAGACTTGGAAATTTTAAAGCAATCTAGTGATTTA	60
Qy	61	TTGGATTTGTTTGAGGTGCTTGTGTTTGGTAAAGACGGCGAAAAAGACACAATGAAAAA	120
Db	61	TTGGATTTGTTTGAGGTGCTTGTGTTTGGTAAAGACGGCGAAAAAGACACAATGAAAAA	120
Qy	121	CTGACCAAGCTCCATAGAAATACAAAGGCATCGCGATGATTACGCTAAATACGCGAAAGA	180
Db	121	CTCAACAGCTCCATAGAAATACAAAGGCATCGCGATGATTACGCTAAATACGCGAAAGA	180
Qy	181	ATCCCTGAAGATTGGCAATACTATGCGAGCAATAGTTTTCGAGTTTCATTAAAGGCGAA	240
Db	181	ATCCCTGAAGATTGGCAATACTATGCGAGCAATAGTTTTCGAGTTTCATTAAAGGTTAA	240
Qy	241	GGAGTCTTATCAAAAGAGATTTTATGCGATGTCGCGATAAATTAAGGTCAAATTACAAAC	300
Db	241	GGAGTCTTATCAAAAGAGATTTTATGCGATGTCGCGATAAATTAAGGTCAAATTACAAAC	300
Qy	301	AAGAAAACTGAAACGACCTTTAAATTGAACAAACATCGCTTCTTAAATCTTAGAAGAAGT	360
Db	301	AAGAAAACTGAAACGACCTTTAAATTGAACAAACATCGCTTCTTAAATCTTAGAAGAAGC	360
Qy	361	TTGGAAGAAATGGATGATGAAGAGATGGAAGAAATGTCGATGAATATCCATAAAAAC	420
Db	361	CTGAAGAAATGGATGATGAAGAGATGGAAGAAATGTCGATGAATATGTCATAAAAAC	420
Qy	421	ACGGACAATTTAAACAGACAAGCCCTTAAGCGCGCGACTTTAAACGCTGTTTAAATGGG	480
Db	421	ACGGACAATTTGAACAGACAAGCCCTTAAGCGCGCGACTTTAAACGCTGTTTAAATGGGA	480
Qy	481	GGTTTTAAATCTTATCAATTAGCTGTCAATGTTGCGAATCGGTCGCAAAAACCATTTCTA	540
Db	481	GGCTTTAAATCTTATCAATTAGCTGTCAATGTTGCGAATCGGTTGCAAAAACCATTTCTA	540
Qy	541	GGGCGTGTTTTATCGCTTGGCGGCAATCAGGTGCTTACAAGACTCTGAGCTTTTAAACA	600
Db	541	GGGCGTGTTTTATCGCTTGGCGGCAATCAAGTGCCTTACAAGAACTCTGAGCTTTTAAACA	600
Qy	601	GGTCTGTTGGCTGGATCATTTACAGGCGTATGGACAGCGATTGATATTCAGGGCGCGCT	660
Db	601	GGCCCTGTTGGCTGGATCATTTACAGGCGTATGGACAGCGATTGATATTCAGGGCGCGCT	660
Qy	661	TATAGGGTAAACCATACCGGCATGCAATTGTGGTTGCCACTTTACGCTTAAAAACACAGCAA	720
Db	661	TATAGGGTAAACCATACCGGCATGCAATTGTGGTTGCCACTTTACGCTTAAAAACGCAACA	720
Qy	721	GCCAAATGAGATTAAGAAGTCGTTGCAAAATAGAAATCCATT	759
Db	721	GCCAAATGAAGTAAAGAAGTCGTTGCAAAATAGAAATCCGTT	759

```

RESULT 11
US-08-821-931-48
; Sequence 48, Application US/08821931
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH ET AL
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 1810
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER:
; OPERATING SYSTEM:
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/821,931
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,032
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/561,469
; FILING DATE: 17-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,405
; FILING DATE: 01-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/660,742
; FILING DATE: 06-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/736,791
; FILING DATE: 25-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/739,150
; FILING DATE: 28-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/761,184
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-001CP9CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 762 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1...762
; US-08-821-931-48

```

Query Match	95.8%	Score 727;	DB 17;	Length 762;
Best Local Similarity	97.4%	Pred. No. 9.6e-212;		
Matches 739: Conservative	0;	Mismatches 20;	Indels	0;
Matches 739: Gaps	0;			

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QY 1 ATGGCATACAAATATGATAGAGACTTGGAAATTTTAAAGCAATGGAATCTAGTGATTTA 60
Db 1 ATGGCATACAAATATGATAGAGACTTGGAAATTTTAAAGCAATGGAATCTAGTGATTTA 60
QY 61 TTGGATTTGTTGAGGTGCTGTTTGGTAAAGCGGCGGAAAGACACAAATGAAAAA 120
Db 61 TTGGATTTGTTGAGGTGCTGTTTGGTAAAGCGGCGGAAAGACACAAATGAAAAA 120
QY 121 CTGACAGCTCCATAGATACAAAGGCGATGCGGATGATTACGTAATACGCGAGAAAG 180
Db 121 CTCACAGCTCCATAGATACAAAGGCGATGCGGATGATTACGTAATACGCGAGAAAG 180
QY 181 ATCGCTGAAGAGTTCGAATATATGCGGCAATAGTTTTCGAGTTTCAATTAAGCGGAA 240
Db 181 ATCGCTGAAGAGTTCGAATATATGCGGCAATAGTTTTCGAGTTTCAATTAAGCGGAA 240
QY 241 GGAGTCTTATACAAAGAGATTTTATGCGATGTCGATGATTAATTAAGGTCATTAACAAC 300
Db 241 GGAGTCTTATACAAAGAGATTTTATGCGATGTCGATGATTAATTAAGGTCATTAACAAC 300
QY 301 AAGAAATCTGAACACACTTAAATGAAACAAACATGCTTCTTAAATCTTGAAGAAGT 360
Db 301 AAGAAATCTGAACACACTTAAATGAAACAAACATGCTTCTTAAATCTTGAAGAAGT 360
QY 361 TTGGAAGAAATGATGATGAAGAGTGAAGAAATGTCGATGAATTAATCCATAAAAAAC 420
Db 361 CTAGAAGAAATGATGATGAAGAGTGAAGAAATGTCGATGAATTAATCCATAAAAAAC 420
QY 421 ACGGCAATTTAAACAGACAGCCTTAAAGCGGCGACTTTAAAGCTGTTTAAATGGGG 480
Db 421 ACGGCAATTTAAACAGACAGCCTTAAAGCGGCGACTTTAAAGCTGTTTAAATGGGG 480
QY 481 GGTTTTAAATCTTCAATAGCTGCTCAATGTCGATGCGGATGCGGTCGCAAAACCATTTA 540
Db 481 GGTTTTAAATCTTCAATAGCTGCTCAATGTCGATGCGGATGCGGTCGCAAAACCATTTA 540
QY 541 GGGCGTGTGTTATCGCTTGGCGGCAATCAGGTGCTTACAGAACTCTGAGCTTTTAAAC 600
Db 541 GGGCGTGTGTTATCGCTTGGCGGCAATCAGGTGCTTACAGAACTCTGAGCTTTTAAAC 600
QY 601 GGTCTGTTGGCTGATCAATACAGCGCTATGACAGCGATGATGATGATGACGGCGCGCT 660
Db 601 GGTCTGTTGGCTGATCAATACAGCGCTATGACAGCGATGATGATGATGACGGCGCGCT 660
QY 661 TATAGGTAAACATACCGGATGCAATGTTGTTGCACTTTACGCTTAAACACAGCAA 720
Db 661 TATAGGTAAACATACCGGATGCAATGTTGTTGCACTTTACGCTTAAACACAGCAA 720
QY 721 GCCAATGAGATAGAAAGTCTGTTGCAATAGATCCATT 759
Db 721 GCCAATGAGATAGAAAGTCTGTTGCAATAGATCCGTT 759
```

RESULT 12

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US-08-821-931-649
; Sequence 649, Application US/08821931
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH ET AL
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 1810
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: ,
```

```
; OPERATING SYSTEM:
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/821,931
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,032
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/561,469
; FILING DATE: 17-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,405
; FILING DATE: 01-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/660,742
; FILING DATE: 06-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/736,791
; FILING DATE: 25-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/739,150
; FILING DATE: 28-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/761,184
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-001CP9CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 649:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 762 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1...762
; US-08-821-931-649
```

```
Query Match 95.8%; Score 727; DB 17; Length 762;
Best Local Similarity 97.4%; Pred. No. 9.6e-212; Mismatches 20; Indels 0; Gaps 0;
Matches 739; Conservative 0;

QY 1 ATGGCATACAAATATGATAGAGACTTGGAAATTTTAAAGCAATGGAATCTAGTGATTTA 60
Db 1 ATGGCATACAAATATGATAGAGACTTGGAAATTTTAAAGCAATGGAATCTAGTGATTTA 60
QY 61 TTGGATTTGTTGAGGTGCTGTTTGGTAAAGCGGCGGAAAGACACAAATGAAAAA 120
Db 61 TTGGATTTGTTGAGGTGCTGTTTGGTAAAGCGGCGGAAAGACACAAATGAAAAA 120
QY 121 CTGACAGCTCCATAGATACAAAGGCGATGCGGATGATTACGTAATACGCGAGAAAG 180
Db 121 CTCACAGCTCCATAGATACAAAGGCGATGCGGATGATTACGTAATACGCGAGAAAG 180
QY 181 ATCGCTGAAGAGTTCGAATATATGCGGCAATAGTTTTCGAGTTTCAATTAAGCGGAA 240
Db 181 ATCGCTGAAGAGTTCGAATATATGCGGCAATAGTTTTCGAGTTTCAATTAAGCGGAA 240
QY 241 GGAGTCTTATACAAAGAGATTTTATGCGATGTCGATGATTAATTAAGGTCATTAACAAC 300
Db 241 GGAGTCTTATACAAAGAGATTTTATGCGATGTCGATGATTAATTAAGGTCATTAACAAC 300
```

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QY 301 AAGAAACTGAACGACTTTAAATGAAACAAACATGCTTTCTAAATCTTAGAAGAAGT 360
Db |||
QY 301 AAGAAACTGAACGACTTTAAATGAAACAAACATGCTTTCTAAATCTTAGAAGAAGT 360
Db |||
QY 361 TTGGAAGAAATGGATGATGAAGAAGTGAAGAAATGTCGATGAATATCCATAAAAAC 420
Db |||
QY 361 CTAGAAGAAATGGATGATGAAGAAGTGAAGAAATGTCGATGAATATCCATAAAAAC 420
Db |||
QY 421 ACGGACAAATTAACACAGCAAGCCCTTAAGCGCGGCACTTTAAACGCTTTTAAATGGG 480
Db |||
QY 421 ACGGACAAATTAACACAGCAAGCCCTTAAGCGCGGCACTTTAAACGCTTTTAAATGGG 480
Db |||
QY 481 GGTCTTAAATCTTAAATAGCTGCTCAATGCTGCAATGCGTGCAGAAACCACTTCTA 540
Db |||
QY 481 GGTCTTAAATCTTAAATAGCTGCTCAATGCTGCAATGCGTGCAGAAACCACTTCTA 540
Db |||
QY 541 GGGCGTGGTTTATCGCTTGGCGGCAATCAGTGTCTTACAGAACTCTGAGCTTTTAA 600
Db |||
QY 541 GGGCGTGGTTTATCGCTTGGCGGCAATCAGTGTCTTACAGAACTCTGAGCTTTTAA 600
Db |||
QY 601 GGTCTGTGGCTGGATCATTAAGCGGTATGAGCAGCGATGATATGCGAGGCGCGCT 660
Db |||
QY 601 GGTCTGTGGCTGGATCATTAAGCGGTATGAGCAGCGATGATATGCGAGGCGCGCT 660
Db |||
QY 661 TATAGGCTTAACCATACCGCATGCTTGTGCTGCTTACGCTTAAACACAGCAA 720
Db |||
QY 661 TATAGGCTTAACCATACCGCATGCTTGTGCTGCTTACGCTTAAACACAGCAA 720
Db |||
QY 721 GCCAATGAGATAAGAAGTGTGCTGCAATAGAATCCATT 759
Db |||
QY 721 GCCAATGAGATAAGAAGTGTGCTGCAATAGAATCCATT 759
Db |||
```

RESULT 13

US-08-993-002A-4400
; Sequence 4400, Application US/08993002A

GENERAL INFORMATION:

; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031

CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875

COMPUTER READABLE FORM:

; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/993.002A
; FILING DATE:

PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400

TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 4400:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 762 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1...762
US-08-993-002A-4400

Query Match 95.8%; Score 727; DB 18; Length 762;

Best Local Similarity 97.4%; Pred. No. 9.6e-212;

Matches 739; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

```
QY 1 ATGGCATCAATATGATAGAGACTTGGAAATTTTAAAGCAATGGAATCTAGTGAATTTA 60
Db |||
QY 1 ATGGCATCAATATGATAGAGACTTGGAAATTTTAAAGCAATGGAATCTAGTGAATTTA 60
Db |||
QY 61 TTGGATTTGTTGAGGTGCTTGTGTTTGGTAAAGACGGCGAAAGACACACATGAAAAA 120
Db |||
QY 61 TTGGATTTGTTGAGGTGCTTGTGTTTGGTAAAGACGGCGAAAGACACACATGAAAAA 120
Db |||
QY 121 CTGACCACTCCATAGAATACAAAAGGCATGCGATGATTACGCTAAATACGACAGAAAGA 180
Db |||
QY 121 CTCACAAGCTCCATAGAATACAAAAGGCATGCGATGATTACGCTAAATACGACAGAAAGA 180
Db |||
QY 181 ATCGCTGAAGAGTTGCAATACTATGGAGCAATAGTTTTCGAGTTTTCATTAAGGCGAA 240
Db |||
QY 181 ATCGCTGAAGAGTTGCAATACTATGGAGCAATAGTTTTCGAGTTTTCATTAAGGCGAA 240
Db |||
QY 241 GGAGTCTTATACAAAGAGATTTTATGCGATGTTGCGATAAAATTAAGGTCAATTAACAAC 300
Db |||
QY 241 GGAGTCTTATACAAAGAGATTTTATGCGATGTTGCGATAAAATTAAGGTCAATTAACAAC 300
Db |||
QY 301 AAGAAAACCTGAAACGACTTTAAATGAAACAAAACATGCTTTCTAAATCTTAGAAGAAGT 360
Db |||
QY 301 AAGAAAACCTGAAACGACTTTAAATGAAACAAAACATGCTTTCTAAATCTTAGAAGAAGT 360
Db |||
QY 361 TTGGAAGAAATGGATGATGAAGAAGTGAAGAAATGTCGATGAATATCCATAAAAAC 420
Db |||
QY 361 CTAGAAGAAATGGATGATGAAGAAGTGAAGAAATGTCGATGAATATCCATAAAAAC 420
Db |||
QY 421 ACGGACAAATTAACACAGCAAGCCCTTAAGCGCGGCACTTTAAACGCTTTTAAATGGG 480
Db |||
QY 421 ACGGACAAATTAACACAGCAAGCCCTTAAGCGCGGCACTTTAAACGCTTTTAAATGGG 480
Db |||
QY 481 GGTCTTAAATCTTAAATAGCTGCTCAATGCTGCAATGCGTGCAGAAACCACTTCTA 540
Db |||
QY 481 GGTCTTAAATCTTAAATAGCTGCTCAATGCTGCAATGCGTGCAGAAACCACTTCTA 540
Db |||
QY 541 GGGCGTGGTTTATCGCTTGGCGGCAATCAGTGTCTTACAGAACTCTGAGCTTTTAA 600
Db |||
QY 541 GGGCGTGGTTTATCGCTTGGCGGCAATCAGTGTCTTACAGAACTCTGAGCTTTTAA 600
Db |||
QY 601 GGTCTGTGGCTGGATCATTAAGCGGTATGAGCAGCGATGATATGCGAGGCGCGCT 660
Db |||
QY 601 GGTCTGTGGCTGGATCATTAAGCGGTATGAGCAGCGATGATATGCGAGGCGCGCT 660
Db |||
QY 661 TATAGGCTTAACCATACCGCATGCTTGTGCTGCTTACGCTTAAACACAGCAA 720
Db |||
QY 661 TATAGGCTTAACCATACCGCATGCTTGTGCTGCTTACGCTTAAACACAGCAA 720
Db |||
QY 721 GCCAATGAGATAAGAAGTGTGCTGCAATAGAATCCATT 759
Db |||
QY 721 GCCAATGAGATAAGAAGTGTGCTGCAATAGAATCCATT 759
Db |||
```

RESULT 14

US-08-993-002A-4401

; Sequence 4401, Application US/08993002A

GENERAL INFORMATION:

; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES

TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 10031

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: Windows NT 4.0

SOFTWARE: UNIX

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/993,002A

FILING DATE:

PRIOR APPLICATION NUMBER:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: GTN-018

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 4401:

SEQUENCE CHARACTERISTICS:

LENGTH: 762 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Helicobacter pylori

FEATURE:

NAME/KEY: misc_feature

LOCATION: 1...762

US-08-993-002A-4401

Query Match 95.8%; Score 727; DB 18; Length 762;

Best Local Similarity 97.4%; Pred. No. 9.6e-212;

Matches 739; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGGCATCAATATGATAGAGACTTGGAAATTTTAAAGCAATTCGAATCTAGTGAATTA 60

DB 1 ATGGCATCAATATGATAGAGACTTGGAAATTTTAAAGCAATTCGAATCTAGTGAATTA 60

QY 61 TTGGATTGTTTGAAGTCTGTTTGGTAAAGACGCGGAAAAAGACACAATGAAAAA 120

DB 61 TTGGATTGTTTGAAGTCTGTTTGGTAAAGACGCGGAAAAAGACACAATGAAAAA 120

QY 121 CTGACAGCTCCATAGATAAACAAGGATCGCGATGATTAACGTAATATAGCGAAGA 180

DB 121 CTGACAGCTCCATAGATAAACAAGGATCGCGATGATTAACGTAATATAGCGAAGA 180

QY 181 ATCGCTGAAGTTCGAATCTATGGGAGCAATAGTTTGGAGTTTCATTAAGGCGAA 240

DB 181 ATCGCTGAAGTTCGAATCTATGGGAGCAATAGTTTGGAGTTTCATTAAGGCGAA 240

QY 241 GGAGTCTTATCAAGAGATTTTATGCGATGTCGTGCGATAAATTAAGGTCAATACAA 300

DB 241 GGAGTCTTATCAAGAGATTTTATGCGATGTCGTGCGATAAATTAAGGTCAATACAA 300

QY 301 AAGAAAACTGAACGACTTTAATTAAGCAACAAACATGCTTTCTAAATCTTGAAGAAGT 360

DB 301 AAGAAAACTGAACGACTTTAATTAAGCAACAAACATGCTTTCTAAATCTTGAAGAAGT 360

QY 361 TTGGAGAAATGGATGATGAAGAGTGAAGAAATGTGCGATGAATATCCATAAAAAA 420

DB 361 CTAGAGAAATGGATGATGAAGAGTGAAGAAATGTGCGATGAATATCCATAAAAAA 420

QY 421 ACGGCAATTTAAACAGACAGAGCTTTAAGCGCGGCACTTTAAACGCTGTTTAAATGGG 480

DB 421 ACGGCAATTTAAACAGACAGAGCTTTAAGCGCGGCACTTTAAACGCTGTTTAAATGGG 480

QY 481 GGTCTTAAATCTTATCAATAGCTGTCATTTGGCGAATCGGTCGCAAAACCATTTCTA 540

DB 481 GGTCTTAAATCTTATCAATAGCTGTCATTTGGCGAATCGGTCGCAAAACCATTTCTA 540

QY 541 GGGCGTGGTTTATCGCTTGGGCAATCAGGTCTTACAGAACTCTGAGCTTTTAAACA 600

DB 541 GGGCGTGGTTTATCGCTTGGGCAATCAGGTCTTACAGAACTCTGAGCTTTTAAACA 600

QY 601 GGTCTTGGTGGTGGATCATTCAGGCGTATGACAGCGATTTGATTTGAGGCGCGCT 660

DB 601 GGTCTTGGTGGTGGATCATTCAGGCGTATGACAGCGATTTGATTTGAGGCGCGCT 660

QY 661 TATAGGTAACCATACCGGCAATCAGGTCTTGGCGAATGAAATGAAATCCATT 720

DB 661 TATAGGTAACCATACCGGCAATCAGGTCTTGGCGAATGAAATGAAATCCATT 720

QY 721 GCGAATGAAGTAAGAGTGGTGGCGAATGAAATGAAATCCATT 759

DB 721 GCGAATGAAGTAAGAGTGGTGGCGAATGAAATGAAATCCATT 759

RESULT 15

US-10-335-977-4400

Sequence 4400, Application US/10335977

GENERAL INFORMATION:

APPLICANT: DOUGLAS SMITH et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES

RELATING TO HELICOBACTER PYLORI FOR

DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 10031

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: Windows NT 4.0

SOFTWARE: UNIX

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/335,977

FILING DATE: 30-Dec-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/993,002

FILING DATE: 17-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: GTN-018

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 4400:

SEQUENCE CHARACTERISTICS:

LENGTH: 762 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Helicobacter pylori

```
;
;
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...762
; SEQUENCE DESCRIPTION: SEQ ID NO: 4400:
US-10-335-977-4400

Query Match          95.8%; Score 727; DB 49; Length 762;
Best Local Similarity 97.4%; Pred. No. 9.6e-212; Indels 0; Gaps 0;
Matches 739; Conservative 0; Mismatches 20;

Qy 1 ATGCATACAAATATGATAGAGACTTGGAAATTTTAAAGCAATTTGGAATCTAGTGATTTA 60
Db 1 ATGCATACAAATATGATAGAGACTTGGAAATTTTAAAGCAATTTGGAATCTAGTGATTTA 60

Qy 61 TTGGATTGTTTGGAGTGTCTTTTGGTAAAGACGGGAAAGAAAGACACAAATGAAAAA 120
Db 61 TTGGATTGTTTGGAGTGTCTTTTGGTAAAGACGGGAAAGAAAGACACAAATGAAAAA 120

Qy 121 CTGACCAAGCTCCATAGAAATCAAAAGGATGGCGATGATTACGCTAAATACGCAGAAAGA 180
Db 121 CTGACCAAGCTCCATAGAAATCAAAAGGATGGCGATGATTACGCTAAATACGCAGAAAGA 180

Qy 181 ATCGCTCAAGAGTTGCAATACTATGGAGCAATAGTTTTTGGAGTTTCATTAAAGGCGAA 240
Db 181 ATCGCTCAAGAGTTGCAATACTATGGAGCAATAGTTTTTGGAGTTTCATTAAAGGCGAA 240

Qy 241 GGAGTCTTATACAAAGAGATTTTATGCGATGTGTGCGATATAATTTAAAGTCAATTTACAC 300
Db 241 GGAGTCTTATACAAAGAGATTTTATGCGATGTGTGCGATATAATTTAAAGTCAATTTACAC 300

Qy 301 AAGAAACTGAAAGCACTTTAAATTTGAACAAACATGCTTTCTAAATCTTAGAAGAGAGT 360
Db 301 AAGAAACTGAAAGCACTTTAAATTTGAACAAACATGCTTTCTAAATCTTAGAAGAGAGC 360

Qy 361 TTGAAGAAATGGATGATGAAGAGTGAAGAAATGTGCGATGAATTTATCCATAAAAAC 420
Db 361 CTAGAAGAAATGGATGATGAAGAGTGAAGAAATGTGCGATGAATTTCTCCATAAAAAC 420

Qy 421 ACGGACAAATTTAAACAGACAGCCCTTAAGCGCGGCACTTTAAACGCTTTTAAATGGGG 480
Db 421 ACGGACAAATTTGAACAGACAGACCTTAAGCGCGGCACTTTAAACGCTTTTAAATGGGA 480

Qy 481 GGTTTTAAATCTTATCAATAGCTGTCTATTTGGGATGCGTCCGAAACCAATCTTA 540
Db 481 GGCTTTAAATCTTATCAATAGCTGTCTATTTGGGATGCGTTCGAAATCCGTTTCAATCTTA 540

Qy 541 GGGCGTGTGTTTATCGCTTGGCGGCAATCAGGTGCTTCAAGAACTCTGAGCTTTTAAACA 600
Db 541 GGGCGTGTGTTTATCGCTTGGCGGCAATCAAGTCTTCAAGAACTCTGAGCTTTTAAACA 600

Qy 601 GGTCTGTGTGGTGGATCATTTACAGGCGATATGGACAGCGATTTGATFATTTGCAGGGCCGCT 660
Db 601 GGCCTGTGTGGTGGATCATTTACAGGCGATATGGACAGCGATTTGATFATTTGCAGGGCCGCT 660

Qy 661 TATAGGGTAAACCATACCGGATGCAATTTGGTGGCTTTACGCTTAAAGCAACAGCA 720
Db 661 TATAGGGTAAACCATACCGGATGCAATTTGGTGGCTTTACGCTTAAAGCAACAGCA 720

Qy 721 GCCAATGAGATAGAGTGTGCAATAGATCCATT 759
Db 721 GCCAATGAGATAGAGTGTGCAATAGATCCGTT 759
```

Search completed: August 3, 2006, 10:55:37
Job time : 5923 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
C 1	43.4	5.7	556	6	US-10-363-345B-23587	Sequence 23587, A
C 2	43.4	5.7	556	6	US-10-363-345B-23588	Sequence 23588, A
C 3	42.8	5.6	1564	6	US-10-363-345B-8863	Sequence 8863, Ap
C 4	42.8	5.6	1564	6	US-10-363-345B-8864	Sequence 8864, Ap
C 5	42.4	5.6	429	7	US-11-486-448-1386	Sequence 1386, Ap
C 6	42	5.5	587	6	US-10-363-345B-12619	Sequence 12619, A
C 7	42	5.5	587	6	US-10-363-345B-12620	Sequence 12620, A
C 8	41.6	5.5	645	7	US-11-486-448-7023	Sequence 7023, Ap
C 9	40.8	5.4	576	6	US-10-363-345B-40153	Sequence 40153, A
C 10	40.8	5.4	576	6	US-10-363-345B-40154	Sequence 40154, A
C 11	40.8	5.4	713	6	US-10-363-345B-6193	Sequence 6193, Ap
C 12	40.8	5.4	713	6	US-10-363-345B-6194	Sequence 6194, Ap
C 13	40.6	5.3	786	6	US-10-363-345B-20053	Sequence 20053, A
C 14	40.6	5.3	786	6	US-10-363-345B-20054	Sequence 20054, A
C 15	40.6	5.3	822	6	US-10-363-345B-11443	Sequence 11443, A
C 16	40.6	5.3	822	6	US-10-363-345B-11444	Sequence 11444, A
C 17	40.6	5.3	822	6	US-10-363-345B-38409	Sequence 38409, A
C 18	40.6	5.3	822	6	US-10-363-345B-38410	Sequence 38410, A
C 19	40.2	5.3	580	6	US-10-363-345B-21455	Sequence 21455, A
C 20	40.2	5.3	580	6	US-10-363-345B-21456	Sequence 21456, A
C 21	40	5.3	780	7	US-11-416-490-20	Sequence 20, Appl
C 22	39.6	5.2	1762	6	US-10-363-345B-7529	Sequence 7529, Ap
C 23	39.6	5.2	1762	6	US-10-363-345B-7530	Sequence 7530, Ap
C 24	39.4	5.2	523643	1	PCT-US03-41389-308	Sequence 308, App
C 25	39.2	4.5	778	6	US-10-363-345B-2179	Sequence 2179, Ap

```
QY 401 ATGAATTATCCATAAAAAACGCGACAATTTAAACAGACAA 441
Db 193 AAAAAACGTAAAAAATAAAAAAATAAAAAAATAAAAAA 153

RESULT 2
US-10-363-345B-23588
; Sequence 23588, Application US/10363345B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: 82010
; CURRENT APPLICATION NUMBER: US/10/363,345B
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40723
; SEQ ID NO 23588
; LENGTH: 556
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 23588
; NAME/KEY: unsure
; LOCATION: (503, 506, 513..514, 517, 520..521, 523..524, 552)
US-10-363-345B-23588

Query Match 5.7%; Score 43.4; DB 6; Length 556;
Best Local Similarity 45.5%; Pred. No. 0.035;
Matches 155; Conservative 0; Mismatches 186; Indels 0; Gaps 0;

QY 101 AAAAAACACACATGAAAACTGACCGAGCTCCATAGATAACAAAAGGCGATGATT 160
Db 64 AAAAAAATAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 123

QY 161 ACGTAAATACGCAAGAAAGTCTGCAAGAGTTGCAATCTATGGGAGCAATAGTTTG 220
Db 124 AAAAAAATAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 183

QY 221 CGAGTTTCATTAAGCGAGGAGCTTTATACAAAGAGATTTTATGCGATGTCGATA 280
Db 184 AAAAAAATAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 243

QY 281 AATTAAAGTCAATTACACAGAAACTGAAACGACTTTTAAATTGAACAAACATGCTTT 340
Db 244 AAAAAAATAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 303

QY 341 CTAAATCTTAGAAGAGTTTGAAGAAATGGATGATGAAGAAGTGAAGAAATGTGCG 400
Db 304 AAAAAAATAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 363

QY 401 ATGAATTATCCATAAAAAACGCGACAATTTAAACAGACAA 441
Db 364 AAAAAACGTAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 404

RESULT 3
US-10-363-345B-8863/c
; Sequence 8863, Application US/10363345B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: 82010
; CURRENT APPLICATION NUMBER: US/10/363,345B
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40723
```

```
; SEQ ID NO 8863
; LENGTH: 1564
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 8863
; NAME/KEY: unsure
; LOCATION: (9, 21, 31, 38, 54, 161, 265, 288, 328, 342, 390, 1069, 1108)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1199, 1204, 1211..1212, 1222, 1250, 1280..1281, 1348)
US-10-363-345B-8863

Query Match 5.6%; Score 42.8; DB 6; Length 1564;
Best Local Similarity 45.5%; Pred. No. 0.067;
Matches 152; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

QY 108 ACACAATGAAAACTGACCGAGCTCCATAGATAACAAAAGGCGATGATGATTACGCTAA 167
Db 810 AAAAAATTAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 751

QY 168 ATACGCAGAAAAATCGCTGAAGAGTTGCAATCTATGGGAGCAATAGTTTTCGAGTTT 227
Db 750 AACGAAATTACAAAACGTAAACGAGTAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 691

QY 228 CATTAAAGCGAAGAGTCTTATACAAAGAGATTTTATCGGATGTGCGATATAAATAA 287
Db 690 CAATAATACAAAAAATACGAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA 631

QY 288 GGTCAATTACACAGAAAACTGAAACGACTTTAATTGAACAAACATGCTTTCTAAAT 347
Db 630 AACGATAAAAAATAACGAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA 571

QY 348 CTAGAAAAAGATTTGGGAAGAAATGCGATCATGAAGAAGTGAAGAAGATGTCGATGAAT 407
Db 570 AAAAAAATAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 511

QY 408 ATCCATAAAAAACGCGACAATTTAAACAGACAA 441
Db 510 AATAAAAAAACAACGAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA 477

RESULT 4
US-10-363-345B-8864
; Sequence 8864, Application US/10363345B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: 82010
; CURRENT APPLICATION NUMBER: US/10/363,345B
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40723
; SEQ ID NO 8864
; LENGTH: 1564
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 8864
; NAME/KEY: unsure
; LOCATION: (217, 284..285, 315, 343, 353..354, 361, 366, 457, 496, 575)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1223, 1237, 1277, 1300, 1404, 1511, 1527, 1534, 1544, 1556)
US-10-363-345B-8864

Query Match 5.6%; Score 42.8; DB 6; Length 1564;
```

Best Local Similarity 45.5%; Pred. No. 0.067; Mismatches 182; Indels 0; Gaps 0;
Matches 152; Conservative 0;
QY 108 ACACAAATGAAAGCTGACAGCTCCATAGATACAAAAGGCATGCGATGATTACGCTAA 167
Db 755 AAAAATTTAAATATAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 814
QY 168 ATACGCAGAAAGATCGCTGAGAGTTGCAATCTATATGGAGCAATAGTTTTCGAGTTT 227
Db 815 AAACGAAATTCACAAACGTAACGACGTAAAAAATAAATAAATAAATAAATAAATAA 874
QY 228 CATTAAAGCGAAGAGTCTTATACAAAGAGATTTTATCGGATGTCGGATTAATATA 287
Db 875 CAAATAATACAAAAATACGAAAAAAGAAAAAATATATACATAAATAAATAATACGAAT 934
QY 288 GGTCAATTTACACAGAAAGCTGAAACGACTTTAATTCGAACAAACATGCTTTCTAAAT 347
Db 935 AAACGATAAAAAATAATACGAAAAATTTATAAAAAAATAAATAAATAATTTAAAAA 994
QY 348 CTTAGAAAGAGTTTGGAGAAATGATGATGAAGAGTGAAGAAATGTCGATCAATT 407
Db 995 AAAAATAAAAAACGAAAAATTAACGAAACGAAAAACGAAAAAATAAATAAATAA 1054
QY 408 ATCCATAAAAAACGCGCAATTTTAAACAGACAA 441
Db 1055 AAATAAAAAAACAACGAAAAATCAAAAAACGA 1088

RESULT 5

US-11-486-448-1386/c
; Sequence 1386, Application US/11486448
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yongwei
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53534)B
; CURRENT APPLICATION NUMBER: US/11/486,448
; CURRENT FILING DATE: 2006-07-14
; NUMBER OF SEQ ID NOS: 117596
; SEQ ID NO 1386
; LENGTH: 639
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C1040_7
US-11-486-448-1386

Query Match 5.6%; Score 42.4; DB 7; Length 639;
Best Local Similarity 53.7%; Pred. No. 0.067; Mismatches 76; Indels 0; Gaps 0;
Matches 88; Conservative 0;
QY 278 ATAAATTAAGGTCAATTACACAAAGAACTGAAACGACTTTAATTCACAAACATGCG 337
Db 595 AAAAATAAAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 536
QY 338 TTTCTAAATCTTGAAGAAGTTTGGAGAAATGCGATGATGAAGAGTGAAGAAATGT 397
Db 535 AACATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 476
QY 398 GCGATGAATTCATCAAAAAACGCGCAATTTTAAACAGACAA 441
Db 475 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 432

RESULT 6

US-10-363-345B-12619/c
; Sequence 12619, Application US/10363345B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin

; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: 82010
; CURRENT APPLICATION NUMBER: US/10/363,345B
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40723
; SEQ ID NO 12619
; LENGTH: 587
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 12619
; NAME/KEY: unsure
; LOCATION: (556..557, 559..)
US-10-363-345B-12619

Query Match 5.5%; Score 42; DB 6; Length 587;
Best Local Similarity 45.1%; Pred. No. 0.084;
Matches 156; Conservative 0; Mismatches 190; Indels 0; Gaps 0;
QY 91 AAAGACGGCGAAAAAGACACATGAATAAAGTACACGAGCTCCATAGATACAAAAGCAT 150
Db 418 AAAAAACGAAAAACGAAAAACACGTAAAAACCGAAAAAATAAATAAATAAATAA 359
QY 151 GCGGATGATTACGCTAAATACGCAGAAAGAAATCGTGAAGAGTTGCAATCTATGCGAGC 210
Db 358 TAGCAAAAAACGATAAAAAACGCAAAAAAACHAAAAAAGAAAAAAGAAAAAAGAAAA 299
QY 211 AATAGTTTTGCGAGTTTTCATTAAAGGCGAAGAGTCTTATACAAAGAGATTTTATGCGAT 270
Db 298 AACGACGCTAAAAAAGAAAAACGAAAAAATAAATAAATAAATAAATAAATAAATA 239
QY 271 GTGTCGATAAATAAAGTCAATTACACAGAAAAAAGTGAAGAGTCTTAAATGAAACA 330
Db 238 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 179
QY 331 AACATGCTTTCTAAATCTTAGAAGAAGTTTGGAGAAATGCGATGATGAAGAGTGA 390
Db 178 AAACGCTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 119
QY 391 GAAATGTCGATGAATTTATCCATAAAAAACACGCAATTTTAAACA 436
Db 118 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 73

RESULT 7

US-10-363-345B-12620
; Sequence 12620, Application US/10363345B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: 82010
; CURRENT APPLICATION NUMBER: US/10/363,345B
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40723
; SEQ ID NO 12620
; LENGTH: 587
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 12620
; NAME/KEY: unsure
; LOCATION: (27..28, 30..)
US-10-363-345B-12620
Query Match 5.5%; Score 42; DB 6; Length 587;

```

Best Local Similarity 45.1%; Pred. No. 0.084;
Matches 156; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

QY 91 AAAGACGGCGAAAGAAAGACACAATAGAAAACTGACCGAGCTCCATAGAAATACAAAAGGCAT 150
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 170 AAAAAACGAAACGAAACGAAACACGTAACAAACCGAAAAAAGAAAAATTTAAATATCAT 229
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 151 GCGCATGATTACGCTAAATTCGCGAAGAAAGAAATCGCTGAAGAGTTGCAATACTATGGGAGC 210
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 230 TAGCGAAAAAACGATAAAAAACGCAAAACCAAAAAAAGAAAAACGAAAAAAGAAAAA 289
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 211 AATAGTTTTGCGAGTTTTCAATTAAGGCGAGGAGTCTTATACAAAGAGATTTTATGCGAT 270
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 290 ACGACGTAACAAAAACGAAAAAAGAAAAAAGAAAAATTAACAAAAAATATAAATATA 349
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 271 GTGTGCGATAAATTTAAAGGTCATTTACAAACAAGAAAACTGAAACGAGCTTTAATTGAACAA 330
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 350 AAAAAAATTTAAAAAAGAAAAAATAAAAAATAAAAAATTCGAAAAAAGAAAAATAAATA 409
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 331 ACGATGCTTCTTAAAAATCTTAGAAGAAAGTTTGAAGAAATGGATGATGAAGAGTGAAA 390
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 410 AAAACGCTCTAAAAAAGAAAAATAAAAAATAATAAATAAATAAAGAAAAAATAAAATTTAA 469
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 391 GAAATGTGCGATGAATTTATCCATAAAAAAACAACGACCAATTTAAACA 436
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 470 AAAATAAAAAAAGAAAAAAGAAAAACGACGAAAAAATAAATAAATAAATAAACA 515
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8
US-11-486-448-7023/c
; Sequence 7023, Application US/11486448
; GENERAL INFORMATION:
; APPLICANT: Kowalic, David K.
; APPLICANT: Cao, Yongwei
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53534)B
; CURRENT APPLICATION NUMBER: US/11/486,448
; CURRENT FILING DATE: 2006-07-14
; NUMBER OF SEQ ID NOS: 117596
; SEQ ID NO 7023
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: uC-gsromu33B044d09b1
US-11-486-448-7023

```

```

; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3'
; FILE REFERENCE: 82010
; CURRENT APPLICATION NUMBER: US/10/363,345B
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40723
; SEQ ID NO 40153
; LENGTH: 576
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 40153
US-10-363-345B-40153

Query Match          5.4%; Score 40.8; DB 6; Length 576;
Best Local Similarity 53.0%; Pred. No. 0.17; Indels 0; Gaps 0;
Matches 87; Conservative 0; Mismatches 77;

Qy 278 ATAAATTAAAGGTCACATTACAACAAGAAAACTGAAACGACTTTTAATTGAAACAAAAACATGC 337
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 338 TTTCTAAAATCTTGAAGAAGTTTGGAGAATAATGGATGATGAAGAAGTGAAGNAATGT 397
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 507 GAATATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 448
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 398 GCGATGAATTATCCATATAAAAAACACGACAACTTTTAAACAGACAA 441
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 447 ACGATAATCGACCGTAAAAAATAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 404
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 10
US-10-363-345B-40154
; Sequence 40154, Application US/10363345B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3'
; FILE REFERENCE: 82010
; CURRENT APPLICATION NUMBER: US/10/363,345B
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40723
; SEQ ID NO 40154
; LENGTH: 576
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 40154
US-10-363-345B-40154

```

RESULT 9
US-10-363-345B-40153/c
; Sequence 40153, Application US/10363345B

```
RESULT 11
US-10-363-345B-6193/c
; Sequence 6193, Application US/10363345B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: 82010
; CURRENT APPLICATION NUMBER: US/10/363,345B
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40723
; SEQ ID NO 6193
; LENGTH: 713
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 6193
US-10-363-345B-6193

Query Match          5.4%; Score 40.8; DB 6; Length 713;
Best Local Similarity 49.1%; Pred. No. 0.18;
Matches 108; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 229 ATTAAGCGGAAGAGTCTTATACAAAGAGATTTTATGCGATGTGTGCGATAAATTAAAG 288
Db 413 AATAAAGGAAAAAATACGAAAAACAAAAAAGACCGGATGAAAAATCGGATAAAAAA 354
QY 289 GTCATTTACACAAAGAACTGAAACGACTTTAATTGACAAACATGCTTTCTAAATC 348
Db 353 ATAAAGAAAAATATAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 294
QY 349 TTAGAAAGAAAGTTTCGAAGAAATGATGATGAAGAGTGAAGAAATGTCGATGAATTA 408
Db 293 AAAAAAACAACCGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 234
QY 409 TCCATTAACAAACGACCAATTTAAACGACAGCCTTAA 448
Db 233 AAAAAAGAAAAACGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 194

RESULT 12
US-10-363-345B-6194
; Sequence 6194, Application US/10363345B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: 82010
; CURRENT APPLICATION NUMBER: US/10/363,345B
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40723
; SEQ ID NO 6194
; LENGTH: 713
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 6194
US-10-363-345B-6194

Query Match          5.4%; Score 40.8; DB 6; Length 713;
Best Local Similarity 49.1%; Pred. No. 0.18;
Matches 108; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 229 ATTAAGCGGAAGAGTCTTATACAAAGAGATTTTATGCGATGTGTGCGATAAATTAAAG 288
Db 413 AATAAAGGAAAAAATACGAAAAACAAAAAAGACCGGATGAAAAATCGGATAAAAAA 354
QY 289 GTCATTTACACAAAGAACTGAAACGACTTTAATTGACAAACATGCTTTCTAAATC 348
Db 353 ATAAAGAAAAATATAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 294
QY 349 TTAGAAAGAAAGTTTCGAAGAAATGATGATGAAGAGTGAAGAAATGTCGATGAATTA 408
Db 293 AAAAAAACAACCGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 234
QY 409 TCCATTAACAAACGACCAATTTAAACGACAGCCTTAA 448
Db 233 AAAAAAGAAAAACGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 194

RESULT 13
US-10-363-345B-20053/c
; Sequence 20053, Application US/10363345B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: 82010
; CURRENT APPLICATION NUMBER: US/10/363,345B
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40723
; SEQ ID NO 20053
; LENGTH: 786
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 20053
US-10-363-345B-20053

Query Match          5.3%; Score 40.6; DB 6; Length 786;
Best Local Similarity 49.8%; Pred. No. 0.21;
Matches 103; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 227 TCATTAAAGCGGAAGAGTCTTATACAAAGAGATTTTATGCGATGTGTGCGATAAATTAA 286
Db 672 TTAATAAACGCGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 613
QY 287 AGGTCAATTACAAAGAAACCTGAACGACTTTAATTGAACAAACATGCTTTCTAAAA 346
Db 612 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 553
QY 347 TCTTAGAAGAAAGTTTGGAGAAGATGATGATGAAGAGTGAAGAAATGTCGATGAAT 406
Db 552 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 493
QY 407 TATCCATAAAAAACACGACCAATTTAA 433
Db 492 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 466

RESULT 14
US-10-363-345B-20054
; Sequence 20054, Application US/10363345B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: 82010
; CURRENT APPLICATION NUMBER: US/10/363,345B
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40723
; SEQ ID NO 20054
; LENGTH: 786
```

```
Db 301 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 360
QY 289 GTCAATTACAAAGAAACCTGAACGACTTTAATTGAACAAACATGCTTTCTAAATC 348
Db 361 ATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 420
QY 349 TTAGAAAGAAAGTTTGGAGAAGATGATGATGAAGAGTGAAGAAATGTCGATGAATTA 408
Db 421 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 480
QY 409 TCCATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 448
Db 481 AAAAAACGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 520
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RESULT 13
US-10-363-345B-20053/c
; Sequence 20053, Application US/10363345B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: 82010
; CURRENT APPLICATION NUMBER: US/10/363,345B
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40723
; SEQ ID NO 20053
; LENGTH: 786
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 20053
US-10-363-345B-20053
```

```
Query Match          5.3%; Score 40.6; DB 6; Length 786;
Best Local Similarity 49.8%; Pred. No. 0.21;
Matches 103; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 227 TCATTAAAGCGGAAGAGTCTTATACAAAGAGATTTTATGCGATGTGTGCGATAAATTAA 286
Db 672 TTAATAAACGCGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 613
QY 287 AGGTCAATTACAAAGAAACCTGAACGACTTTAATTGAACAAACATGCTTTCTAAAA 346
Db 612 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 553
QY 347 TCTTAGAAGAAAGTTTGGAGAAGATGATGATGAAGAGTGAAGAAATGTCGATGAAT 406
Db 552 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 493
QY 407 TATCCATAAAAAACACGACCAATTTAA 433
Db 492 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 466
```

```
RESULT 14
US-10-363-345B-20054
; Sequence 20054, Application US/10363345B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: 82010
; CURRENT APPLICATION NUMBER: US/10/363,345B
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40723
; SEQ ID NO 20054
; LENGTH: 786
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 20054
US-10-363-345B-20054

Query Match          5.3%; Score 40.6; DB 6; Length 786;
Best Local Similarity 49.8%; Pred. No. 0.21; Mismatches 0; Gaps 0;
Matches 103; Conservative 0; Indels 104;

QY 227 TCATTAAAGCGGAGGAGTCTTATACAAAGAGATTTTATCGATGTGTGGCATATAAATTA 286
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 115 TTAATAACCGGAAATAAATAACCAAAAAACGATCGAAACGAAACGATATAAAT 174

QY 287 AGGTCAATTACAAACAGAACTGAAACGACTTTAATTGAACAAAAATGCTTTCTAAAA 346
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 175 AAAAAAATAAAAAAATAACGAAAAAATAAAAAACGCAAAAAATCGCTACTACGAA 234

QY 347 TCTTAGAAGAGTTTGGAGAAATGATGATGAAGAGTGAAGAAATGTCGATGAAT 406
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 235 AATAATAAAAAAATAAAAAATAACGAAAAATAAAAACTAAAAAATAAAAAACGATAAA 294

QY 407 TATCCATAAAAAACACGACAAATTTAA 433
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 295 AAAAAAATAAAAAATAAAAAAATAAAAAA 321

RESULT 15
US-10-363-345B-31443/c
; Sequence 31443, Application US/10363345B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: 82010
; CURRENT APPLICATION NUMBER: US/10/363,345B
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40723
; SEQ ID NO 31443
; LENGTH: 822
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 31443
US-10-363-345B-31443

Query Match          5.3%; Score 40.6; DB 6; Length 822;
Best Local Similarity 49.8%; Pred. No. 0.21;
Matches 103; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 227 TCATTAAAGCGGAGGAGTCTTATACAAAGAGATTTTATCGATGTGTGGCATATAAATTA 286
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 799 TTAATAAACCGGAAATAAATAACCAAAAAACGATCGAAACGAAACGATATAAATTA 740

QY 287 AGGTCAATTACAAACAGAACTGAAACGACTTTAATTGAACAAACATGCTTTCTAAAA 346
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 739 AAAAAAATAAAAAAATAACGAAAAAATAAAAAACGCAAAAAATCGCTACTACGAA 680

QY 347 TCTTAGAAGAGTTTGGAGAAATGATGATGAAGAGTGAAGAAATGTCGATGAAT 406
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 679 AATAATAAAAAAATAAAAAATAACGAAAAATAAAAACTAAAAAATAAAAAACGATAAA 620

QY 407 TATCCATAAAAAACACGACAAATTTAA 433
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 619 AAAAAAATAAAAAATAAAAAAATAAAAAA 593
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Search completed: August 3, 2006, 10:58:47
Job time : 184 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 3, 2006, 12:03:35 ; Search time 49 Seconds
(without alignments)

451.944 Million cell updates/sec

Title: US-09-732-091-4

Perfect score: 1279

Sequence: 1 MAYKYDRDLFLKQLESSDL.....LRLKTTQANGKKSLQIESI 253

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /EMC Celerra_SIDS3/ptodata/2/iaa/5 COMB.pdp:*
- 2: /EMC Celerra_SIDS3/ptodata/2/iaa/6 COMB.pdp:*
- 3: /EMC Celerra_SIDS3/ptodata/2/iaa/7 COMB.pdp:*
- 4: /EMC Celerra_SIDS3/ptodata/2/iaa/H COMB.pdp:*
- 5: /EMC Celerra_SIDS3/ptodata/2/iaa/PCTUS COMB.pdp:*
- 6: /EMC Celerra_SIDS3/ptodata/2/iaa/RE COMB.pdp:*
- 7: /EMC Celerra_SIDS3/ptodata/2/iaa/backfiles1.pdp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	364	28.5	273	2	US-09-252-991A-29841
2	346.5	27.1	321	2	US-09-252-991A-29840
3	247	19.3	258	2	US-09-489-039A-8852
4	100	7.8	739	2	US-09-543-681A-6437
5	99	7.7	222	2	US-08-944-604-16
6	99	7.7	274	2	US-09-134-001C-5279
7	98	7.7	386	2	US-09-248-796A-17815
8	96	7.5	173	1	US-08-658-639-12
9	96	7.5	173	2	US-08-944-604-12
10	95	7.4	2125	2	US-09-1919-172-29
11	95	7.4	2704	2	US-09-538-092-1260
12	93	7.3	381	2	US-09-710-279-3056
13	91.5	7.2	1086	2	US-09-543-681A-7696
14	90	7.0	216	2	US-09-710-279-2624
15	89.5	7.0	281	2	US-09-198-452A-749
16	89.5	7.0	281	2	US-09-438-185A-707
17	89.5	7.0	543	2	US-09-328-352-5845
18	89.5	7.0	546	2	US-09-345-236B-98
19	89.5	7.0	546	2	US-09-345-236B-121
20	89.5	7.0	560	2	US-09-446-301A-50
21	89.5	7.0	1402	2	US-09-248-796A-14503
22	88.5	6.9	552	2	US-09-446-301A-4
23	88.5	6.9	552	2	US-09-099-932-4
24	88.5	6.9	552	2	US-10-392-970-4
25	88	6.9	488	2	US-09-489-039A-13363
26	87.5	6.8	732	1	US-08-533-669A-18

27	87.5	6.8	732	2	US-09-307-143-4
28	87.5	6.8	732	2	US-09-183-861-18
29	87.5	6.8	732	2	US-09-022-765-18
30	87.5	6.8	732	2	US-09-551-974A-18
31	87.5	6.8	732	2	US-09-565-501A-18
32	87.5	6.8	732	2	US-09-639-206A-18
33	87.5	6.8	732	2	US-09-874-923-18
34	87.5	6.8	732	2	US-08-798-841-18
35	87.5	6.8	752	2	US-09-949-016-7993
36	87.5	6.8	854	2	US-10-094-749-2559
37	87	6.8	280	2	US-09-830-230A-596
38	87	6.8	302	2	US-09-830-230A-595
39	87	6.8	491	2	US-09-029-267-2
40	87	6.8	431	2	US-09-248-796A-22920
41	86.5	6.8	394	2	US-09-134-001C-3626
42	86.5	6.8	420	2	US-09-248-796A-15323
43	86.5	6.8	1042	2	US-09-792-024-106
44	86	6.7	1164	2	US-09-538-092-399
45	85	6.6	183	2	US-09-270-767-33130

ALIGNMENTS

RESULT 1

US-09-252-991A-29841
; Sequence 29841, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29841
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29841

Query Match 28.5%; Score 364; DB 2; Length 273;

Best Local Similarity 35.4%; Pred. No. 1.9e-30;

Matches 85; Conservative 49; Mismatches 88; Indels 18; Gaps 4;

QY 10 EFLKQLESSDLLDLFVLFVFGKDGKRNHKLSTSSIEYKHGDDYAKYAEIAEELQYVG 69

DB 28 QLLERSVNDLBLEPLVEYIL-----KARTESLSKQVDFKRWHPHRYASAILDLRLFG 81

QY 70 SNSPSAFIKGEVLYKEILCDVCKLKNVYKTKTTLLIEQNMLSKILERSLEEMDDDEV 129

DB 82 GNSFANLWRKSGSYTEVVRDVAGKLVKGVSGMELIELEAMVQSILRQALEKSSGDR 141

QY 130 KEMCDEL-----SIKNTDNLNRQALSAAATLTFKMGFKSYQLAVIVANAVAKTILGRG 183

DB 142 RELEELRAGLDKTKWTALLNGSALSG--LVVPAVARMILYRTSTVIVNSMAQQLLGHG 199

QY 184 LSLA-----GNQVLTRTSLFPGVMIITGVWTAIDTAGPAYRVVTIPACIVVATLRUKTQ 239

DB 200 LRSVAVGCTFAGGRAVAALAGVGVAGVWTAIDTAGPAYRVVTIPCVLHIAMLRLKAR 259

RESULT 2

US-09-252-991A-29840
; Sequence 29840, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.

1 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
2 FILE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
3 CURRENT APPLICATION NUMBER: US/09/252.991A
4 PRIOR FILING DATE: 1999-02-18
5 PRIOR APPLICATION NUMBER: US 60/074,788
6 PRIOR FILING DATE: 1998-02-18
7 PRIOR APPLICATION NUMBER: US 60/094,190
8 PRIOR FILING DATE: 1998-07-27
9 NUMBER OF SEQ ID NOS: 33142
10 SEQ ID NO 29840
11 LENGTH: 321
12 TYPE: PRT
13 ORGANISM: Pseudomonas aeruginosa
14 US-09-252-991A-29840

Query Match 27.1%; Score 346.5; DB 2; Length 321;
Best Local Similarity 34.3%; Pred. No. 1.8e-28;
Matches 82; Conservative 42; Mismatches 112; Indels 3; Gaps 3;
QY 1 MAYKYDRDL-EFLKQLESSLDDLDFEVLVFGKDGKRNHKLTSSTIEYKRHGGDDYAKYAE 59
DB 53 MAIHDDADLADVLSSDDIRLLIDVITDNGRISLSSVCRQLSAAKEGVVGEFERG 112
QY 60 RIAEELQYGSNSFASPIK-GEGLVYKEILCDVCDKLKVNKKTTETTLIEQNMLSKILE 118
DB 113 MVAEELMRFGNSLMNLFRCGSGVPYKELSDVASHVGVSKESTGDCARMEMAIITKVE 172
QY 119 RSLEEMDDEEVKEMCDLSIKNTDNLNRQALSATLTLFRMGGPKSYQLAVIVANAVAKT 178
DB 173 QSIGRMEEDKATTFESIGTSYRSGMGPPVAL-AALIASLSASGWTSYGLAAMVASATMSS 231
QY 179 ILGRGLSLAGNQLVTRTSLFPTGPGVMIITGWTATDIAGPAYRVTTIPACIVATILK 237
DB 232 LVGRGVALAGGATIGRGLSLVGTGPGWAIAGIWTAFDLASPAYRVTLPCVIQIGHMRQK 290

RESULT 3
US-09-489-039A-8852
; Sequence 8852, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8852
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8852

Query Match 19.3%; Score 247; DB 2; Length 258;
Best Local Similarity 28.2%; Pred. No. 5.7e-18;
Matches 70; Conservative 48; Mismatches 100; Indels 30; Gaps 6;
QY 3 YKYDRDL-EFLKQLESSLDDLDFEVLVFGKDGKRNHKLTSSTIEYKRHGGDDYAKYAE 59
DB 14 YLEDDDLAFLPECSAEHLAFTRLTHGNGKPRLSSTLLRNETHFLAMEGHPERYRRNQ 73
QY 60 RIAEELQYGSNSFASPIKGEGLVYKEILCDVCDKLKVNKKTTETTLIEQNMLSKILER 119
DB 74 LIAGELQHFGGDSANTLRRHGKPYRAILLDVCKRLKAKVDKQLSTPQIEQOLLAHFLQH 133
QY 120 SLEEMDDEEVKEMCDLSIKN--TDNL-----NRQALSATLTLFRMGGPKSYQLAVIV 171
DB 134 SWNKINAEQKQAFLAANVECRSHELDSLMHLLRHRKLSGEGVTLLL-----DERLTAIL 186

QY 172 ANAVAKTILGRGLSLAGNQLVTRTSLFPTGPGVMIITGWTATDIAGPAYRVTTIPACIV 231
DB 187 RTHAAVSVIGHGLVRGAG-----LGGPLGAALNSVKA---VSGSAYRVTTIPAVLHI 234
QY 232 ATLRLKTQ 239
DB 235 ACLRQMLQ 242
RESULT 4
US-09-543-681A-6437
; Sequence 6437, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 6437
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6437

Query Match 7.8%; Score 100; DB 2; Length 739;
Best Local Similarity 25.6%; Pred. No. 0.15;
Matches 54; Conservative 42; Mismatches 65; Indels 50; Gaps 10;
QY 6 DRDLLEFLKQLESSLDDLDFEVLVFGKDGKRNHKLTSSTIEYKRHGGDDYAKYAE 65
DB 517 DKVSDFLVSLVNSLSDGLKEL---GLD--KKIIEEMKNSIQ-----DKLRKATKILVT 565
QY 66 QYQSGNSFASPIKGEGLVYKEILCDVCDK-----LKVNKKTTETTL--IEQNMLS 114
DB 566 VLFVAATLSPVIGPAM---KQISDAVNKISNQRIQLKVLNDGLEAVLGMKIDIII 622
QY 115 KILERSLEEMDDEEVKEMCDLSIKNTDNLNRQAL-----SAATLTLFRMGGPKSYQLA 168
DB 623 KALEEALKID----KQLAKEISKASIMLNKTVVASKLTNSAATVTNVIYGS----- 671
QY 169 VIVANAVAKTILGRGLSLAGNQLVTRTSLF 199
DB 672 -VIASKIIQ-----SIAGSKKLTAVLDII 694

RESULT 5
US-08-944-604-16
; Sequence 16, Application US/08944604
; Patent No. 6218131
; GENERAL INFORMATION:
; APPLICANT: KEESSE, SUSAN
; APPLICANT: OEAR, ROBERT
; APPLICANT: WU, YING-JYE
; TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESS: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1260
; LENGTH: 2704
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q03001
US-09-538-092-1260

Query Match 7.4%; Score 95; DB 2; Length 2704;
Best Local Similarity 25.4%; Pred No. 3.7;
Matches 46; Conservative 35; Mismatches 62; Indels 38; Gaps 9;

QY 2 AYKDRDLEFLK--QLESDDLDF-----EVLVFGKDGKRNHNEKLTSSIEYKRHGGDDYA 55
DB 1565 SFRDEKELERLQICQKSDHLKEQEKSHQELQLQNIKAENKNDKIQLRNELEKSNECA 1624
QY 56 KYAERIAEL--QYVGSNSFASFIKGG--VLYKEILCDVCDKLV----- 97
DB 1625 EMLKQKVELTRQNNETKLMMQRIQAESENI VLEKQTIQORCEALKIQADGFKDQLRSTN 1684
QY 98 -NYNKTKTTLEONMLSKI--LERSLEEMDD--BEVKEMCDLSI-----KNTDNLNR 146
DB 1685 EHLHKQTKT---EQDFQRKIKLEEDLAKSQNLVSEFFKQCDQNNIIQNTKKEVRNLNA 1741
QY 147 Q 147
DB 1742 E 1742

RESULT 12
US-09-710-279-3056
; Sequence 3056, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3056
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-710-279-3056

Query Match 7.3%; Score 93; DB 2; Length 381;
Best Local Similarity 24.0%; Pred No. 0.31;
Matches 53; Conservative 30; Mismatches 74; Indels 64; Gaps 10;

QY 4 KYDRDLEFLKQLESDDLDFEVLVFGKDGKRNHNEKLTSSIEYKRHGGDDYAK--YAPRI 61
DB 19 KVDHNEIYLKTKDKSFDMDTI-----SNLYNSKFTIGYGFPERYQQDLLNLQIERT 71
QY 62 ABEQYVGSN-SFASFIKGGVLYKEILCDVCDKLVKNYKKTETTLI---EQNMLSKIL 117

DB 72 QNVLQFNSDPNIQNF-----DEML-----NKLQKVLISASESGTKKIV 112
QY 118 ERSLEEMDDDEEVKEMCDLSIKNTDNLNRQALSAATITLFFMGGFKSYQLAVIVAN-AVA 176
DB 113 DHFVEELYSEEPKQKIN-----ICGLVDYKIGGLEPTQLIVIAARPSVG 157
QY 177 KT-----ILGRG-----LSLAGNOVLTRTSLFLTG 201
DB 158 KTGCFALNMMLNIASOGYKTSFFSLETGTGVSVLKRLMSAETG 198

RESULT 13
US-09-543-681A-7696
; Sequence 7696, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709,1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7696
; LENGTH: 1086
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7696

Query Match 7.2%; Score 91.5; DB 2; Length 1086;
Best Local Similarity 19.5%; Pred No. 2.2;
Matches 43; Conservative 38; Mismatches 73; Indels 67; Gaps 9;

QY 3 KYDRDLEFLKQLESDDLDFEVLVFGKDGKRNHNEKLTSSIEYKRHGGDDYAKYAERIA 62
DB 786 FAYDRGKE-IEQMQ-----FETTLIGK--SRAEQEKLNA----- 816
QY 63 BELQYVGSNSFASFIKGGVLYKEILCDVCDKLVKNYKKTETTLIIONMLSKILERSLE 122
DB 817 -----LRQIDVLYQQASVDLGEKELVNLQRNVLT--KQIIEELRKREAM 860
QY 123 EMD-----DEEVKEMCDLSIKNTDNLNRQALSAATITLFFMGGFKSYQLAVI 170
DB 861 KGDPMAGLKQGLSDFSESAMDVNVNVRTTNALNNMSDALADFALTGKGSFKDFANAVI 920
QY 171 --VANAVAKTILGRGLSLAGNOVLTRTSLFLTGPGVGMIIITG 209
DB 921 SDITRMVMKMLIFKAIEAGG-----QAMGF---DMGWMMSKG 953

RESULT 14
US-09-710-279-2624
; Sequence 2624, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2624
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic

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OM protein - protein search, using sw model

Run on: August 3, 2006, 12:15:20 ; Search time 176 Seconds
(without alignments)
665.871 Million cell updates/sec

Title: US-09-732-091-4
Perfect score: 1279
Sequence: 1 MAYKYDRDLEFLKQLESSDL.....LRLKTOOANGDKKSLQIESI 253

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1279	100.0	253	3	US-09-732-091-4
2	1279	100.0	253	4	US-10-433-970-4
3	1279	100.0	265	3	US-09-732-091-44
4	1279	100.0	265	4	US-10-433-970-44
5	1270	99.3	253	4	US-10-335-977-9162
6	1270	99.3	256	4	US-10-335-977-9163
7	1270	99.3	256	4	US-10-335-977-9164
8	1264	98.8	253	4	US-10-433-970-48
9	1264	98.8	265	4	US-10-433-970-45
10	722	56.5	248	4	US-10-335-977-7699
11	716	56.0	237	4	US-10-335-977-7698
12	472.5	36.9	155	3	US-09-882-227-414
13	252	19.7	49	3	US-09-732-091-20
14	252	19.7	49	4	US-10-433-970-20
15	198	15.5	38	3	US-09-732-091-17
16	198	15.5	38	4	US-10-433-970-17
17	194	15.2	41	3	US-09-732-091-19
18	194	15.2	41	4	US-10-433-970-19
19	152	11.9	30	3	US-09-732-091-18
20	152	11.9	30	4	US-10-433-970-18
21	150	11.7	30	3	US-09-732-091-16
22	150	11.7	30	4	US-10-433-970-16
23	99	7.7	274	4	US-10-724-972A-5261
24	98.5	7.7	1009	4	US-10-282-122A-43832
25	97.5	7.6	815	4	US-10-437-963-191043
26	97	7.6	916	4	US-10-282-122A-76490
27	96.5	7.5	373	4	US-10-369-493-42

28	96.5	7.5	701	4	US-10-032-585-7400	Sequence 7400, Ap
29	96.5	7.5	1102	4	US-10-156-761-14395	Sequence 14395, A
30	95	7.4	517	4	US-10-282-122A-54543	Sequence 54543, A
31	95	7.4	2125	3	US-09-919-172-29	Sequence 29, Appl
32	95	7.4	2125	5	US-10-752-986-29	Sequence 29, Appl
33	95	7.4	2649	4	US-10-205-219-169	Sequence 169, App
34	95	7.4	2649	4	US-10-341-434-220	Sequence 220, App
35	95	7.4	2649	4	US-10-341-434-230	Sequence 230, App
36	95	7.4	2649	5	US-10-756-149-4786	Sequence 4786, Ap
37	95	7.4	2649	5	US-10-287-436A-378	Sequence 378, App
38	95	7.4	2649	5	US-10-287-436A-1079	Sequence 1079, Ap
39	93.5	7.3	1196	4	US-10-282-122A-52737	Sequence 52737, A
40	93	7.3	381	5	US-10-793-626-3056	Sequence 3056, Ap
41	93	7.3	610	4	US-10-282-122A-47217	Sequence 47217, A
42	92.5	7.2	430	4	US-10-369-493-5229	Sequence 5229, Ap
43	92.5	7.2	996	3	US-09-815-242-5251	Sequence 5251, Ap
44	92.5	7.2	1009	3	US-09-815-242-12141	Sequence 12141, A
45	92	7.2	380	5	US-10-732-923-3177	Sequence 3177, Ap

ALIGNMENTS

RESULT 1
US-09-732-091-4
; Sequence 4, Application US/09732091
; Patent No. US20020107368A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Jing-Hui
; APPLICANT: Walker, Richard I.
; APPLICANT: Jackson, W. James
; TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses
; TITLE OF INVENTION: thereof
; FILE REFERENCE: 7969-088
; CURRENT APPLICATION NUMBER: US/09/732,091
; CURRENT FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Helicobacter sp.
US-09-732-091-4

Query Match	100.0%;	Score	1279;	DB	3;	Length	253;
Best Local Similarity	100.0%;	Pred. No.	3.7e-108;	Mismatches	0;	Indels	0;
Matches	253;	Conservative	0;				
QY	1	MAYKYDRDLEFLKQLESSDL	LDLFEVLVFGKDGKXKHNKLTSSIEYKRGHDDYAKYAE	60			
Db	1	MAYKYDRDLEFLKQLESSDL	LDLFEVLVFGKDGKXKHNKLTSSIEYKRGHDDYAKYAE	60			
QY	61	IAEELQYGSNSFASFIKGEVLYKEILCDVCDKLVKNYNNKTTTLLIEQNMLSKILERS	120				
Db	61	IAEELQYGSNSFASFIKGEVLYKEILCDVCDKLVKNYNNKTTTLLIEQNMLSKILERS	120				
QY	121	LEEMDEEVEKMCDELISKNTDNLNRQALSAATLTLFKMGFKSYQLAVIVANAVAKTIL	180				
Db	121	LEEMDEEVEKMCDELISKNTDNLNRQALSAATLTLFKMGFKSYQLAVIVANAVAKTIL	180				
QY	181	GRGLSLAGNQVLTRTLFLTGPVGMITGTWTAIDIAGPAYRVTIIPACIVATLRLKTOQ	240				
Db	181	GRGLSLAGNQVLTRTLFLTGPVGMITGTWTAIDIAGPAYRVTIIPACIVATLRLKTOQ	240				
QY	241	ANGDKKSLQIESI	253				
Db	241	ANGDKKSLQIESI	253				

RESULT 2
US-10-433-970-4
; Sequence 4, Application US/10433970
; Publication No. US20040138415A1

```
; GENERAL INFORMATION:
; APPLICANT: Tian, Jing-Hui
; APPLICANT: Walker, Richard
; APPLICANT: Jackson, James
; TITLE OF INVENTION: HELICOBACTER PROTEINS, GENE SEQUENCES AND USES
; FILE REFERENCE: 7969-091-999
; CURRENT APPLICATION NUMBER: US/10/433,970
; CURRENT FILING DATE: 2003-06-06
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Helicobacter sp.
US-10-433-970-4
Query Match      100.0%; Score 1279; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 3.7e-108;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAYKYDRDLFLKQLESSDLDLFEVLVFGKDGKGRHNEKLTSSIEYKRHGDDYAKYAE 60
DB 1 MAYKYDRDLFLKQLESSDLDLFEVLVFGKDGKGRHNEKLTSSIEYKRHGDDYAKYAE 60
QY 61 IAEELQYYSNSFASFIKGEGVLYKEILCDVCDKLVKNVKNKTTTTLIEQNMLSKILERS 120
DB 61 IAEELQYYSNSFASFIKGEGVLYKEILCDVCDKLVKNVKNKTTTTLIEQNMLSKILERS 120
QY 121 LEEMDDEEVKEMCDELSIKNTDNLNRQALSAAATLTLFKMGGFKSYQLAVIVANAVAKTIL 180
DB 121 LEEMDDEEVKEMCDELSIKNTDNLNRQALSAAATLTLFKMGGFKSYQLAVIVANAVAKTIL 180
QY 121 IAEELQYYSNSFASFIKGEGVLYKEILCDVCDKLVKNVKNKTTTTLIEQNMLSKILERS 120
DB 121 IAEELQYYSNSFASFIKGEGVLYKEILCDVCDKLVKNVKNKTTTTLIEQNMLSKILERS 120
QY 181 GRGLSLAGNOVLTRTSLFTGPGVWIIITGVWTAIDAGPAYRVITIPACIVVATLRLKTOQ 240
DB 181 GRGLSLAGNOVLTRTSLFTGPGVWIIITGVWTAIDAGPAYRVITIPACIVVATLRLKTOQ 240
QY 193 GRGLSLAGNOVLTRTSLFTGPGVWIIITGVWTAIDAGPAYRVITIPACIVVATLRLKTOQ 252
DB 193 GRGLSLAGNOVLTRTSLFTGPGVWIIITGVWTAIDAGPAYRVITIPACIVVATLRLKTOQ 252
QY 241 ANGDKKSLQIESI 253
DB 241 ANGDKKSLQIESI 253
; RESULT 4
US-10-433-970-44
; Sequence 44, Application US/10433970
; Publication No. US20040138415A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Jing-Hui
; APPLICANT: Walker, Richard
; APPLICANT: Jackson, James
; TITLE OF INVENTION: HELICOBACTER PROTEINS, GENE SEQUENCES AND USES
; FILE REFERENCE: 7969-091-999
; CURRENT APPLICATION NUMBER: US/10/433,970
; CURRENT FILING DATE: 2003-06-06
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Helicobacter sp.
US-10-433-970-44
Query Match      100.0%; Score 1279; DB 4; Length 265;
Best Local Similarity 100.0%; Pred. No. 4e-108;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAYKYDRDLFLKQLESSDLDLFEVLVFGKDGKGRHNEKLTSSIEYKRHGDDYAKYAE 60
DB 13 MAYKYDRDLFLKQLESSDLDLFEVLVFGKDGKGRHNEKLTSSIEYKRHGDDYAKYAE 72
QY 61 IAEELQYYSNSFASFIKGEGVLYKEILCDVCDKLVKNVKNKTTTTLIEQNMLSKILERS 120
DB 73 IAEELQYYSNSFASFIKGEGVLYKEILCDVCDKLVKNVKNKTTTTLIEQNMLSKILERS 132
QY 121 LEEMDDEEVKEMCDELSIKNTDNLNRQALSAAATLTLFKMGGFKSYQLAVIVANAVAKTIL 180
DB 133 LEEMDDEEVKEMCDELSIKNTDNLNRQALSAAATLTLFKMGGFKSYQLAVIVANAVAKTIL 192
QY 181 GRGLSLAGNOVLTRTSLFTGPGVWIIITGVWTAIDAGPAYRVITIPACIVVATLRLKTOQ 240
DB 193 GRGLSLAGNOVLTRTSLFTGPGVWIIITGVWTAIDAGPAYRVITIPACIVVATLRLKTOQ 252
QY 241 ANGDKKSLQIESI 253
DB 253 ANGDKKSLQIESI 265
; RESULT 5
US-10-335-977-9162
; Sequence 9162, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO HELICOBACTER PYLORI FOR
```

```

DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 9162:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...253
SEQUENCE DESCRIPTION: SEQ ID NO: 9162:
US-10-335-977-9162

```

Query Match	99.3%	Score 1270;	DB 4;	Length 253;
Best Local Similarity	99.2%;	Pred. No. 2.5e-107;		
Matches 251;	Conservative 1;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	MAYKYDRDLLEFLKQLSSDLLDLFEVLVRGKDGKEKHNEKLTSSIEYKRHHGDDYAKYAER	60	
Db	1	MAYKYDRDLLEFLKQLSSDLLDLFEVLVRGKDGKEKHNEKLTSSIEYKRHHGDDYAKYAER	60	
Qy	61	IABELOYGSGNSPASTPIKGEGLVYKEILCDVCKLVNKNKTTETTLIEQNMLSKILERS	120	
Db	61	IABELOYGSGNSPASTPIKGEGLVYKEILCDVCKLVNKNKTTETTLIEQNMLSKILERS	120	
Qy	121	LREMDDEEVKEMCDELSIKNTDNLNQALSAATLTLFKMGGFYSQYLAIVANAVAKTIL	180	
Db	121	LREMDDEEVKEMCDELSIKNTDNLNQALSAATLTLFKMGGFYSQYLAIVANAVAKTIL	180	
Qy	181	GRGLSLAGNQVLTRTLTSFLTGPVGWIIITGYWTAIDIAGPAYRYVTIPACIVVATLRUKTQQ	240	
Db	181	GRGLSLAGNQVLTRTLTSFLTGPVGWIIITGYWTAIDIAGPAYRYVTIPACIVVATLRUKTQQ	240	
Qy	241	ANGDKKSQIQIESI	253	
Db	241	ANEDKKSQIQIESV	253	

RESULT 6
US-10-335-977-9163
; Sequence 9163, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al

```

1 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
2
3 RELATING TO HELICOBACTER PYLORI FOR
4 DIAGNOSTICS AND THERAPEUTICS
5
6 NUMBER OF SEQUENCES: 10031
7
8 CORRESPONDENCE ADDRESS:
9
10 ADDRESSEE: LAHIVE & COCKFIELD
11
12 STREET: 28 State Street
13
14 CITY: Boston
15
16 STATE: Massachusetts
17
18 COUNTRY: USA
19
20 ZIP: 02109-1875
21
22 COMPUTER READABLE FORM:
23
24 MEDIUM TYPE: CD-ROM ISO9660
25
26 COMPUTER: IBM PC Compatible
27
28 OPERATING SYSTEM: Windows NT 4.0
29
30 SOFTWARE: UNIX
31
32 CURRENT APPLICATION DATA:
33
34 FILING APPLICATION NUMBER: US/10/335,977
35
36 FILING DATE: 30-Dec-2002
37
38 PRIOR APPLICATION DATA:
39
40 APPLICATION NUMBER: 08/993,002
41
42 FILING DATE: 17-DEC-1997
43
44 ATTORNEY/AGENT INFORMATION:
45
46 NAME: Mandragouras, Amy E.
47
48 REGISTRATION NUMBER: 36,207
49
50 REFERENCE/DOCKET NUMBER: GTN-018
51
52 TELECOMMUNICATION INFORMATION:
53
54 TELEPHONE: (617)227-7400
55
56 TELEFAX: (617)742-4214
57
58 INFORMATION FOR SEQ ID NO: 9163:
59
60 SEQUENCE CHARACTERISTICS:
61
62 LENGTH: 253 amino acids
63
64 TYPE: amino acid
65
66 TOPOLOGY: linear
67
68 MOLECULE TYPE: protein
69
70 HYPOTHETICAL: YES
71
72 ORIGINAL SOURCE:
73
74 ORGANISM: Helicobacter pylori
75
76 FEATURE:
77
78 NAME/KEY: misc feature
79
80 LOCATION: (B) LOCATION 1...253
81
82 SEQUENCE DESCRIPTION: SEQ ID NO: 9163:
83
84 US-10-335-977-9163

```

Query Match	99.3%;	Score 1270;	DB 4;	Length 253;
Best Local Similarity	99.2%;	Pred. No. 2.5e-107;		
Matches 251;	Conservative 1;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	MAYKYDRDLFLKQLRSSDLLDLFEVLVFGKDGKGRHNEKLTSSIEYKRHGDDYAKYAER	60	
Db	1	MAYKYDRDLFLKQLRSSDLLDLFEVLVFGKDGKGRHNEKLTSSIEYKRHGDDYAKYAER	60	
Qy	61	IASELOYGSGNSFASFTKGGVLYKETLDCVCKLKVYNNKKTETTTLIEQNMLSKILLERS	120	
Db	61	IASELOYGSGNSFASFTKGGVLYKETLDCVCKLKVYNNKKTETTTLIEQNMLSKILLERS	120	
Qy	121	LEEMDDEEVKEMCDELISKNTDNLNQALSAATLTLPKMGGFKSYQLAVIVANAVAKTIL	180	
Db	121	LEEMDDEEVKEMCDELISKNTDNLNQALSAATLTLPKMGGFKSYQLAVIVANAVAKTIL	180	
Qy	181	GRGLSLAGNQVLRTRLTSFLTPGPGWIIITGVWTAIDIAGPAYRVTIPACIVVATLRKLTQQ	240	
Db	181	GRGLSLAGNQVLRTRLTSFLTPGPGWIIITGVWTAIDIAGPAYRVTIPACIVVATLRKLTQQ	240	
Qy	241	ANGDKKSLQIESI	253	
Db	241	ANEDKKSLQIESV	253	

RESULT 7
US-10-335-977-9164
; Sequence 9164, Application US/10335977
; Publication No. US20040052799A1

GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 9164:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...256
SEQUENCE DESCRIPTION: SEQ ID NO: 9164:
US-10-335-977-9164

Query Match 99.3%; Score 1270; DB 4; Length 256;
Best Local Similarity 99.2%; Pred. No. 2.5e-107;
Matches 251; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAYKYDRDLFLKQLESDLLDLFEVLVFGDKGKRRHNEKLTSSIEYKRHGGDDYAKYAE 60
DB 4 MAYKYDRDLFLKQLESDLLDLFEVLVFGDKGKRRHNEKLTSSIEYKRHGGDDYAKYAE 63
QY 61 IAELOYGSGNSFASFIKGEGLVYKEILCDVCDKLVNKKTTTTLIEQNMLSKILERS 120
DB 64 IAELOYGSGNSFASFIKGEGLVYKEILCDVCDKLVNKKTTTTLIEQNMLSKILERS 123
QY 121 LEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLFLFMGGFKSYQLAVIVANAVAKTIL 180
DB 124 LEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLFLFMGGFKSYQLAVIVANAVAKTIL 183
QY 181 GRGLSLAGNOVLTRLTSLFTGPGVGIITGVWTAIDAGPAYRVTTIPACIVVATLRLKTTQ 240
DB 184 GRGLSLAGNOVLTRLTSLFTGPGVGIITGVWTAIDAGPAYRVTTIPACIVVATLRLKTTQ 243
QY 241 ANGDKKSLQIESI 253
DB 244 ANEDKKSLQIESV 256
RESULT 8
US-10-433-970-48

Sequence 48, Application US/10433970
Publication No. US20040138415A1
GENERAL INFORMATION:
APPLICANT: Tian, Jing-Hui
APPLICANT: Walker, Richard
APPLICANT: Jackson, James
TITLE OF INVENTION: HELICOBACTER PROTEINS, GENE SEQUENCES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 7969-091-999
CURRENT APPLICATION NUMBER: US/10/433,970
CURRENT FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: 09/732,091
PRIOR FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 48
LENGTH: 253
TYPE: PRT
ORGANISM: Helicobacter sp.
US-10-433-970-48

Query Match 98.8%; Score 1264; DB 4; Length 253;
Best Local Similarity 98.8%; Pred. No. 8.7e-107;
Matches 250; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAYKYDRDLFLKQLESDLLDLFEVLVFGDKGKRRHNEKLTSSIEYKRHGGDDYAKYAE 60
DB 1 MAYKYDRDLFLKQLESDLLDLFEVLVFGDKGKRRHNEKLTSSIEYKRHGGDDYAKYAE 60
QY 61 IAELOYGSGNSFASFIKGEGLVYKEILCDVCDKLVNKKTTTTLIEQNMLSKILERS 120
DB 61 IAELOYGSGNSFASFIKGEGLVYKEILCDVCDKLVNKKTTTTLIEQNMLSKILERS 120
QY 121 LEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLFLFMGGFKSYQLAVIVANAVAKTIL 180
DB 121 LEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLFLFMGGFKSYQLAVIVANAVAKTIL 180
QY 181 GRGLSLAGNOVLTRLTSLFTGPGVGIITGVWTAIDAGPAYRVTTIPACIVVATLRLKTTQ 240
DB 181 GRGLSLAGNOVLTRLTSLFTGPGVGIITGVWTAIDAGPAYRVTTIPACIVVATLRLKTTQ 240
QY 241 ANGDKKSLQIESI 253
DB 241 ANEDKKSLQIESI 253

RESULT 9
US-10-433-970-46
Sequence 46, Application US/10433970
Publication No. US20040138415A1
GENERAL INFORMATION:
APPLICANT: Tian, Jing-Hui
APPLICANT: Walker, Richard
APPLICANT: Jackson, James
TITLE OF INVENTION: HELICOBACTER PROTEINS, GENE SEQUENCES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 7969-091-999
CURRENT APPLICATION NUMBER: US/10/433,970
CURRENT FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: 09/732,091
PRIOR FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 46
LENGTH: 265
TYPE: PRT
ORGANISM: Helicobacter sp.
US-10-433-970-46

Query Match 98.8%; Score 1264; DB 4; Length 265;
Best Local Similarity 98.8%; Pred. No. 9.3e-107;
Matches 250; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAYKYDRDLFLKQLBSSDLLDLFEVLVFGKDGKRNHNEKLTSSIEYKRGHDDYAKYAE 60
DB 13 MAYKYDRDLFLKQLBSSDLLDLFEVLVFGKDGKRNHNEKLTSSIEYKRGHDDYAKYAE 72
QY 61 IAEELQYCGSNFASPIKGEVLYKEILCDVCDKLVNKNKTTETTLIEQNMLSKILERS 120
DB 73 IAEELQYCGSNFASPIKGEVLYKEILCDVCDKLVNKNKTTETTLIEQNMLSKILERS 132
QY 121 LBEEMDDEEYKEMCDELSIKNTDNLNRQALSAAATLTLFKMGGFKSYQLAVIVANAVAKTIL 180
DB 133 LBEEMDDEEYKEMCDELSIKNTDNLNRQALSAAATLTLFKMGGFKSYQLAVIVANAVAKTIL 192
QY 181 GRGLSLAGNQLVTRTSLFTGPVGMIIITGVWTAIDAGPAYRTIPACIVVATLRKTOQ 240
DB 193 GRGLSLAGNQLVTRTSLFTGPVGMIIITGVWTAIDAGPAYRTIPACIVVATLRKTOQ 252
QY 241 ANGDKKSQIESI 253
DB 253 ANEDKKSQIESI 265

RESULT 10

US-10-335-977-7699
; Sequence 7699, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335,977
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 7699:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...248
; SEQUENCE DESCRIPTION: SEQ ID NO: 7699:

Query Match 56.5%; Score 722; DB 4; Length 248;
Best Local Similarity 60.3%; Pred. No. 2.3e-57;

Matches 141; Conservative 36; Mismatches 53; Indels 4; Gaps 2;
QY 8 DLEFLKQLBSSDLLDLFEVLVFGKDGKRNHNEKLTSSIEYKRGHDDYAKYAEELQY 67
DB 11 DLEFLKQLBSSDLLDLFEVLVFGKDGKRNHNEKLTSSIEYKRGHDDYAKYAEELQY 70
QY 68 YGNSNFASPIKGEVLYKEILCDVCDKLVNKNKTTETTLIEQNMLSKILERSLEEMDDE 127
DB 71 YGNSNFASPIKGEVLYKEILCDVCDKLVNKNKTTETTLIEQNMLSKILERSLEEMDDE 130
QY 128 EYKEMCDELSIKNTDNLNRQALSAAATLTLFKMGGFKSYQLAVIVANAVAKTILGRGL 184
DB 131 EYKEMCDELSIKNTDNLNRQALSAAATLTLFKMGGFKSYQLAVIVANAVAKTILGRGL 190
QY 185 -SLAGNQLVTRTSLFTGPVGMIIITGVWTAIDAGPAYRTIPACIVVATLRK 237
DB 191 SSVGVKVALKTTDLILAGPIGWITGALVINSINLAGPAYRTIPACIVVATLRK 244

RESULT 11

US-10-335-977-7698
; Sequence 7698, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335,977
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 7698:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...237
; SEQUENCE DESCRIPTION: SEQ ID NO: 7698:

US-10-335-977-7698
Query Match 56.0%; Score 716; DB 4; Length 237;
Best Local Similarity 60.1%; Pred. No. 7.7e-57;
Matches 140; Conservative 36; Mismatches 53; Indels 4; Gaps 2;

QY 9 LEFLKQLESDLLDLFEVLVFGKDGKRRHNEKLTSSIEYKRRHGGDDYAKYAEIRIAEELQYY 68
Db 1 LEFLKRLSSDLKDLFDALVYDEGDTLRMEELTSLTEYQRYGHDYAKYPRRIAEELQRY 60
QY 69 GSNFSASFIRKGBGVLYKEILCDVCDLKVNYNKKTETTLTLEQNMLSKILERSLEEMDDE 128
Db 61 GSNFSANFFRDEGVLYKEILCDACDHLDDINYNERSATSLIEQNMLSKLLKDSLEKMSGRE 120
QY 129 VKEMCDLSIKNTDNL---NRQALSAATLTLFRMGPKSYOLAVIVANAVAKTTLGRCL- 184
Db 121 IKELCDGLGPNFDKVGNGKQVLIAVSLTLFRAGGSHSYALAVADAMVRQTLGHGLS 180
QY 185 SLAGNOVLTTLSLFTGPGVMIITGVWTAIDAGPAYRVVTIPACIVVATLRK 237
Db 181 SVGKVALKKTLDILAGPIGWITGALVSNLAGPAYRVVTPACVIVATLRKK 233

RESULT 12
US-09-882-227-414
; Sequence 414, Application US/09882227
; Publication No. US20030158396A1
; GENERAL INFORMATION:
; APPLICANT: Kleanthous, Harold
; APPLICANT: Al-Garawi, Anas
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean-Francois
; APPLICANT: Oomen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding No. US20030158396A1 Helicobacter Polypeptides in the
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 06132/047002
; CURRENT APPLICATION NUMBER: US/09/882,227
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 08/902,615
; PRIOR FILING DATE: 1997-07-29
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 414
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-882-227-414

Query Match 36.9%; Score 472.5; DB 3; Length 155;
Best Local Similarity 63.3%; Pred. No. 7e-35; Indels 3; Gaps 1;
Matches 93; Conservative 22; Mismatches 29
QY 38 NEKLTSSIEYKRRHGGDDYAKYAEIRIAEELQYYGNSFSFIRKGBGVLYKEILCDVCDLKLV 97
Db 2 NEDLTNSTEYKRYGHDYAKYPRRIAEELQRYGNSFANFFRDEGVLYKEILCDACDHLKV 61
QY 98 NNNKKTETTLIEQNMLSKILERSLEEMDDEEVKEMCDLSIKNTDNL---NRQALSAATL 154
Db 62 NYNEESATSLIEQNMLSKLLKDSLEKMSRREIKELCNELGWNTIDKVGNGKQVLIASTL 121
QY 155 TLFKMGKPKSYOLAVIVANAVAKTILG 181
Db 122 TLFKAGGSHSYALAVSADAMVRQTLG 148

RESULT 13
US-09-732-091-20
; Sequence 20, Application US/09732091
; Patent No. US20020107368A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Jing-Hui
; APPLICANT: Walker, Richard I.
; APPLICANT: Jackson, W. James
; TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses
; TITLE OF INVENTION: thereof
; FILE REFERENCE: 7969-088
; CURRENT APPLICATION NUMBER: US/09/732,091
; CURRENT FILING DATE: 2000-12-07

; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Helicobacter sp.
US-09-732-091-20
Query Match 19.7%; Score 252; DB 3; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.9e-15; Indels 0; Gaps 0;
Matches 49; Conservative 0; Mismatches 0
QY 203 VGMIIITGVWTAIDAGPAYRVVTIPACIVVATLRKLTQQANGKKSLOIE 251
Db 1 VGMIIITGVWTAIDAGPAYRVVTIPACIVVATLRKLTQQANGKKSLOIE 49

RESULT 14
US-10-433-970-20
; Sequence 20, Application US/10433970
; Publication No. US20040138415A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Jing-Hui
; APPLICANT: Walker, Richard
; APPLICANT: Jackson, James
; TITLE OF INVENTION: HELICOBACTER PROTEINS, GENE SEQUENCES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 7969-091-999
; CURRENT APPLICATION NUMBER: US/10/433,970
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 09/732,091
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Helicobacter sp.
US-10-433-970-20

Query Match 19.7%; Score 252; DB 4; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.9e-15; Indels 0; Gaps 0;
Matches 49; Conservative 0; Mismatches 0
QY 203 VGMIIITGVWTAIDAGPAYRVVTIPACIVVATLRKLTQQANGKKSLOIE 251
Db 1 VGMIIITGVWTAIDAGPAYRVVTIPACIVVATLRKLTQQANGKKSLOIE 49

RESULT 15
US-09-732-091-17
; Sequence 17, Application US/09732091
; Patent No. US20020107368A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Jing-Hui
; APPLICANT: Walker, Richard I.
; APPLICANT: Jackson, W. James
; TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses
; TITLE OF INVENTION: thereof
; FILE REFERENCE: 7969-088
; CURRENT APPLICATION NUMBER: US/09/732,091
; CURRENT FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Helicobacter sp.
US-09-732-091-17

Query Match 15.5%; Score 198; DB 3; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.1e-10; Indels 0; Gaps 0;
Matches 38; Conservative 0; Mismatches 0

Qy 53 DYAKYAEIRIAEELQYYGNSPFASFKGEVLYKEILCD 90
 | | | | | | | | | | | | | | | | | | | | | |
Dd 1 DYAKYAEIRIAEELQYYGNSPFASFKGEVLYKEILCD 38

Search completed: August 3, 2006, 12:18:40
Job time : 177 secs

GenCore version 5.1.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 3, 2006, 12:15:50 ; Search time 31 Seconds
(without alignments)
546.105 Million cell updates/sec

Title: US-09-732-091-4
Perfect score: 1279
Sequence: 1 MAYKDRDLFLKQLLESSDL.....LRLKTOQANGKKSQIESI 253

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 236815 seqs, 66914042 residues

Total number of hits satisfying chosen parameters: 236815

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB pep.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	98	7.7	413	6	US-10-471-571A-1526	Sequence 1526, Ap
2	96.5	7.5	282	6	US-10-449-902-33147	Sequence 33147, A
3	94	7.3	576	6	US-10-531-357A-2	Sequence 2, Appl
4	91.5	7.2	187	6	US-10-953-349-4873	Sequence 4873, Ap
5	91.5	7.2	187	7	US-11-056-355B-43591	Sequence 43591, A
6	91.5	7.2	187	7	US-11-056-355B-98508	Sequence 98508, A
7	91.5	7.2	187	7	US-11-056-355B-109747	Sequence 109747, A
8	91.5	7.2	241	6	US-10-953-349-4872	Sequence 4872, Ap
9	91.5	7.2	241	7	US-11-056-355B-43590	Sequence 43590, A
10	91.5	7.2	241	7	US-11-056-355B-98507	Sequence 98507, A
11	91.5	7.2	241	7	US-11-056-355B-109746	Sequence 109746, A
12	91.5	7.2	257	7	US-11-056-355B-98506	Sequence 98506, A
13	91.5	7.2	257	7	US-11-056-355B-109745	Sequence 109745, A
14	91.5	7.2	261	6	US-10-953-349-4871	Sequence 4871, Ap
15	91.5	7.2	261	7	US-11-056-355B-43589	Sequence 43589, A
16	87.5	6.8	462	7	US-11-056-355B-83110	Sequence 83110, A
17	87.5	6.8	489	7	US-11-056-355B-83109	Sequence 83109, A
18	87.5	6.8	732	7	US-11-105-233-171	Sequence 171, App
19	87	6.8	247	6	US-10-471-571A-972	Sequence 972, App
20	87	6.8	402	6	US-10-471-571A-2786	Sequence 2786, Ap
21	87	6.8	1182	7	US-11-056-355B-48406	Sequence 48406, A
22	87	6.8	1200	7	US-11-056-355B-48405	Sequence 48405, A
23	87	6.8	1294	7	US-11-056-355B-48404	Sequence 48404, A
24	85.5	6.7	457	7	US-11-330-403-3995	Sequence 3995, Ap
25	84.5	6.6	454	7	US-11-056-355B-80275	Sequence 80275, A

ALIGNMENTS

RESULT 1

US-10-471-571A-1526 483 7 US-11-056-355B-80274 Sequence 80274, A
; Sequence 1526, Application US/10471571A Sequence 23, Appl
; Publication No. US20060115490A1 Sequence 354, App
; GENERAL INFORMATION: Sequence 9557, Ap
; APPLICANT: CHIRON SPA Sequence 8304, Ap
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS Sequence 48918, A
; FILE REFERENCE: P02692WO US/10/471,571A Sequence 48917, A
; CURRENT APPLICATION NUMBER: 2003-09-12 Sequence 14767, A
; PRIOR APPLICATION NUMBER: GB-0107661.1 Sequence 2242, Ap
; PRIOR FILING DATE: 2001-03-27 Sequence 117364, A
; NUMBER OF SEQ ID NOS: 5642 Sequence 38278, A
; SOFTWARE: Seqwin99, version 1.03 Sequence 106124, A
; SEQ ID NO 1526 Sequence 117363, A
; LENGTH: 413 Sequence 106123, A
; TYPE: PRT Sequence 2240, Ap
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(413)
; OTHER INFORMATION: replicative DNA helicase
US-10-471-571A-1526

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Best Local Similarity	24.0%;	Pred. No. 2;		
Matches	53;	Conservative 26;	Mismatches 78;	Indels 64;
Gaps	8;			
QY	4	KYDRLEFLKQLLESSDLDL-----LFEVLVFGKDGKGRHNEKLTSTSIYKRRHGDYAKY	57	
Db	50	KIDHQEYLYKATKDEFLDADTTIKLYNSDFICYGFFERYQOELLESYQLN-----KA	102	
QY	58	ABRIAELOYGNSNFASPIKGEVLYKEILCDVKLVNKNKTETTTLEIONMLSKIL	117	
Db	103	NELVTEFKQPTNQNFNNLI-----DELKDLKTTITNKEDGT-----KKFV	143	
QY	118	ERSLEHMDDEEVKEMCDSELSIKNTDNLNQALSAATILTFKMGGFKSYQLAVIVAN-AVA	176	
Db	144	BEFVBEEL-----YSDSPKQIKTKGYKMDYKIGGLEPSQLIVIAARPSVG	188	
QY	177	KT-----TLGRG-----LSLAGNQVLRTRLSFLTG	201	
Db	189	KTGFALNMLNIAQNGYKTSFFSLETTGTSLVKRLMSTTIG	229	

RESULT 2

US-10-449-902-33147
; Sequence 33147, Application US/10449902

QY 73 FASFIKGEVLYKEILCDVCDKLKVNNKKTETTLIEQNMLSKILERSLEEMDDEEVKEM 132
Db 169 WKSLEETE-----KKVYLDKAAELKAEYKNSLESNDADAEDEE--EKQSDDDVDAEEKQV 222

QY 133 CD-----ELSIKNTDNLNQA 148
Db 223 DDDDEVEEKEVENTDDDKKEA 243

RESULT 13
US-11-056-355B-109745
; Sequence 109745, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 109745
; LENGTH: 257
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(257)
; OTHER INFORMATION: Ceres Seq. ID no. 13600904
US-11-056-355B-109745

Query Match 7.2%; Score 91.5; DB 7; Length 257;
Best Local Similarity 23.4%; Pred. No. 3.7;
Matches 33; Conservative 25; Mismatches 44; Indels 39; Gaps 5;

QY 34 EKRHNEKLTSSIEYK-----RHGDDYAKYABRIAEELQYVGSNS 72
Db 116 KKTNDKSSSTSNKPKPLTAFFIWMDFRKTFSKSEHNGSLAKDAKI-----GGEK 168

QY 73 FASFIKGEVLYKEILCDVCDKLKVNNKKTETTLIEQNMLSKILERSLEEMDDEEVKEM 132
Db 169 WKSLEETE-----KKVYLDKAAELKAEYKNSLESNDADAEDEE--EKQSDDDVDAEEKQV 222

QY 133 CD-----ELSIKNTDNLNQA 148
Db 223 DDDDEVEEKEVENTDDDKKEA 243

RESULT 14
US-10-953-349-4871
; Sequence 4871, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4871
; LENGTH: 261
; TYPE: PRP
; ORGANISM: Arabidopsis thaliana
US-10-953-349-4871

Query Match 7.2%; Score 91.5; DB 6; Length 261;
Best Local Similarity 23.4%; Pred. No. 3.8;
Matches, 33; Conservative 25; Mismatches 44; Indels 39; Gaps 5;

QY 34 EKRHNEKLTSSIEYK-----RHGDDYAKYABRIAEELQYVGSNS 72
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QY 73 FASFIKGEVLYKEILCDVCDKLKVNNKKTETTLIEQNMLSKILERSLEEMDDEEVKEM 132
Db 173 WKSLEETE-----KKVYLDKAAELKAEYKNSLESNDADAEDEE--EKQSDDDVDAEEKQV 226

QY 133 CD-----ELSIKNTDNLNQA 148
Db 227 DDDDEVEEKEVENTDDDKKEA 247

RESULT 15
US-11-056-355B-43589
; Sequence 43589, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 43589
; LENGTH: 261
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(261)
; OTHER INFORMATION: Ceres Seq. ID no. 13492489
US-11-056-355B-43589

Query Match 7.2%; Score 91.5; DB 7; Length 261;
Best Local Similarity 23.4%; Pred. No. 3.8;
Matches 33; Conservative 25; Mismatches 44; Indels 39; Gaps 5;

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QY 73 FASFIKGEVLYKEILCDVCDKLKVNNKKTETTLIEQNMLSKILERSLEEMDDEEVKEM 132
Db 173 WKSLEETE-----KKVYLDKAAELKAEYKNSLESNDADAEDEE--EKQSDDDVDAEEKQV 226

QY 133 CD-----ELSIKNTDNLNQA 148
Db 227 DDDDEVEEKEVENTDDDKKEA 247

Search completed: August 3, 2006, 12:19:18
Job time : 32 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 3, 2006, 12:04:10 ; Search time 604 Seconds
(without alignments)
639.603 Million cell updates/sec

Title: US-09-732-091-4
Perfect score: 1279
Sequence: 1 MAYKYDRDLFLKLESSL.....LRKLTQANGDKKSLQIESI 253

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 8366291 seqs, 1526956180 residues
Total number of hits satisfying chosen parameters: 8366291

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Pending Patents AA Main:*
- 1: /EMC_Celerra_SIDS3/ptodata/2/paa/PCTUS COMB.pcp:*
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 - 43: /EMC_Celerra_SIDS3/ptodata/2/paa/US113 COMB.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1279	100.0	253	27	US-09-732-091-4
3	1279	100.0	253	34	US-10-433-970-4
4	1279	100.0	265	1	PCT-US01-48392-44
5	1279	100.0	265	27	US-09-732-091-44
6	1279	100.0	265	34	US-10-433-970-44
7	1270	99.3	253	1	PCT-US96-18542-205
8	1270	99.3	253	14	US-08-487-032A-785
9	1270	99.3	253	15	US-08-561-469A-785
10	1270	99.3	253	17	US-08-761-184-870
11	1270	99.3	253	17	US-08-761-184-1471
12	1270	99.3	253	18	US-08-821-931-870
13	1270	99.3	253	18	US-08-821-931-1471
14	1270	99.3	253	19	US-08-993-002A-9162
15	1270	99.3	253	19	US-08-993-002A-9163
16	1270	99.3	253	33	US-10-335-977-9162
17	1270	99.3	253	33	US-10-335-977-9163
18	1270	99.3	256	17	US-08-761-184-1215
19	1270	99.3	256	18	US-08-821-931-1215
20	1270	99.3	256	19	US-08-993-002A-9164
21	1270	99.3	256	33	US-10-335-977-9164
22	1264	98.8	253	1	PCT-US01-48392-48
23	1264	98.8	253	34	US-10-433-970-48
24	1264	98.8	265	1	PCT-US01-48392-46
25	1264	98.8	265	34	US-10-433-970-46
26	722	56.5	248	19	US-08-993-002A-7699
27	722	56.5	248	33	US-10-335-977-7699
28	716	56.0	237	19	US-08-993-002A-7698
29	716	56.0	237	33	US-10-335-977-7698
30	615	48.1	209	14	US-08-487-032C-831
31	472.5	36.9	155	1	PCT-US98-06371-1148
32	472.5	36.9	155	19	US-08-902-615A-414
33	472.5	36.9	155	28	US-09-882-227-414
34	364	28.5	273	33	US-10-366-683-29841
35	364	28.5	273	34	US-10-419-128-29841
36	346.5	27.1	321	33	US-10-366-683-29840
37	346.5	27.1	321	34	US-10-419-128-29840
38	252	19.7	49	1	PCT-US01-48392-20
39	252	19.7	49	27	US-09-732-091-20
40	252	19.7	49	34	US-10-433-970-20
41	247	19.3	258	34	US-10-446-203-8852
42	198	15.5	38	1	PCT-US01-48392-17
43	198	15.5	38	27	US-09-732-091-17
44	198	15.5	38	34	US-10-433-970-17
45	194	15.2	41	1	PCT-US01-48392-19

ALIGNMENTS

RESULT 1
PCT-US01-48392-4
; Sequence 4, Application PC/TUS0148392
; GENERAL INFORMATION:

; APPLICANT: AntexBiologicals, Inc.
; TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses
; FILE OF INVENTION: thereof
; FILE REFERENCE: 7969-091-228
; CURRENT APPLICATION NUMBER: PCT/US01/48392
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 09/732,091
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Helicobacter sp.
PCT-US01-48392-4

Query Match 100.0%; Score 1279; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.8e-118;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MAYKYDRDLFLKQLESSDLLDLFEVLVFGKDGKGRHNEKLTSSIEYKRHGGDDYAKYAE 60
QY 61 IAEELQYGSNSFASFIKGEVLYKEILCDVCDKLVNKKTTETTLIEQNMLSKILERS 120
DB 61 IAEELQYGSNSFASFIKGEVLYKEILCDVCDKLVNKKTTETTLIEQNMLSKILERS 120
QY 121 LEEMDEEVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGPKSYQLAVIVANAVAKTIL 180
DB 121 LEEMDEEVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGPKSYQLAVIVANAVAKTIL 180
QY 181 GRGLSLAGNQVLTRTLSPFLTGPVGMIIITGVWTAIDIAIAGPAYRVITPACIVVATLRLKTOQ 240
DB 181 GRGLSLAGNQVLTRTLSPFLTGPVGMIIITGVWTAIDIAIAGPAYRVITPACIVVATLRLKTOQ 240
QY 241 ANGDKKSLQIESI 253
DB 241 ANGDKKSLQIESI 253

RESULT 2

US-09-732-091-4
; Sequence 4, Application US/09732091
; GENERAL INFORMATION:
; APPLICANT: Tian, Jing-Hui
; APPLICANT: Walker, Richard I.
; APPLICANT: Jackson, W. James
; TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses
; FILE OF INVENTION: thereof
; FILE REFERENCE: 7969-088
; CURRENT APPLICATION NUMBER: US/09/732,091
; CURRENT FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Helicobacter sp.
US-09-732-091-4

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Best Local Similarity 100.0%; Pred. No. 4.8e-118;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MAYKYDRDLFLKQLESSDLLDLFEVLVFGKDGKGRHNEKLTSSIEYKRHGGDDYAKYAE 60
QY 61 IAEELQYGSNSFASFIKGEVLYKEILCDVCDKLVNKKTTETTLIEQNMLSKILERS 120
DB 61 IAEELQYGSNSFASFIKGEVLYKEILCDVCDKLVNKKTTETTLIEQNMLSKILERS 120

QY 121 LEEMDEEVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGPKSYQLAVIVANAVAKTIL 180
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QY 181 GRGLSLAGNQVLTRTLSPFLTGPVGMIIITGVWTAIDIAIAGPAYRVITPACIVVATLRLKTOQ 240
DB 181 GRGLSLAGNQVLTRTLSPFLTGPVGMIIITGVWTAIDIAIAGPAYRVITPACIVVATLRLKTOQ 240
QY 241 ANGDKKSLQIESI 253
DB 241 ANGDKKSLQIESI 253

RESULT 3

US-10-433-970-4
; Sequence 4, Application US/10433970
; GENERAL INFORMATION:
; APPLICANT: Tian, Jing-Hui
; APPLICANT: Walker, Richard
; APPLICANT: Jackson, James
; TITLE OF INVENTION: HELICOBACTER PROTEINS, GENE SEQUENCES AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: 7969-091-999
; CURRENT APPLICATION NUMBER: US/10/433,970
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 09/732,091
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Helicobacter sp.
US-10-433-970-4

Query Match 100.0%; Score 1279; DB 34; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.8e-118;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAYKYDRDLFLKQLESSDLLDLFEVLVFGKDGKGRHNEKLTSSIEYKRHGGDDYAKYAE 60
DB 1 MAYKYDRDLFLKQLESSDLLDLFEVLVFGKDGKGRHNEKLTSSIEYKRHGGDDYAKYAE 60
QY 61 IAEELQYGSNSFASFIKGEVLYKEILCDVCDKLVNKKTTETTLIEQNMLSKILERS 120
DB 61 IAEELQYGSNSFASFIKGEVLYKEILCDVCDKLVNKKTTETTLIEQNMLSKILERS 120
QY 121 LEEMDEEVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGPKSYQLAVIVANAVAKTIL 180
DB 121 LEEMDEEVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGPKSYQLAVIVANAVAKTIL 180
QY 181 GRGLSLAGNQVLTRTLSPFLTGPVGMIIITGVWTAIDIAIAGPAYRVITPACIVVATLRLKTOQ 240
DB 181 GRGLSLAGNQVLTRTLSPFLTGPVGMIIITGVWTAIDIAIAGPAYRVITPACIVVATLRLKTOQ 240
QY 241 ANGDKKSLQIESI 253
DB 241 ANGDKKSLQIESI 253

RESULT 4

PCT-US01-48392-44
; Sequence 44, Application PC/TUS0148392
; GENERAL INFORMATION:
; APPLICANT: AntexBiologicals, Inc.
; TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses
; FILE OF INVENTION: thereof
; FILE REFERENCE: 7969-091-228
; CURRENT APPLICATION NUMBER: PCT/US01/48392
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 09/732,091
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 48

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Helicobacter sp.
PCT-US01-48392-44

Query Match      100.0%; Score 1279; DB 1; Length 265;
Best Local Similarity 100.0%; Pred. No. 5.2e-118;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAYKYDRDLLEFLKQLESSDLLDLFEVLVFGKDGKRNHNEKLTSSIEYKRGHGGDYAKYAE 60
DB 13 MAYKYDRDLLEFLKQLESSDLLDLFEVLVFGKDGKRNHNEKLTSSIEYKRGHGGDYAKYAE 72
QY 61 IAEELQYGSNSPASFKEGVLVYKEILCDVCDKLVNKNKTTTTLIEQNMLSKILERS 120
DB 73 IAEELQYGSNSPASFKEGVLVYKEILCDVCDKLVNKNKTTTTLIEQNMLSKILERS 132
QY 121 LEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGPKSYQLAVIVANAVAKTIL 180
DB 133 LEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGPKSYQLAVIVANAVAKTIL 192
QY 181 GRGLSLAGNQVLTRTLSTFLTGPVGVWITGVTWTAIDIAGPAYRVTIPACIVVATLRLKTOQ 240
DB 193 GRGLSLAGNQVLTRTLSTFLTGPVGVWITGVTWTAIDIAGPAYRVTIPACIVVATLRLKTOQ 252

RESULT 5
US-09-732-091-44
; Sequence 44, Application US/09732091
; GENERAL INFORMATION:
; APPLICANT: Tian, Jing-Hui
; APPLICANT: Walker, Richard I.
; APPLICANT: Jackson, W. James
; TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses
; FILE REFERENCE: 7969-088
; CURRENT APPLICATION NUMBER: US/09/732,091
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Helicobacter sp.
US-09-732-091-44

Query Match      100.0%; Score 1279; DB 27; Length 265;
Best Local Similarity 100.0%; Pred. No. 5.2e-118;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAYKYDRDLLEFLKQLESSDLLDLFEVLVFGKDGKRNHNEKLTSSIEYKRGHGGDYAKYAE 60
DB 13 MAYKYDRDLLEFLKQLESSDLLDLFEVLVFGKDGKRNHNEKLTSSIEYKRGHGGDYAKYAE 72
QY 61 IAEELQYGSNSPASFKEGVLVYKEILCDVCDKLVNKNKTTTTLIEQNMLSKILERS 120
DB 73 IAEELQYGSNSPASFKEGVLVYKEILCDVCDKLVNKNKTTTTLIEQNMLSKILERS 132
QY 121 LEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGPKSYQLAVIVANAVAKTIL 180
DB 133 LEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGPKSYQLAVIVANAVAKTIL 192
QY 181 GRGLSLAGNQVLTRTLSTFLTGPVGVWITGVTWTAIDIAGPAYRVTIPACIVVATLRLKTOQ 240
DB 193 GRGLSLAGNQVLTRTLSTFLTGPVGVWITGVTWTAIDIAGPAYRVTIPACIVVATLRLKTOQ 252

RESULT 6
US-10-433-970-44
; Sequence 44, Application US/10433970
; GENERAL INFORMATION:
; APPLICANT: Tian, Jing-Hui
; APPLICANT: Walker, Richard
; APPLICANT: Jackson, James
; TITLE OF INVENTION: HELICOBACTER PROTEINS, GENE SEQUENCES AND USES
; FILE REFERENCE: 7969-091-999
; CURRENT APPLICATION NUMBER: US/10/433,970
; CURRENT FILING DATE: 2003-06-06
; PRIOR FILING DATE: 09/732,091
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Helicobacter sp.
US-10-433-970-44

Query Match      100.0%; Score 1279; DB 34; Length 265;
Best Local Similarity 100.0%; Pred. No. 5.2e-118;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAYKYDRDLLEFLKQLESSDLLDLFEVLVFGKDGKRNHNEKLTSSIEYKRGHGGDYAKYAE 60
DB 13 MAYKYDRDLLEFLKQLESSDLLDLFEVLVFGKDGKRNHNEKLTSSIEYKRGHGGDYAKYAE 72
QY 61 IAEELQYGSNSPASFKEGVLVYKEILCDVCDKLVNKNKTTTTLIEQNMLSKILERS 120
DB 73 IAEELQYGSNSPASFKEGVLVYKEILCDVCDKLVNKNKTTTTLIEQNMLSKILERS 132
QY 121 LEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGPKSYQLAVIVANAVAKTIL 180
DB 133 LEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGPKSYQLAVIVANAVAKTIL 192
QY 181 GRGLSLAGNQVLTRTLSTFLTGPVGVWITGVTWTAIDIAGPAYRVTIPACIVVATLRLKTOQ 240
DB 193 GRGLSLAGNQVLTRTLSTFLTGPVGVWITGVTWTAIDIAGPAYRVTIPACIVVATLRLKTOQ 252

RESULT 7
PCT-US96-18542-205
; Sequence 205, Application PC/TUS9618542
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 268
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER:
; OPERATING SYSTEM:
; SOFTWARE:
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: PCT/US96/18542
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/561,469
; FILING DATE: 17-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-001CPPC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 205:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1...253
;
PCT-US96-18542-205
;
Query Match 99.3%; Score 1270; DB 1; Length 253;
Best Local Similarity 99.2%; Pred. No. 3.8e-117;
Matches 251; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAYKYDRDLFLFKQLLESSDLLDLFEVLVFGKDGKRRHNEKLTSSIEYKRHGDDYAKYAE 60
Db 1 MAYKYDRDLFLFKQLLESSDLLDLFEVLVFGKDGKRRHNEKLTSSIEYKRHGDDYAKYAE 60
QY 61 IAEELQYIGNSFASFIKGEVLYKEILCDVCDKLVNKKTTTLLIEQNMLSKILERS 120
Db 61 IAEELQYIGNSFASFIKGEVLYKEILCDVCDKLVNKKTTTLLIEQNMLSKILERS 120
QY 121 LEEMDEEVKEMCDLSIKNTDNLNRQALSAATLTLFKMGGPKSYQLAVIVANAVAKTIL 180
Db 121 LEEMDEEVKEMCDLSIKNTDNLNRQALSAATLTLFKMGGPKSYQLAVIVANAVAKTIL 180
QY 181 GRGLSLAGNOVLTRTLSPFTGPGVGIITGVTWTAIDIAAGPAYRVTIIPACIVVATLRLKTOO 240
Db 181 GRGLSLAGNOVLTRTLSPFTGPGVGIITGVTWTAIDIAAGPAYRVTIIPACIVVATLRLKTOO 240
QY 241 ANGDKKSLQIESI 253
Db 241 ANEDKSLQIESV 253

RESULT 8
US-08-487-032A-785
; Sequence 785, Application US/08487032A
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 880
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/561,469A
; FILING DATE: 17-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,032
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; APPLICATION NUMBER: US/08/487,032A
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 785:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORGANISM: Helicobacter pylori
; ORGANISM: Helicobacter pylori
;
US-08-487-032A-785
;
Query Match 99.3%; Score 1270; DB 14; Length 253;
Best Local Similarity 99.2%; Pred. No. 3.8e-117;
Matches 251; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAYKYDRDLFLFKQLLESSDLLDLFEVLVFGKDGKRRHNEKLTSSIEYKRHGDDYAKYAE 60
Db 1 MAYKYDRDLFLFKQLLESSDLLDLFEVLVFGKDGKRRHNEKLTSSIEYKRHGDDYAKYAE 60
QY 61 IAEELQYIGNSFASFIKGEVLYKEILCDVCDKLVNKKTTTLLIEQNMLSKILERS 120
Db 61 IAEELQYIGNSFASFIKGEVLYKEILCDVCDKLVNKKTTTLLIEQNMLSKILERS 120
QY 121 LEEMDEEVKEMCDLSIKNTDNLNRQALSAATLTLFKMGGPKSYQLAVIVANAVAKTIL 180
Db 121 LEEMDEEVKEMCDLSIKNTDNLNRQALSAATLTLFKMGGPKSYQLAVIVANAVAKTIL 180
QY 181 GRGLSLAGNOVLTRTLSPFTGPGVGIITGVTWTAIDIAAGPAYRVTIIPACIVVATLRLKTOO 240
Db 181 GRGLSLAGNOVLTRTLSPFTGPGVGIITGVTWTAIDIAAGPAYRVTIIPACIVVATLRLKTOO 240
QY 241 ANGDKKSLQIESI 253
Db 241 ANEDKSLQIESV 253

RESULT 9
US-08-561-469A-785
; Sequence 785, Application US/08561469A
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 994
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,469A
; FILING DATE: 17-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,032
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
```

```
/ NAME: Mandragouras, Amy E.
/ REGISTRATION NUMBER: 36,207
/ REFERENCE/DOCKET NUMBER: GTN-001CP
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617)227-7400
/ TELEFAX: (617)227-5941
/ INFORMATION FOR SEQ ID NO: 785:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 253 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: YES
/ ORIGINAL SOURCE:
/ ORGANISM: Helicobacter pylori
/
US-08-561-469A-785

Query Match          99.3%; Score 1270; DB 15; Length 253;
Best Local Similarity 99.2%; Pred. No. 3.8e-117;
Matches 251; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAYKYDRDLFLKQLSSDLLDLFEVLVFGDGEKRNKLTSSIEYKRGHDDYAKYAE 60
   |||||||
Db 1 MAYKYDRDLFLKQLSSDLLDLFEVLVFGDGEKRNKLTSSIEYKRGHDDYAKYAE 60
   |||||||
QY 61 IAEELQYGSNSPASFIKGEGVLYKEILCDVCDKLVKNYKTKTETTLIEQNMLSKILERS 120
   |||||||
Db 61 IAEELQYGSNSPASFIKGEGVLYKEILCDVCDKLVKNYKTKTETTLIEQNMLSKILERS 120
   |||||||
QY 121 LEEMDDEEVKEMCDLSIKNTDNLNRQALSAAFTLTFKMGFKSYQLAVIVANAVAKTIL 180
   |||||||
Db 121 LEEMDDEEVKEMCDLSIKNTDNLNRQALSAAFTLTFKMGFKSYQLAVIVANAVAKTIL 180
   |||||||
QY 181 GRGLSLAGNQVLTRTLSTFLTGPVGIITGVWTAIDTAGPAYRVITPACIVVATLRLKTTQQ 240
   |||||||
Db 181 GRGLSLAGNQVLTRTLSTFLTGPVGIITGVWTAIDTAGPAYRVITPACIVVATLRLKTTQQ 240
   |||||||
QY 241 ANGDKKSQIESI 253
   |||||||
Db 241 ANEDKKSQIESV 253

RESULT 10
US-08-761-184-870
/ Sequence 870, Application US/08761184
/ GENERAL INFORMATION:
/ APPLICANT: DOUGLAS SMITH ET AL
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
/ TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI AND
/ TITLE OF INVENTION: THERAPEUTIC USES THEREOF
/ NUMBER OF SEQUENCES: 1810
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: LAHIVE & COCKFIELD
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02109-1875
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: CD/ROM ISO9660
/ COMPUTER:
/ OPERATING SYSTEM:
/ SOFTWARE:
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/761,184
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/487,032
/ FILING DATE: 07-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/561,469
/ FILING DATE: 17-NOV-1995
/ PRIOR APPLICATION DATA:

/ NAME: Mandragouras, Amy E.
/ REGISTRATION NUMBER: 36,207
/ REFERENCE/DOCKET NUMBER: GTN-001CP
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617)227-7400
/ TELEFAX: (617)227-5941
/ INFORMATION FOR SEQ ID NO: 785:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 253 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: YES
/ ORIGINAL SOURCE:
/ ORGANISM: Helicobacter pylori
/
US-08-561-469A-785

Query Match          99.3%; Score 1270; DB 15; Length 253;
Best Local Similarity 99.2%; Pred. No. 3.8e-117;
Matches 251; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAYKYDRDLFLKQLSSDLLDLFEVLVFGDGEKRNKLTSSIEYKRGHDDYAKYAE 60
   |||||||
Db 1 MAYKYDRDLFLKQLSSDLLDLFEVLVFGDGEKRNKLTSSIEYKRGHDDYAKYAE 60
   |||||||
QY 61 IAEELQYGSNSPASFIKGEGVLYKEILCDVCDKLVKNYKTKTETTLIEQNMLSKILERS 120
   |||||||
Db 61 IAEELQYGSNSPASFIKGEGVLYKEILCDVCDKLVKNYKTKTETTLIEQNMLSKILERS 120
   |||||||
QY 121 LEEMDDEEVKEMCDLSIKNTDNLNRQALSAAFTLTFKMGFKSYQLAVIVANAVAKTIL 180
   |||||||
Db 121 LEEMDDEEVKEMCDLSIKNTDNLNRQALSAAFTLTFKMGFKSYQLAVIVANAVAKTIL 180
   |||||||
QY 181 GRGLSLAGNQVLTRTLSTFLTGPVGIITGVWTAIDTAGPAYRVITPACIVVATLRLKTTQQ 240
   |||||||
Db 181 GRGLSLAGNQVLTRTLSTFLTGPVGIITGVWTAIDTAGPAYRVITPACIVVATLRLKTTQQ 240
   |||||||
QY 241 ANGDKKSQIESI 253
   |||||||
Db 241 ANEDKKSQIESV 253

RESULT 11
US-08-761-184-1471
/ Sequence 1471, Application US/08761184
/ GENERAL INFORMATION:
/ APPLICANT: DOUGLAS SMITH ET AL
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
/ TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI AND
/ TITLE OF INVENTION: THERAPEUTIC USES THEREOF
/ NUMBER OF SEQUENCES: 1810
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: LAHIVE & COCKFIELD
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02109-1875
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER:
OPERATING SYSTEM:
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/761,184
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,032
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/561,469
FILING DATE: 17-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,405
FILING DATE: 01-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/660,742
FILING DATE: 06-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/736,791
FILING DATE: 25-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/739,150
FILING DATE: 28-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-001CP9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1471:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1...253
US-08-761-184-1471

Query Match 99.3%; Score 1270; DB 17; Length 253;
Best Local Similarity 99.2%; Pred. No. 3.8e-117;
Matches 251; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAYKYDRDLLEFLKQLESSDLLDLFEVLVFGKDGKGRHNEKLTSSIEYKRHGDDYAKYAE 60
DB 1 MAYKYDRDLLEFLKQLESSDLLDLFEVLVFGKDGKGRHNEKLTSSIEYKRHGDDYAKYAE 60
QY 61 TAEELQYYSNSFASFKGEGVLYKEILCDVCDKLVKNVYKKTETTLIEQNMLSKILERS 120
DB 61 TAEELQYYSNSFASFKGEGVLYKEILCDVCDKLVKNVYKKTETTLIEQNMLSKILERS 120
QY 121 LEEMDEEVKENCDELSTKNTDNLNQAALTLTKFMGGKSKYQLAVIVANAKTLL 180
DB 121 LEEMDEEVKENCDELSTKNTDNLNQAALTLTKFMGGKSKYQLAVIVANAKTLL 180
QY 181 GRGLSLAGNQLVTRLTSLFTGPGVWITGWTATDIAAGPAYRTIPACIVWATRLKTOQ 240
DB 181 GRGLSLAGNQLVTRLTSLFTGPGVWITGWTATDIAAGPAYRTIPACIVWATRLKTOQ 240
QY 241 ANGDKKSLQIESI 253
DB 241 ANEDKKSLQIESV 253

RESULT 12

US-08-821-931-870
Sequence 870, Application US/08821931
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH ET AL
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI AND
TITLE OF INVENTION: THERAPEUTIC USES THEREOF
NUMBER OF SEQUENCES: 1810
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER:
OPERATING SYSTEM:
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,931
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,032
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/561,469
FILING DATE: 17-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,405
FILING DATE: 01-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/660,742
FILING DATE: 06-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/736,791
FILING DATE: 25-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/739,150
FILING DATE: 28-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/761,184
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-001CP9CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 870:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1...253
US-08-821-931-870

Query Match 99.3%; Score 1270; DB 18; Length 253;
Best Local Similarity 99.2%; Pred. No. 3.8e-117;
Matches 251; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAYKYDRDLLEFLKQLESSDLLDLFEVLVFGKDGKGRHNEKLTSSIEYKRHGDDYAKYAE 60
DB 1 MAYKYDRDLLEFLKQLESSDLLDLFEVLVFGKDGKGRHNEKLTSSIEYKRHGDDYAKYAE 60

QY 61 IABELQYGSNSPASFIKGEVLYKEILCDVCDKLKVNYNKKTETTTTLEQNMLSKILERS 120
Db 61 IABELQYGSNSPASFIKGEVLYKEILCDVCDKLKVNYNKKTETTTTLEQNMLSKILERS 120
QY 121 LEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGFKSYQLAVIVANAVAKTIL 180
Db 121 LEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGFKSYQLAVIVANAVAKTIL 180
QY 181 GRGLSLAGNOVLTRTSLFELTGPVGMWITGVWTAIDIAGPAYRVTIIPACIVVATLRLKTOQ 240
Db 181 GRGLSLAGNOVLTRTSLFELTGPVGMWITGVWTAIDIAGPAYRVTIIPACIVVATLRLKTOQ 240
QY 241 ANGDKKSLQIESI 253
Db 241 ANEDKSLQIESV 253

RESULT 13

US-08-821-931-1471
; Sequence 1471, Application US/08821931
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH ET AL
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 1810
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; OPERATING SYSTEM:
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/821,931
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,032
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/561,469
; FILING DATE: 17-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,405
; FILING DATE: 01-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/660,742
; FILING DATE: 06-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/736,791
; FILING DATE: 25-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/739,150
; FILING DATE: 28-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/761,184
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-001CP9CN
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1471:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1...253
US-08-821-931-1471

Query Match 99.3%; Score 1270; DB 18; Length 253;
Best Local Similarity 99.2%; Pred. No. 3.8e-117;
Matches 251; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAYKYDRDLLEFLKQLSESSDLLDFEVLVFGKDEGRHNEKLTSSIEYKRGHGGDYAKYAE 60
Db 1 MAYKYDRDLLEFLKQLSESSDLLDFEVLVFGKDEGRHNEKLTSSIEYKRGHGGDYAKYAE 60
QY 61 IABELQYGSNSPASFIKGEVLYKEILCDVCDKLKVNYNKKTETTTTLEQNMLSKILERS 120
Db 61 IABELQYGSNSPASFIKGEVLYKEILCDVCDKLKVNYNKKTETTTTLEQNMLSKILERS 120
QY 121 LEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGFKSYQLAVIVANAVAKTIL 180
Db 121 LEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGFKSYQLAVIVANAVAKTIL 180
QY 181 GRGLSLAGNOVLTRTSLFELTGPVGMWITGVWTAIDIAGPAYRVTIIPACIVVATLRLKTOQ 240
Db 181 GRGLSLAGNOVLTRTSLFELTGPVGMWITGVWTAIDIAGPAYRVTIIPACIVVATLRLKTOQ 240
QY 241 ANGDKKSLQIESI 253
Db 241 ANEDKSLQIESV 253

RESULT 14

US-08-993-002A-9162
; Sequence 9162, Application US/08993002A
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,002A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 9162:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid

```
;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1...253
US-08-993-002A-9162

Query Match          99.3%; Score 1270; DB 19; Length 253;
Best Local Similarity 99.2%; Pred. No. 3.8e-117;
Matches 251; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAYKYDRDLFLKQLESDDLDFEVLVFGDGEKRNHNEKLTSSIEYKRHGDDYAKYAE 60
   |||
DB 1 MAYKYDRDLFLKQLESDDLDFEVLVFGDGEKRNHNEKLTSSIEYKRHGDDYAKYAE 60
   |||

QY 61 IAEELQYYGNSFASFIKGEGVLYKEILCDVCDKLKVNYNKKTTTLLIEQNMLSKILERS 120
   |||
DB 61 IAEELQYYGNSFASFIKGEGVLYKEILCDVCDKLKVNYNKKTTTLLIEQNMLSKILERS 120
   |||

QY 121 LEEMDDEEVKEMCDLSIKNTDNLNRQALSAATLTLFMGGFKSYQLAVIVANAVAKTIL 180
   |||
DB 121 LEEMDDEEVKEMCDLSIKNTDNLNRQALSAATLTLFMGGFKSYQLAVIVANAVAKTIL 180
   |||

QY 181 GRGLSLAGNOVLTRTSLFTGPGVMIITGVWTAIDAGPAYRVVTIPACIVVATLRLKTOQ 240
   |||
DB 181 GRGLSLAGNOVLTRTSLFTGPGVMIITGVWTAIDAGPAYRVVTIPACIVVATLRLKTOQ 240
   |||

QY 241 ANGDKKSLQIESI 253
   |||
DB 241 ANEDKKSQIESV 253
   |||
```

RESULT 15

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US-08-993-002A-9163
; Sequence 9163, Application US/08993002A
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,002A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 9163:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
```

```
;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1...253
US-08-993-002A-9163

Query Match          99.3%; Score 1270; DB 19; Length 253;
Best Local Similarity 99.2%; Pred. No. 3.8e-117;
Matches 251; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAYKYDRDLFLKQLESDDLDFEVLVFGDGEKRNHNEKLTSSIEYKRHGDDYAKYAE 60
   |||
DB 1 MAYKYDRDLFLKQLESDDLDFEVLVFGDGEKRNHNEKLTSSIEYKRHGDDYAKYAE 60
   |||

QY 61 IAEELQYYGNSFASFIKGEGVLYKEILCDVCDKLKVNYNKKTTTLLIEQNMLSKILERS 120
   |||
DB 61 IAEELQYYGNSFASFIKGEGVLYKEILCDVCDKLKVNYNKKTTTLLIEQNMLSKILERS 120
   |||

QY 121 LEEMDDEEVKEMCDLSIKNTDNLNRQALSAATLTLFMGGFKSYQLAVIVANAVAKTIL 180
   |||
DB 121 LEEMDDEEVKEMCDLSIKNTDNLNRQALSAATLTLFMGGFKSYQLAVIVANAVAKTIL 180
   |||

QY 181 GRGLSLAGNOVLTRTSLFTGPGVMIITGVWTAIDAGPAYRVVTIPACIVVATLRLKTOQ 240
   |||
DB 181 GRGLSLAGNOVLTRTSLFTGPGVMIITGVWTAIDAGPAYRVVTIPACIVVATLRLKTOQ 240
   |||

QY 241 ANGDKKSLQIESI 253
   |||
DB 241 ANEDKKSQIESV 253
   |||
```

Search completed: August 3, 2006, 12:14:59

Job time : 605 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	97.5	7.6	311	1	PCT-US06-18535-32605	Sequence 32605, A
2	97.5	7.6	311	7	US-11-431-855-32605	Sequence 32605, A
3	95	7.4	2649	7	US-11-188-417A-25	Sequence 25, Appl
4	92	7.2	309	7	US-11-434-137-9630	Sequence 9630, Ap
5	92	7.2	309	7	US-11-434-184-9630	Sequence 9630, Ap
6	92	7.2	309	7	US-11-434-203-9630	Sequence 9630, Ap
7	92	7.2	309	7	US-11-434-127-9630	Sequence 9630, Ap
8	92	7.2	309	7	US-11-434-199-9630	Sequence 9630, Ap
9	92	7.2	327	7	US-11-434-137-5500	Sequence 5500, Ap
10	92	7.2	327	7	US-11-434-184-5500	Sequence 5500, Ap
11	92	7.2	327	7	US-11-434-203-5500	Sequence 5500, Ap
12	92	7.2	327	7	US-11-434-127-5500	Sequence 5500, Ap
13	92	7.2	327	7	US-11-434-199-5500	Sequence 5500, Ap
14	91.5	7.2	241	7	US-11-479-226-1446	Sequence 1446, Ap
15	91.5	7.2	375	7	US-11-434-137-10134	Sequence 10134, A
16	91.5	7.2	375	7	US-11-434-184-10134	Sequence 10134, A
17	91.5	7.2	375	7	US-11-434-203-10134	Sequence 10134, A
18	91.5	7.2	375	7	US-11-434-127-10134	Sequence 10134, A
19	91.5	7.2	375	7	US-11-434-199-10134	Sequence 10134, A
20	91.5	7.2	390	7	US-11-434-137-4944	Sequence 4944, Ap
21	91.5	7.2	390	7	US-11-434-184-4944	Sequence 4944, Ap
22	91.5	7.2	390	7	US-11-434-203-4944	Sequence 4944, Ap
23	91.5	7.2	390	7	US-11-434-127-4944	Sequence 4944, Ap
24	91.5	7.2	390	7	US-11-434-199-4944	Sequence 4944, Ap
25	90	7.0	271	7	US-11-365-965-569	Sequence 569, App

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QY 189 NOVLTRTSLTGPVGMIIITGVMTAI 214
Db 236 MRLVGAKNSYIRGP--FFPEGAWGI 259

RESULT 11
US-11-434-203-5500
; Sequence 5500, Application US/11434203
; GENERAL INFORMATION:
; APPLICANT: Telford, John
; APPLICANT: Masignani, Vega
; APPLICANT: Ros, Immaculada Margarit Y
; APPLICANT: Fraser, Claire
; APPLICANT: Tettelin, Hervé
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/11/434,203
; CURRENT FILING DATE: 2006-05-16
; PRIOR APPLICATION NUMBER: US 10/415,182
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: PCT/GB01/04789
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: GB-0026333.5
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: GB-0028727.6
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: GB-0105640.7
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 12025
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 5500
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
US-11-434-203-5500

Query Match 7.2%; Score 92; DB 7; Length 327;
Best Local Similarity 21.8%; Pred. No. 3.6;
Matches 45; Conservative 35; Mismatches 60; Indels 66; Gaps 11;

QY 31 KDGKRN-----EKLTSIEYKRGDDYAKYAERIAEELQYGSNSFA 74
Db 98 KDKLNDPDYHKYDKIRISGVEKT-----YSSKAEQLKEVQKEVGSDDVID 146

QY 75 SFIKGEGVLYKEILCDVCDKLVNKNKTETTLIEQNMLSKILERSLEEMDDEEVKEMCD 134
Db 147 D-----TYKDALLDV-----YVGTSSAKVSKS-VSEAIR-IEGVD--YTKEPID 188

QY 135 ELSIKN-TDNLNRQALSAATLTFKMGGPKSYQLAVIVA-----NAVAKTILGRGLSLAG 188
Db 189 STKLSNLTNI-----RIWFGGVALLIVLAIFLISNTIRMSRRTDIEI 235

QY 189 NOVLTRTSLTGPVGMIIITGVMTAI 214
Db 236 MRLVGAKNSYIRGP--FFPEGAWGI 259

RESULT 12
US-11-434-127-5500
; Sequence 5500, Application US/11434127
; GENERAL INFORMATION:
; APPLICANT: Telford, John
; APPLICANT: Masignani, Vega
; APPLICANT: Ros, Immaculada Margarit Y
; APPLICANT: Fraser, Claire
; APPLICANT: Tettelin, Hervé
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/11/434,127
; CURRENT FILING DATE: 2006-05-16
; PRIOR APPLICATION NUMBER: US 10/415,182
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: PCT/GB01/04789
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: GB-0026333.5
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: GB-0105640.7
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 12025
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 5500
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
US-11-434-203-5500

Query Match 7.2%; Score 92; DB 7; Length 327;
Best Local Similarity 21.8%; Pred. No. 3.6;
Matches 45; Conservative 35; Mismatches 60; Indels 66; Gaps 11;

QY 31 KDGKRN-----EKLTSIEYKRGDDYAKYAERIAEELQYGSNSFA 74
Db 98 KDKLNDPDYHKYDKIRISGVEKT-----YSSKAEQLKEVQKEVGSDDVID 146

QY 75 SFIKGEGVLYKEILCDVCDKLVNKNKTETTLIEQNMLSKILERSLEEMDDEEVKEMCD 134
Db 147 D-----TYKDALLDV-----YVGTSSAKVSKS-VSEAIR-IEGVD--YTKEPID 188

QY 135 ELSIKN-TDNLNRQALSAATLTFKMGGPKSYQLAVIVA-----NAVAKTILGRGLSLAG 188
Db 189 STKLSNLTNI-----RIWFGGVALLIVLAIFLISNTIRMSRRTDIEI 235

QY 189 NOVLTRTSLTGPVGMIIITGVMTAI 214
Db 236 MRLVGAKNSYIRGP--FFPEGAWGI 259

RESULT 13
US-11-434-199-5500
; Sequence 5500, Application US/11434199
; GENERAL INFORMATION:
; APPLICANT: Telford, John
; APPLICANT: Masignani, Vega
; APPLICANT: Ros, Immaculada Margarit Y
; APPLICANT: Fraser, Claire
; APPLICANT: Tettelin, Hervé
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/11/434,199
; CURRENT FILING DATE: 2006-05-16
; PRIOR APPLICATION NUMBER: US 10/415,182
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: PCT/GB01/04789
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: GB-0026333.5
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: GB-0105640.7
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 12025
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 5500
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
US-11-434-199-5500

Query Match 7.2%; Score 92; DB 7; Length 327;
Best Local Similarity 21.8%; Pred. No. 3.6;
Matches 45; Conservative 35; Mismatches 60; Indels 66; Gaps 11;

QY 31 KDGKRN-----EKLTSIEYKRGDDYAKYAERIAEELQYGSNSFA 74
Db 98 KDKLNDPDYHKYDKIRISGVEKT-----YSSKAEQLKEVQKEVGSDDVID 146

QY 75 SFIKGEGVLYKEILCDVCDKLVNKNKTETTLIEQNMLSKILERSLEEMDDEEVKEMCD 134
Db 147 D-----TYKDALLDV-----YVGTSSAKVSKS-VSEAIR-IEGVD--YTKEPID 188

QY 135 ELSIKN-TDNLNRQALSAATLTFKMGGPKSYQLAVIVA-----NAVAKTILGRGLSLAG 188
Db 189 STKLSNLTNI-----RIWFGGVALLIVLAIFLISNTIRMSRRTDIEI 235

QY 189 NOVLTRTSLTGPVGMIIITGVMTAI 214
Db 236 MRLVGAKNSYIRGP--FFPEGAWGI 259

RESULT 14
US-11-434-127-5500
; Sequence 5500, Application US/11434127
; GENERAL INFORMATION:
; APPLICANT: Telford, John
; APPLICANT: Masignani, Vega
; APPLICANT: Ros, Immaculada Margarit Y
; APPLICANT: Fraser, Claire
; APPLICANT: Tettelin, Hervé
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/11/434,127
; CURRENT FILING DATE: 2006-05-16
; PRIOR APPLICATION NUMBER: US 10/415,182
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: PCT/GB01/04789
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: GB-0026333.5
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: GB-0105640.7
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 12025
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 5500
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
US-11-434-127-5500

PRIOR APPLICATION NUMBER: PCT/GB01/04789
PRIOR FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: GB-0026333.5
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: GB-0028727.6
PRIOR FILING DATE: 2000-11-24
PRIOR APPLICATION NUMBER: GB-0105640.7
PRIOR FILING DATE: 2001-03-07
NUMBER OF SEQ ID NOS: 12025
SOFTWARE: SeqWin99, version 1.02
SEQ ID NO 5500
LENGTH: 327
TYPE: PRT
ORGANISM: Streptococcus agalactiae
US-11-434-127-5500

Query Match 7.2%; Score 92; DB 7; Length 327;
Best Local Similarity 21.8%; Pred. No. 3.6;
Matches 45; Conservative 35; Mismatches 60; Indels 66; Gaps 11;

QY 31 KDGKRN-----EKLTSIEYKRGDDYAKYAERIAEELQYGSNSFA 74
Db 98 KDKLNDPDYHKYDKIRISGVEKT-----YSSKAEQLKEVQKEVGSDDVID 146

QY 75 SFIKGEGVLYKEILCDVCDKLVNKNKTETTLIEQNMLSKILERSLEEMDDEEVKEMCD 134
Db 147 D-----TYKDALLDV-----YVGTSSAKVSKS-VSEAIR-IEGVD--YTKEPID 188

QY 135 ELSIKN-TDNLNRQALSAATLTFKMGGPKSYQLAVIVA-----NAVAKTILGRGLSLAG 188
Db 189 STKLSNLTNI-----RIWFGGVALLIVLAIFLISNTIRMSRRTDIEI 235

QY 189 NOVLTRTSLTGPVGMIIITGVMTAI 214
Db 236 MRLVGAKNSYIRGP--FFPEGAWGI 259

RESULT 15
US-11-434-199-5500
; Sequence 5500, Application US/11434199
; GENERAL INFORMATION:
; APPLICANT: Telford, John
; APPLICANT: Masignani, Vega
; APPLICANT: Ros, Immaculada Margarit Y
; APPLICANT: Fraser, Claire
; APPLICANT: Tettelin, Hervé
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/11/434,199
; CURRENT FILING DATE: 2006-05-16
; PRIOR APPLICATION NUMBER: US 10/415,182
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: PCT/GB01/04789
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: GB-0026333.5
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: GB-0105640.7
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 12025
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 5500
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
US-11-434-199-5500

PRIOR APPLICATION NUMBER: PCT/GB01/04789
PRIOR FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: GB-0026333.5
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: GB-0028727.6
PRIOR FILING DATE: 2000-11-24
PRIOR APPLICATION NUMBER: GB-0105640.7
PRIOR FILING DATE: 2001-03-07
NUMBER OF SEQ ID NOS: 12025
SOFTWARE: SeqWin99, version 1.02
SEQ ID NO 5500
LENGTH: 327
TYPE: PRT
ORGANISM: Streptococcus agalactiae
US-11-434-127-5500

Query Match 7.2%; Score 92; DB 7; Length 327;
Best Local Similarity 21.8%; Pred. No. 3.6;
Matches 45; Conservative 35; Mismatches 60; Indels 66; Gaps 11;

QY 31 KDGKRN-----EKLTSIEYKRGDDYAKYAERIAEELQYGSNSFA 74
Db 98 KDKLNDPDYHKYDKIRISGVEKT-----YSSKAEQLKEVQKEVGSDDVID 146

QY 75 SFIKGEGVLYKEILCDVCDKLVNKNKTETTLIEQNMLSKILERSLEEMDDEEVKEMCD 134
Db 147 D-----TYKDALLDV-----YVGTSSAKVSKS-VSEAIR-IEGVD--YTKEPID 188

QY 135 ELSIKN-TDNLNRQALSAATLTFKMGGPKSYQLAVIVA-----NAVAKTILGRGLSLAG 188
Db 189 STKLSNLTNI-----RIWFGGVALLIVLAIFLISNTIRMSRRTDIEI 235

QY 189 NOVLTRTSLTGPVGMIIITGVMTAI 214
Db 236 MRLVGAKNSYIRGP--FFPEGAWGI 259

RESULT 16
US-11-434-199-5500
; Sequence 5500, Application US/11434199
; GENERAL INFORMATION:
; APPLICANT: Telford, John
; APPLICANT: Masignani, Vega
; APPLICANT: Ros, Immaculada Margarit Y
; APPLICANT: Fraser, Claire
; APPLICANT: Tettelin, Hervé
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/11/434,199
; CURRENT FILING DATE: 2006-05-16
; PRIOR APPLICATION NUMBER: US 10/415,182
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: PCT/GB01/04789
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: GB-0026333.5
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: GB-0105640.7
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 12025
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 5500
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
US-11-434-199-5500

Db 98 KDKLKNPDYHKVYDKIKRISGEKVT-----YSKAQLEKVEQKEYGSDVID 146
QY 75 SFIKGEGLVYKEILCDVCDKLVNKKTTETTLIEQNMLSKILERSLEEMDDEEVKEMCD 134
Db 147 D-----TYKDALLDV-----YVVGTSAAKVS-KS-VSEAIGR-IEGVD--YTKEPID 188
QY 135 ELSIKN-TDNLNRQALSATLTLFKMGGFKSVQLAVIVA-----NAVAKTILGRGLSLAG 188
Db 189 STKLSNLTNDNI-----RINFGGVALLVLAIFLISNIRMSRRTDIEI 235
QY 189 NOVLTRTSLFSLTGPVGIITGWTAI 214
Db 236 MRLVGAKNYSIRGP--PFPEGAWGCI 259

RESULT 14
US-11-479-226-1446
; Sequence 1446, Application US/11479226
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: REUBER, T. Lynne
; APPLICANT: RATCLIFFE, Oliver J
; APPLICANT: RUFF, Thomas G
; APPLICANT: THOMPSON-MIZE, Rebecca L
; APPLICANT: SUN, Jindong
; TITLE OF INVENTION: TRANSCRIPTION FACTORS FOR INCREASING YIELD
; FILE REFERENCE: MBI-0022-2CIP
; CURRENT FILING DATE: 2006-06-30
; PRIOR APPLICATION NUMBER: 09/713,994
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/166,228
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/197,899
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: 60/227,439
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 2002
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1446
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G1030 Amino Acid Sequence
US-11-479-226-1446

Query Match 7.2%; Score 91.5; DB 7; Length 241;
Best Local Similarity 23.4%; Pred. No. 2.6;
Matches 33; Conservative 25; Mismatches 44; Indels 39; Gaps 5;
QY 34 EKRHNKLTSSIEYK-----RHGDDVAKYAERIAEELQVYGSNS 72
Db 100 KKTNDKSSSTSNKPKRPLTAPFPMSPDKTFKSHNGSLAKDAKI-----GGEK 152
QY 73 PASFKGEGLVYKEILCDVCDKLVNKKTTETTLIEQNMLSKILERSLEEMDDEEVKEM 132
Db 153 WKSLETEE---KKVLDKAAELKAEYKNSLESNDADDEEED--EKQSDDDVDDAEKQV 206
QY 133 CD-----ELSIKNTDNLNRQA 148
Db 207 DDDDEVEKEVENTDDDKKEA 227

RESULT 15
US-11-434-137-10134
; Sequence 10134, Application US/11434137
; GENERAL INFORMATION:
; APPLICANT: Telford, John
; APPLICANT: Masignani, Vega
; APPLICANT: Ros, Immaculada Margarit Y
; APPLICANT: Fraser, Claire

; APPLICANT: Tettelin, Hervé
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/11/434,137
; PRIOR FILING DATE: 2006-05-16
; PRIOR APPLICATION NUMBER: US 10/415,182
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: PCT/GB01/04789
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: GB-0026333.5
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: GB-0028727.6
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: GB-0105640.7
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 12025
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 10134
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
US-11-434-137-10134
Query Match 7.2%; Score 91.5; DB 7; Length 375;
Best Local Similarity 25.7%; Pred. No. 4.7;
Matches 37; Conservative 33; Mismatches 61; Indels 13; Gaps 7;
QY 74 ASFIKGEGLVYKEILCDVCDK-LKVNKKTTETTLIEQNMLSKILERSLEEMDDEEVKEM 132
Db 228 SSVFKGGETIYLDVLPNISVKELEIHFQNEREKS--KNALKILLPERLAEFYAEIDLPEK 285
QY 133 CDELSIKNTDNLNRQALSATLTLFKMGGFKSV--QLAVIVANAVAKTILGR---GLSLA 187
Db 286 VKQSVKIDLEMLIQKLPILVTGRMSLAKSFVTGGVDLKEINPKTLESKKVAGLHFA 345
QY 188 GN--QVLTRTSLF-LTGPV--GWI 206
Db 346 GEVLIDINAHTGGFNITSALCTGVV 369
Search completed: August 3, 2006, 12:15:38
Job time : 34 secs

72798 8-1078 199339 M9

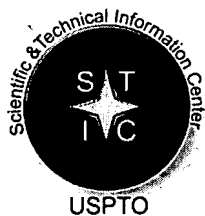
STIC-Biotech/ChemLib

From: Portner, Ginny
Sent: Monday, August 21, 2006 5:35 PM
To: STIC-Biotech/ChemLib
Subject: 10/387,977

please interference search SEQ ID NO 1 and 2. thanks!!

Ginny Portner
Remsen Building
Art Unit 1645
Room E03, B02; Mail Box 3C18
(571) 272-0862

8/22/2006



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 199339

TO: Ginny Portner
Location: rem/3B02/3C18
Art Unit: 1645
August 31, 2006

Case Serial Number: 10/387977

From: P. Sheppard
Location: Remsen Building
Phone: (571) 272-2529

sheppard@uspto.gov

Search Notes

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 25, 2006, 17:49:50 ; Search time 215.372 Seconds
(without alignments)
44.581 Million cell updates/sec

Title: US-10-387-977-1

Perfect score: 118

Sequence: 1 FNGISLANYTHGSETAWGT 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq.8.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*
10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	118	100.0	21	2	AAW83070	Peptide f
2	118	100.0	493	2	AAW83125	Peptide f
3	118	100.0	507	2	AAW83124	Peptide f
4	118	100.0	1706	2	AAW24786	Peptide f
5	118	100.0	1706	9	ADZ10438	P. gingiv
6	118	100.0	1706	9	ADZ10438	P. gingiv
7	118	100.0	1706	9	ADZ10427	P. gingiv
8	118	100.0	1706	9	ADZ10456	P. gingiv
9	118	100.0	1706	9	ADZ10456	P. gingiv
10	114	96.6	435	4	AAW49555	Microbial
11	114	96.6	492	7	ABW02694	Gingipain
12	114	96.6	492	9	ADV16838	Human cys
13	114	96.6	507	7	ABW02695	Porphyrom
14	114	96.6	737	2	AAW70186	Arg-gingi
15	114	96.6	737	2	AAW34846	Arg-gingi
16	114	96.6	737	3	AAW67395	Arg-gingi
17	114	96.6	737	4	AAU08937	P. gingiv
18	114	96.6	991	2	AAW77313	Porphyrom
19	114	96.6	1477	7	ABW02693	Porphyrom
20	114	96.6	1687	2	AAW96033	Porphyrom
21	114	96.6	1687	2	AAW69495	Haemagglu
22	114	96.6	1704	2	AAW70188	Arg-gingi
23	114	96.6	1704	2	AAW34843	Arg-gingi

ALIGNMENTS

RESULT 1

AAW83070
ID AAW83070 standard; peptide; 21 AA.

XX AC AAW83070;

XX DT 03-MAR-1999 (first entry)

XX DE Peptide from the 300kDa complex of cysteine proteinases and adhesins.

XX KW 300 kD multiprotein complex; cysteine proteinase; adhesin;
virulence factor; immune response; P. gingivalis infection;
periodontal disease; passive immunisation; subgingival plaque.

XX OS Synthetic.

XX OS Porphyromonas gingivalis.

XX PN WO9849192-A1.

XX PD 05-NOV-1998.

XX PF 30-APR-1998; 98WO-AU000311.

XX PR 30-APR-1997; 97AU-00006528.

XX PA (UYME) UNIV MELBOURNE.
(VICT-) VICTORIAN DAIRY IND AUTHORITY.
(CSLC-) CSL LTD.

XX PI Reynolds EC, Obrien-Simpson NM, Slakeski N;
WPI; 1999-024043/02.

XX DR Immunogenic composition containing new Porphyromonas gingivalis peptides
- and related antibodies, useful for treatment, prevention and diagnosis
of periodontal disease.

XX PS Claim 1; Page 49; 70pp; English.

XX CC Peptides AAW83070-122 are derived from the 300 kD multiprotein complex of
cysteine proteinases and adhesins. The 300kDa multiprotein complex is the
major virulence factor of Porphyromonas gingivalis. The specification
describes a composition for raising an immune response against P.
gingivalis which contains at least one of the present peptides. The
products are used to treat and prevent P. gingivalis infection
(periodontal disease). Antibodies are used for passive immunisation, and

AAW67396 Arg-gingi
AAU08938 P. gingiv
ADV16836 Human cys
AAW83071 Peptide f
AAW83126 PtiIK48
ADZ10439 P. gingiv
ADZ10409 P. gingiv
ADZ10393 P. gingiv
ADZ10428 P. gingiv
AAW96029 P. gingiv
AAW24787 PtiK anti
AAW69487 Haemagglu
ADV16839 Human cys
AAW96032 P. gingiv
AAW69494 Haemagglu
ADV16837 Human cys
AAW34847 Lys-gingi
AAW72458 Porphyrom
ADN25795 Bacterioc
ADH85853 Enterococ
ADV16133 X. palarg
AAW74922 Human sec

CC as diagnostic reagents for P. gingivalis in subgingival plaque. The
 XX peptides are used to detect P. gingivalis specific antibodies in serum
 SQ Sequence 21 AA;

Query Match 100.0%; Score 118; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 5.9e-11;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNGGISLANYTGHGSETAWGT 21
 |||||
 DB 1 FNGGISLANYTGHGSETAWGT 21

RESULT 2
 AAW831125

ID AAW831125 standard; protein; 493 AA.

XX AAW831125;

XX 03-MAR-1999 (first entry)

XX PrtIIR45 Arginine specific proteinase fragment.

XX 300 kD multiprotein complex; cysteine proteinase; adhesin;
 KW virulence factor; immune response; P. gingivalis infection;
 KW periodontal disease; passive immunisation; subgingival plaque.

XX Porphyromonas gingivalis.

XX WO9849192-A1.

XX 05-NOV-1998.

XX 30-APR-1998; 98WO-AU000311.

XX 30-APR-1997; 97AU-00006528.

XX (UYME) UNIV MELBOURNE.

PA (VICT-) VICTORIAN DAIRY IND AUTHORITY.

PA (CSLC-) CSL LTD.

PI Reynolds EC, Obrien-Simpson NM, Slakeski N;

XX WPI; 1999-024043/02.

XX Immunogenic composition containing new Porphyromonas gingivalis peptides
 PT - and related antibodies, useful for treatment, prevention and diagnosis
 PT of periodontal disease.

XX Example 1; Fig 8; 70pp; English.

XX The present sequence represents a fragment of the PrtIIR45 Arginine
 CC specific proteinase of Porphyromonas gingivalis. The specification
 CC describes peptides derived from the 300 kD multiprotein complex of
 CC cysteine proteinases and adhesins. The 300kDa multiprotein complex is the
 CC major virulence factor of P. gingivalis. The specification describes a
 CC composition for raising an immune response against P. gingivalis which
 CC contains at least one of the present peptides. The products are used to
 CC treat and prevent P. gingivalis infection (periodontal disease).
 CC Antibodies are used for passive immunisation, and as diagnostic reagents
 CC for P. gingivalis in subgingival plaque. The peptides are used to detect
 CC P. gingivalis specific antibodies in serum

XX Sequence 493 AA;

Query Match 100.0%; Score 118; DB 2; Length 493;
 Best Local Similarity 100.0%; Pred. No. 2.5e-09;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNGGISLANYTGHGSETAWGT 21
 |||||
 DB 199 FNGGISLANYTGHGSETAWGT 219

RESULT 3

AAW831124

ID AAW831124 standard; protein; 507 AA.

XX AAW831124;

XX 03-MAR-1999 (first entry)

XX PrtIIR50 Arginine specific proteinase fragment.

XX 300 kD multiprotein complex; cysteine proteinase; adhesin;
 KW virulence factor; immune response; P. gingivalis infection;
 KW periodontal disease; passive immunisation; subgingival plaque.

XX Porphyromonas gingivalis.

XX WO9849192-A1.

XX 05-NOV-1998.

XX 30-APR-1998; 98WO-AU000311.

XX 30-APR-1997; 97AU-00006528.

XX (UYME) UNIV MELBOURNE.

PA (VICT-) VICTORIAN DAIRY IND AUTHORITY.

PA (CSLC-) CSL LTD.

XX Reynolds EC, Obrien-Simpson NM, Slakeski N;

XX WPI; 1999-024043/02.

XX Immunogenic composition containing new Porphyromonas gingivalis peptides
 PT - and related antibodies, useful for treatment, prevention and diagnosis
 PT of periodontal disease.

XX Example 1; Fig 8; 70pp; English.

XX The present sequence represents a fragment of the PrtIIR50 Arginine
 CC specific proteinase of Porphyromonas gingivalis. The specification
 CC describes peptides derived from the 300 kD multiprotein complex of
 CC cysteine proteinases and adhesins. The 300kDa multiprotein complex is the
 CC major virulence factor of P. gingivalis. The specification describes a
 CC composition for raising an immune response against P. gingivalis which
 CC contains at least one of the present peptides. The products are used to
 CC treat and prevent P. gingivalis infection (periodontal disease).
 CC Antibodies are used for passive immunisation, and as diagnostic reagents
 CC for P. gingivalis in subgingival plaque. The peptides are used to detect
 CC P. gingivalis specific antibodies in serum

XX Sequence 507 AA;

Query Match 100.0%; Score 118; DB 2; Length 507;
 Best Local Similarity 100.0%; Pred. No. 2.6e-09;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNGGISLANYTGHGSETAWGT 21
 |||||
 DB 199 FNGGISLANYTGHGSETAWGT 219

RESULT 4

AAW24786

ID AAW24786 standard; protein; 1706 AA.

XX AAW24786;

XX 17-OCT-2003 (revised)

DT 25-NOV-1997 (first entry)

XX PrtR antigenic protein complex.

XX	Periodontal disease; cell surface protein; thiol protease; endopeptidase; PrtR; PrtR45; PrtR44; PrtR15; PrtR17; PrtR27; haemagglutinin; adhesin; therapy; diagnosis; vaccine; antigen.	
XX	Porphyromonas gingivalis; strain W50.	
XX		
FH	Key	Location/Qualifiers
FT	Peptide	1..227
FT		/label= Pro-pro_peptide
FT	Cleavage-site	227..228
FT	Protein	228..719
FT		/label= PrtR45
FT		/note= "45 kDa Arg-specific thiol protease"
FT	Cleavage-site	719..720
FT	Protein	720..1138
FT		/label= PrtR44
FT		/note= "44 kDa adhesin"
FT	Cleavage-site	1138..1139
FT	Protein	1139..1273
FT		/label= PrtR15
FT		/note= "15 kDa adhesin"
FT	Cleavage-site	1273..1274
FT	Protein	1274..1431
FT		/label= PrtR17
FT		/note= "17 kDa adhesin"
FT	Cleavage-site	1431..1432
FT	Protein	1432..1706
FT		/label= PrtR27
FT		/note= "27 kDa adhesin"
XX		
FN	W09716542-Al.	
XX		
XX	09-MAY-1997.	
XX		
XX	30-OCT-1996; 96WO-AU000673.	
XX		
XX	30-OCT-1995; 95AU-00006275.	
XX		
XX	(UYME) UNIV MELBOURNE.	
PA	(VICT-) VICTORIAN DAIRY IND AUTHORITY.	
XX		
PI	Reynolds EC, Bhogal PS, Slakeski N;	
XX		
XX	WPI; 1997-272112/24.	
DR	N-PSDB; AAT78850.	
XX		
PT	New antigenic protein complex from Porphyromonas gingivalis - comprising Arg- and lys- specific thiol endo-peptidase(s), used in the detection, prevention and treatment of periodontal disease.	
XX		
PS	Example 1; Fig 8b; 68pp; English.	
XX		
CC	A PrtR-PrtR cell surface protein of Porphyromonas ginivalis (PG) comprises a 300 kDa complex composed of a 45 kDa arginine-specific thiol protease and 44, 15, 17 and 27 kDa adhesins encoded by the prtR gene (AAT78850), and a 148 kDa lysine-specific thiol protease and 39, 15 and 44 kDa adhesins (see AAT24787) encoded by the prtK gene (AAT78851). A claimed antigenic complex comprises at least one multimeric protein complex of PrtR and PrtK each containing at least one adhesin domain, the complex having a mol.wt. of over 200 kDa, and preferably comprises all 9 proteins of the PrtR-PrtK complex (see also AAT24780-85). It can be used in a claimed composition to elicit an immune response directed against PG, and in a claimed method of reducing the prospect of PG infection and/or severity of disease. Antibodies directed against the complex are claimed for use in treating PG infection. Unlike whole PG cells or other previously prepared antigens based on fimbriae or the capsule, the PrtR-PrtK complex or component parts are safe and effective antigens. (Updated on 17-OCT-2003 to standardise OS field)	
XX		
XX	Sequence 1706 AA;	

Query Match 100.0%; Score 118; DB 2; Length 1706;

Best Local Similarity	100.0%;	Pred. No. 1.1e-08;	
Matches	21; Conservative	0; Mismatches	0; Indels
			0; Gaps
QY	1	FMGGISLANYTGHGSETAWGT	21
DB	426	FMGGISLANYTGHGSETAWGT	446
RESULT 5			
ADZ10438			
ID	ADZ10438	standard; protein; 1706	AA.
XX	AC	ADZ10438;	
XX	DT		
XX	DE	16-JUN-2005	(first entry)
XX	DE	P. gingivalis	arginine specific protease ArgI, SEQ ID 221.
XX	KW	Vaccine; enzyme; therapy; diagnosis;	periodontal disease;
KW	KW	antiinflammatory; mouth disease;	gingivitis; inflammation; mouth disease;
KW	KW	endocarditis; cardiac; cardiovascular	disease; inflammation;
KW	KW	bacterial urinary tract infection;	antibacterial; uropathic;
KW	KW	genitourinary disease; infection;	osteomyelitis; osteopathic;
XX	KW	musculoskeletal disease; antigen.	
OS		Porphyromonas gingivalis.	
XX	XX	WO2005019249-A2.	
PN			
XX	PD	03-MAR-2005.	
XX	PF	10-AUG-2004; 2004WO-US025778.	
XX	PR	15-AUG-2003; 2003US-0495589P.	
XX	PA	(UYFL) UNIV FLORIDA.	
PI		Progulske-Fox A, Hillman JD, Handfield M;	
XX	DR	WPI: 2005-214225/22.	
DR	DR	N-PSDB; ADZ10270.	
XX			
PT	PT	New isolated immunogenic polypeptide, useful for diagnosing, treating,	
PT	PT	preventing, or ameliorating diseases and infections caused by	
PT	PT	Porphyromonas gingivalis e.g. localized prepubertal periodontitis.	
XX			
PS	Claim 1;	SEQ ID NO 221; 73pp; English.	
XX			
CC	CC	The invention relates to an isolated immunogenic Porphyromonas gingivalis	
CC	CC	polypeptide (I) comprising (a) a polypeptide at least about 5 contiguous	
CC	CC	amino acids of an amino acid sequence appearing as ADZ10384 - ADZ10443,	
CC	CC	ADZ10445 - ADZ10478 or ADZ10480-ADZ10571, (b) the polypeptide of (a) and	
CC	CC	a heterologous polypeptide or (c) an amino acid sequence selected from	
CC	CC	ADZ10384 - ADZ10443, ADZ10445 - ADZ10478 or ADZ10480-ADZ10571. Also	
CC	CC	included are an isolated polynucleotide (comprising a sequence that	
CC	CC	encodes (I) (a), (b) or (c)), an expression control sequence operably	
CC	CC	linked to the polynucleotide above (or the polynucleotide above and a	
CC	CC	heterologous polynucleotide), an expression vector comprising the	
CC	CC	polynucleotide, a host cell comprising the expression vector, an antibody	
CC	CC	(antibody fragment, or single-chain antibody) that specifically binds to	
CC	CC	the polypeptide, a composition comprising the antibody (antibody	
CC	CC	fragment, or single-chain antibody) and a pharmaceutical carrier,	
CC	CC	treating or preventing a disease/infection caused by Porphyromonas	
CC	CC	gingivalis, a composition comprising the isolated immunogenic polypeptide	
CC	CC	(or the polynucleotide) and a pharmaceutical carrier, eliciting an immune	
CC	CC	response in an animal, detecting the presence of a first P. gingivalis	
CC	CC	polynucleotide in a test sample, detecting the presence of a P.	
CC	CC	gingivalis antibody in a test sample, detecting the presence of P.	
CC	CC	gingivalis (or a P. gingivalis polypeptide) in a test sample, detecting	
CC	CC	P. gingivalis infection in a subject and detecting P. gingivalis in a	
CC	CC	subject. The immunogenic polypeptide is useful for the diagnosis,	
CC	CC	treatment, prevention, and amelioration of diseases and infections caused	
CC	CC	by P. gingivalis. It is useful for treating or preventing localized	

CC prepubertal periodontitis, generalized prepubertal periodontitis,
 CC localized juvenile periodontitis, generalized juvenile periodontitis,
 CC rapidly progressive adult periodontitis, refractory adult periodontitis,
 CC endocarditis, thyroid gland abscess, urinary tract infection, brain
 CC abscess, or vertebral osteomyelitis. The present sequence is a P.
 CC gingivalis immunogenic protein of the invention.
 XX
 SQ Sequence 1706 AA;

Query Match 100.0%; Score 118; DB 9; Length 1706;
 Best Local Similarity 100.0%; Pred. No. 1.1e-08;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNGGISLANYTGHGSETAWGT 21
 DB 426 FNGGISLANYTGHGSETAWGT 446

RESULT 6
 ADZ10403
 ID ADZ10403 standard; protein; 1706 AA.

XX AC ADZ10403;

XX 16-JUN-2005 (first entry)

XX DE P. gingivalis arginine -specific protease ArgI SEQ ID 186.

XX KW Vaccine; enzyme; therapy; diagnosis; periodontal disease;
 KW antiinflammatory; mouth disease; gingivitis; inflammation; mouth disease;
 KW endocarditis; cardiant; cardiovascular disease; inflammation;
 KW bacterial urinary tract infection; antibacterial; uropathic;
 KW genitourinary disease; infection; osteomyelitis; osteopathic;
 KW musculoskeletal disease; antigen.

XX OS Porphyromonas gingivalis.

XX PN W02005019249-A2.

XX PD 03-MAR-2005.

XX PF 10-AUG-2004; 2004WO-US025778.

XX PR 15-AUG-2003; 2003US-0495589P.

XX PA (UYFL) UNIV FLORIDA.

XX PI Progulske-Fox A, Hillman JD, Handfield M;

XX DR WPI; 2005-214225/22.

XX DR N-PSDB; ADZ10235.

XX PT New isolated immunogenic polypeptide, useful for diagnosing, treating,
 PT preventing, or ameliorating diseases and infections caused by
 PT Porphyromonas gingivalis e.g. localized prepubertal periodontitis.

XX PS Claim 1; SEQ ID NO 186; 73pp; English.

XX CC The invention relates to an isolated immunogenic Porphyromonas gingivalis
 CC polypeptide (I) comprising (a) a polypeptide at least about 5 contiguous
 CC amino acids of an amino acid sequence appearing as ADZ10384 - ADZ10443,
 CC ADZ10445 - ADZ10478 or ADZ10480-ADZ10571, (b) the polypeptide of (a) and
 CC a heterologous polypeptide or (c) an amino acid sequence selected from
 CC ADZ10384 - ADZ10443, ADZ10445 - ADZ10478 or ADZ10480-ADZ10571. Also
 CC included are an isolated polynucleotide (comprising a sequence that
 CC encodes (I) (a), (b) or (c)), an expression control sequence operably
 CC linked to the polynucleotide above (or the polynucleotide above and a
 CC heterologous polynucleotide), an expression vector comprising the
 CC polynucleotide, a host cell comprising the expression vector, an antibody
 CC (antibody fragment, or single-chain antibody) that specifically binds to
 CC the polypeptide, a composition comprising the antibody (antibody
 CC fragment, or single-chain antibody) and a pharmaceutical carrier,
 CC treating or preventing a disease/infection caused by Porphyromonas

CC gingivalis, a composition comprising the isolated immunogenic polypeptide
 CC (or the polynucleotide) and a pharmaceutical carrier, eliciting an immune
 CC response in an animal, detecting the presence of a first P. gingivalis
 CC polynucleotide in a test sample, detecting the presence of a P.
 CC gingivalis antibody in a test sample, detecting the presence of P.
 CC gingivalis (or a P. gingivalis polypeptide) in a test sample, detecting
 CC P. gingivalis infection in a subject and detecting P. gingivalis in a
 CC subject. The immunogenic polypeptide is useful for the diagnosis,
 CC treatment, prevention, and amelioration of diseases and infections caused
 CC by P. gingivalis. It is useful for treating or preventing localized
 CC prepubertal periodontitis, generalized prepubertal periodontitis,
 CC localized juvenile periodontitis, generalized juvenile periodontitis,
 CC rapidly progressive adult periodontitis, refractory adult periodontitis,
 CC endocarditis, thyroid gland abscess, urinary tract infection, brain
 CC abscess, or vertebral osteomyelitis. The present sequence is a P.
 CC gingivalis immunogenic protein of the invention.

XX SQ Sequence 1706 AA;

Query Match 100.0%; Score 118; DB 9; Length 1706;
 Best Local Similarity 100.0%; Pred. No. 1.1e-08;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNGGISLANYTGHGSETAWGT 21

DB 426 FNGGISLANYTGHGSETAWGT 446

RESULT 7

ADZ10427

ID ADZ10427 standard; protein; 1706 AA.

XX AC ADZ10427;

XX DT 16-JUN-2005 (first entry)

XX DE P. gingivalis arginine specific protease ArgI, SEQ ID 210.

XX KW Vaccine; enzyme; therapy; diagnosis; periodontal disease;
 KW antiinflammatory; mouth disease; gingivitis; inflammation; mouth disease;
 KW endocarditis; cardiant; cardiovascular disease; inflammation;
 KW bacterial urinary tract infection; antibacterial; uropathic;
 KW genitourinary disease; infection; osteomyelitis; osteopathic;
 KW musculoskeletal disease; antigen.

XX OS Porphyromonas gingivalis.

XX PN W02005019249-A2.

XX PD 03-MAR-2005.

XX PF 10-AUG-2004; 2004WO-US025778.

XX PR 15-AUG-2003; 2003US-0495589P.

XX PA (UYFL) UNIV FLORIDA.

XX PI Progulske-Fox A, Hillman JD, Handfield M;

XX DR WPI; 2005-214225/22.

XX DR N-PSDB; ADZ10256.

XX PT New isolated immunogenic polypeptide, useful for diagnosing, treating,
 PT preventing, or ameliorating diseases and infections caused by
 PT Porphyromonas gingivalis e.g. localized prepubertal periodontitis.

XX PS Claim 1; SEQ ID NO 210; 73pp; English.

XX CC The invention relates to an isolated immunogenic Porphyromonas gingivalis
 CC polypeptide (I) comprising (a) a polypeptide at least about 5 contiguous
 CC amino acids of an amino acid sequence appearing as ADZ10384 - ADZ10443,
 CC ADZ10445 - ADZ10478 or ADZ10480-ADZ10571, (b) the polypeptide of (a) and
 CC a heterologous polypeptide or (c) an amino acid sequence selected from

CC ADZ10384 - ADZ10443, ADZ10445 - ADZ10478 or ADZ10480-ADZ10571. Also
 CC included are an isolated polynucleotide (comprising a sequence that
 CC encodes (i) (a), (b) or (c)), an expression control sequence operably
 CC linked to the polynucleotide above (or the polynucleotide above and a
 CC heterologous polynucleotide), an expression vector comprising the
 CC polynucleotide, a host cell comprising the expression vector, an antibody
 CC (antibody fragment, or single-chain antibody) that specifically binds to
 CC the polypeptide, a composition comprising the antibody (antibody
 CC fragment, or single-chain antibody) and a pharmaceutical carrier,
 CC treating or preventing a disease/infection caused by Porphyromonas
 CC gingivalis, a composition comprising the isolated immunogenic polypeptide
 CC (or the polynucleotide) and a pharmaceutical carrier, eliciting an immune
 CC response in an animal, detecting the presence of a first P. gingivalis
 CC polynucleotide in a test sample, detecting the presence of a P.
 CC gingivalis antibody in a test sample, detecting the presence of a P.
 CC gingivalis (or a P. gingivalis polypeptide) in a test sample, detecting
 CC P. gingivalis infection in a subject and detecting P. gingivalis in a
 CC subject. The immunogenic polypeptide is useful for the diagnosis,
 CC treatment, prevention, and amelioration of diseases and infections caused
 CC by P. gingivalis. It is useful for treating or preventing localized
 CC prepubertal periodontitis, generalized prepubertal periodontitis,
 CC localized juvenile periodontitis, generalized juvenile periodontitis,
 CC rapidly progressive adult periodontitis, refractory adult periodontitis,
 CC endocarditis, thyroid gland abscess, urinary tract infection, brain
 CC abscess, or vertebral osteomyelitis. The present sequence is a P.
 CC gingivalis immunogenic protein of the invention.

XX SQ Sequence 1706 AA;

Query Match 100.0%; Score 118; DB 9; Length 1706;
 Best Local Similarity 100.0%; Pred. No. 1.le-08;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FNGGISLANYTGHGSETAWGT 21
 |||||
 Db 426 FNGGISLANYTGHGSETAWGT 446

RESULT 8

ID ADZ10456
 XX ADZ10456 standard; protein; 1706 AA.

AC ADZ10456;

DT 16-JUN-2005 (first entry)

DE P. gingivalis arginine-specific protease ArgI SEQ ID 239.

KW Vaccine; enzyme; therapy; diagnosis; periodontal disease;
 KW antiinflammatory; mouth disease; gingivitis; inflammation; mouth disease;
 KW endocarditis; cardiant; cardiovascular disease; inflammation;
 KW bacterial urinary tract infection; antibacterial; uropathic;
 KW genitourinary disease; infection; osteomyelitis; osteopathic;
 KW musculoskeletal disease; antigen.

XX Porphyromonas gingivalis.

PN WO2005019249-A2.

XX 03-MAR-2005.

PF 10-AUG-2004; 2004WO-US025778.

XX 15-AUG-2003; 2003US-0495589P.

XX (UYFL) UNIV FLORIDA.

XX Progulske-Fox A, Hillman JD, Handfield M;

DR WPI: 2005-214225/22.

XX N-PSDB; ADZ10287.

PT New isolated immunogenic polypeptide, useful for diagnosing, treating,

PT preventing, or ameliorating diseases and infections caused by
 XX Porphyromonas gingivalis e.g. localized prepubertal periodontitis.
 PS Claim 1; SEQ ID NO 239; 73pp; English.

CC The invention relates to an isolated immunogenic Porphyromonas gingivalis
 CC polypeptide (I) comprising (a) a polypeptide at least about 5 contiguous
 CC amino acids of an amino acid sequence appearing as ADZ10384 - ADZ10443,
 CC ADZ10445 - ADZ10478 or ADZ10480-ADZ10571, (b) the polypeptide of (a) and
 CC a heterologous polypeptide or (c) an amino acid sequence selected from
 CC ADZ10384 - ADZ10443, ADZ10445 - ADZ10478 or ADZ10480-ADZ10571. Also
 CC included are an isolated polynucleotide (comprising a sequence that
 CC encodes (i) (a), (b) or (c)), an expression control sequence operably
 CC linked to the polynucleotide above (or the polynucleotide above and a
 CC heterologous polynucleotide), an expression vector comprising the
 CC polynucleotide, a host cell comprising the expression vector, an antibody
 CC (antibody fragment, or single-chain antibody) that specifically binds to
 CC the polypeptide, a composition comprising the antibody (antibody
 CC fragment, or single-chain antibody) and a pharmaceutical carrier,
 CC treating or preventing a disease/infection caused by Porphyromonas
 CC gingivalis, a composition comprising the isolated immunogenic polypeptide
 CC (or the polynucleotide) and a pharmaceutical carrier, eliciting an immune
 CC response in an animal, detecting the presence of a first P. gingivalis
 CC polynucleotide in a test sample, detecting the presence of a P.
 CC gingivalis antibody in a test sample, detecting the presence of a P.
 CC gingivalis (or a P. gingivalis polypeptide) in a test sample, detecting
 CC P. gingivalis infection in a subject and detecting P. gingivalis in a
 CC subject. The immunogenic polypeptide is useful for the diagnosis,
 CC treatment, prevention, and amelioration of diseases and infections caused
 CC by P. gingivalis. It is useful for treating or preventing localized
 CC prepubertal periodontitis, generalized prepubertal periodontitis,
 CC localized juvenile periodontitis, generalized juvenile periodontitis,
 CC rapidly progressive adult periodontitis, refractory adult periodontitis,
 CC endocarditis, thyroid gland abscess, urinary tract infection, brain
 CC abscess, or vertebral osteomyelitis. The present sequence is a P.
 CC gingivalis immunogenic protein of the invention.

XX SQ Sequence 1706 AA;

Query Match 100.0%; Score 118; DB 9; Length 1706;
 Best Local Similarity 100.0%; Pred. No. 1.le-08;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FNGGISLANYTGHGSETAWGT 21
 |||||
 Db 426 FNGGISLANYTGHGSETAWGT 446

RESULT 9

AEB91466

ID AEB91466 standard; protein; 1706 AA.

XX AEB91466;

XX 20-OCT-2005 (first entry)

DE Microbial pathogen adhesin protein sequence, SEQ ID NO:176.

XX algorithm; adhesin; pharmaceutical; vaccine; drug screening;
 KW bordetella pertussis infection; antibacterial; pneumonia;
 KW antiinflammatory; respiratory-gen.; gastric ulcer; antilucer;
 KW gastrointestinal-gen.; urinary tract infection; antimicrobial; uropathic.

XX Porphyromonas gingivalis.

XX WO2005076010-A2.

XX 18-AUG-2005.

XX 07-FEB-2005; 2005WO-IN000037.

XX 06-FEB-2004; 2004IN-DE000173.

PR 20-JUL-2004; 2004US-0589227P.

XX (COUL) COUNCIL SCI & IND RES SOUTH AFRICA.
 XX Sachdeva G, Kumar K, Jain P, Brahmachari SK, Ramachandran S;
 XX WPI; 2005-597835/61.
 XX Computational method for identifying adhesin and adhesin like molecules,
 PT comprises computing sequence-based attributes of protein sequences using
 PT neural network software and training an artificial neural network.
 XX Claim 16; SEQ ID NO 176; 402pp; English.
 XX The present invention relates to a computational method (M1) for
 CC identifying adhesin and adhesin-like proteins, by computing the sequence-
 CC based attributes of protein sequences using five attribute modules of a
 CC neural network software, training an artificial neural network (ANN) for
 CC each of the computed five attributes, and identifying the adhesin and
 CC adhesin-like proteins having probability of being an adhesin (Pad) as
 CC equal or greater than 0.51. Also claimed is a set of 274 annotated genes
 CC encoding adhesin and adhesin-like proteins, having 274 fully defined 162-
 CC 1151 base pair (SEQ ID NO: 385-658) sequences; a set of 105 hypothetical
 CC genes encoding adhesin and adhesin-like proteins, having 105 fully
 CC defined 306-15876 base pairs (SEQ ID NO: 659-763); a set of 279 annotated
 CC adhesin and adhesin-like proteins, having 279 fully defined 53-3716 base
 CC pair (SEQ ID NO: 1-279); a set of 105 hypothetical adhesin and adhesin-
 CC like proteins, having 105 fully defined 106-5291 base pair (SEQ ID NO:
 CC 280-384) sequences; and a fully connected multilayer feed forward ANN (I)
 CC based on (M1). (M1) is useful for identifying adhesin and adhesin-like
 CC proteins, of therapeutic potential, and identifying and short-listing
 CC proteins for further testing in development of new vaccine formulations
 CC to eliminate diseases caused by various pathogenic organisms. (M1) is
 CC useful for identifying putative adhesins that are important in drug
 CC discovery and preventing therapeutics for whooping cough, pneumonia,
 CC gastric ulcer and urinary tract infections. (M1) identifies adhesins from
 CC distantly related organisms, and from bacteria belonging to a wide
 CC phylogenetic spectrum. (M1) is capable of predicting adhesive nature of
 CC unique proteins. The present sequence is a microbial pathogen adhesin
 CC protein sequence.
 XX Sequence 1706 AA;
 SQ Query Match 100.0%; Score 118; DB 9; Length 1706;
 Best Local Similarity 100.0%; Pred. No. 1.1e-08;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FNGGISLANYTGHGSETAWGT 21
 DB 426 FNGGISLANYTGHGSETAWGT 446
 RESULT 10
 AAB49555
 ID AAB49555 standard; protein; 435 AA.
 AC AAB49555;
 XX 09-MAR-2001 (first entry)
 DT Gingipain R.
 DE Gingipain R; antiinflammatory; cardiant; RgpB; cysteine protease;
 KW Periodontitis; gingipain R inhibitor; periodontal disease;
 KW Cardiovascular disease.
 XX Porphyromonas gingivalis.
 OS WO200071682-A2.
 PN 30-NOV-2000.
 PD 19-MAY-2000; 2000WO-EP004561.
 PF
 XX

20-MAY-1999; 99EP-00109944.
 (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 (UYGE-) UNIV GEORGIA RES FOUND INC.
 XX Eichinger A, Beisel H, Bode W, Huber R, Moroder L, Travis J;
 PI Potempa J, Alefelder S, Pleiner E, Stuerzebecher J;
 XX WPI; 2001-061353/07.
 XX New crystal structure of gingipain R useful to obtain crystal structure
 PT data for design and/or identification of gingipain R inhibitors useful
 PT for treatment and/or prevention of periodontitis.
 XX Disclosure; Fig 3; 46pp; English.
 XX The present sequence is gingipain R (RgpB) from Porphyromonas gingivalis.
 CC Gingipain R is a cysteine protease and plays a pivotal role in the
 CC aetiology of periodontitis. The crystal structure of the present protein
 CC is useful to obtain crystal structure data for the design and/or
 CC identification of gingipain R inhibitors, using a computer aided
 CC modelling program. The identified gingipain R inhibitors are useful for
 CC the treatment and/or prevention of periodontal diseases, especially
 CC periodontitis, and/or cardiovascular diseases that occur after a primary
 CC periodontal disease
 XX Sequence 435 AA;
 SQ Query Match 96.6%; Score 114; DB 4; Length 435;
 Best Local Similarity 95.2%; Pred. No. 8.9e-09;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FNGGISLANYTGHGSETAWGT 21
 DB 199 FNGGISLANYTGHGSETAWGT 219
 RESULT 11
 ABW02694
 ID ABW02694 standard; protein; 492 AA.
 AC ABW02694;
 XX 11-MAR-2004 (first entry)
 DT Porphyromonas gingivalis 95 kDa RgpA protein 50 kDa catalytic domain.
 XX Activated protein C; APC; arginine-specific cysteine proteinase; RgpA;
 KW 95-kDa gingipain R; HRP; RgpB; 50 kDa-gingipain R; blood coagulation;
 KW RGP-2; septicemia; disseminated intravascular coagulation; gene therapy;
 KW anticoagulant; thrombolytic; antibacterial; immunosuppressive; enzyme.
 XX Porphyromonas gingivalis.
 OS US6627193-B1.
 PN 30-SEP-2003.
 PD 13-JAN-2000; 2000US-00482500.
 PF 13-JAN-1999; 99US-0115869P.
 PR (UYGE-) UNIV GEORGIA RES FOUND INC.
 XX Travis J, Imamura T, Potempa J;
 XX WPI; 2003-874308/81.
 XX Producing activated protein C in blood, useful for controlling blood
 PT coagulation, comprises contacting the blood with an amount of an arginine
 PT -specific cysteine proteinase derived from Porphyromonas gingivalis.
 XX Claim 8; SEQ ID NO 2; Opp; English.
 PS

XX The present invention relates to a method of producing activated protein
CC C (APC) in a medium comprising protein C. The method involves contacting
CC the medium with an arginine-specific cysteine proteinase, referred as
CC Rgpa (also referred as 95-kDa gingipain R (HRGP)) and RgpB (also referred
CC as 50 kDa-gingipain R (RGP-2)) of bacterial origin. The composition and
CC methods are useful in controlling blood coagulation or in treating
CC septicemia or disseminated intravascular coagulation in patients. The
CC invention is also used in gene therapy. The present sequence is
CC Porphyromonas gingivalis 95 kDa Rgpa protein 50 kDa catalytic domain
XX
SQ Sequence 492 AA;

Query Match 96.6%; Score 114; DB 7; Length 492;
Best Local Similarity 95.2%; Pred. No. 1e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FNGGISLVNYTGHGSETAWGT 21
Db 199 FNGGISLVNYTGHGSETAWGT 219

RESULT 12
ADV16838
ID ADV16838 standard; protein; 492 AA.
XX
AC ADV16838;
XX
XX
DT 24-FEB-2005 (first entry)
XX
DE Human cysteine protease related protein, SEQ ID 3.
XX
KW selectable marker; periodontal disease; angina; antiangiinal;
KW cardiovascular disease; diabetes; antidiabetic; cysteine protease;
KW enzyme.
XX
OS Homo sapiens.
XX
XX WO2004106541-A1.
XX
XX 09-DEC-2004.
XX
XX 31-MAY-2004; 2004WO-JP007867.
XX
XX 30-MAY-2003; 2003JP-00154070.
XX
XX (KYUS-) KYUSHU TLO CO LTD.
XX
XX Yamamoto K;
XX
XX WPI; 2005-021305/02.
XX
XX Novel periodontal disease marker for detecting periodontal disease,
PT comprising cysteine protease derived from Porphyromonas gingivalis,
PT useful for detecting periodontal disease, in saliva.
XX
XX Claim 5; SEQ ID NO 3; 44pp; Japanese.
XX
XX The invention relates to a novel periodontal disease marker for detecting
CC periodontal disease. The marker comprises a cysteine protease derived
CC from a Porphyromonas gingivalis microbe. The invention further comprises:
CC a periodontal disease ward appearance kit, comprising a sampling tool,
CC a periodontal disease marker, synthetic substrate, buffer, and a reducing
CC agent. The periodontal disease marker is useful for detecting and
CC diagnosing periodontal disease from saliva. The periodontal disease
CC marker provides reliable and convenient detection of periodontal disease,
CC and provides simultaneous detection of angina and diabetes. This sequence
CC represents a human cysteine protease related protein of the invention.
XX
SQ Sequence 492 AA;

Query Match 96.6%; Score 114; DB 9; Length 492;
Best Local Similarity 95.2%; Pred. No. 1e-08;

Qy 1 FNGGISLVNYTGHGSETAWGT 21
Db 199 FNGGISLVNYTGHGSETAWGT 219

RESULT 13
ABW02695
ID ABW02695 standard; protein; 507 AA.
XX
AC ABW02695;
XX
XX
DT 11-MAR-2004 (first entry)
XX
DE Porphyromonas gingivalis 50 kDa RgpB protein.
XX
KW Activated protein C; APC; arginine-specific cysteine proteinase; Rgpa;
KW 95-kDa gingipain R; HRGP; RgpB; 50 kDa-gingipain R; blood coagulation;
KW RGP-2; septicemia; disseminated intravascular coagulation; gene therapy;
KW anticoagulant; thrombolytic; antibacterial; immunosuppressive; enzyme.
XX
OS Porphyromonas gingivalis.
XX
XX US6627193-B1.
XX
XX 30-SEP-2003.
XX
XX 13-JAN-2000; 2000US-00482500.
XX
XX 13-JAN-1999; 99US-0115869P.
XX
XX (UYGE-) UNIV GEORGIA RES FOUND INC.
XX
XX Travis J, Imamura T, Potempa J;
XX
XX WPI; 2003-874308/81.
XX
XX Producing activated protein C in blood, useful for controlling blood
PT coagulation, comprises contacting the blood with an amount of an arginine
PT -specific cysteine proteinase derived from Porphyromonas gingivalis.
XX
XX Claim 1; SEQ ID NO 3; 0pp; English.
XX
XX The present invention relates to a method of producing activated protein
CC C (APC) in a medium comprising protein C. The method involves contacting
CC the medium with an arginine-specific cysteine proteinase, referred as
CC Rgpa (also referred as 95-kDa gingipain R (HRGP)) and RgpB (also referred
CC as 50 kDa-gingipain R (RGP-2)) of bacterial origin. The composition and
CC methods are useful in controlling blood coagulation or in treating
CC septicemia or disseminated intravascular coagulation in patients. The
CC invention is also used in gene therapy. The present sequence is
CC Porphyromonas gingivalis 50 kDa RgpB protein
XX
SQ Sequence 507 AA;

Query Match 96.6%; Score 114; DB 7; Length 507;
Best Local Similarity 95.2%; Pred. No. 1.1e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FNGGISLVNYTGHGSETAWGT 21
Db 199 FNGGISLVNYTGHGSETAWGT 219

RESULT 14
AAR70186
ID AAR70186 standard; protein; 737 AA.
XX
AC AAR70186;
XX
XX
DT 25-MAR-2003 (revised)
DT 21-SEP-1995 (first entry)

```

XX DE Arg-gingipain-1.
XX KW Arg-gingipain-1; gingivalis; periodontal disease; vaccine;
XX KW arginine-specific protease.
XX OS Porphyromonas gingivalis.
XX PH Key Location/Qualifiers
XX FT Protein 228..737
XX FT /label= Mat_protein
XX PN WO9507286-A1.
XX XX
XX XX
XX PD 16-MAR-1995.
XX XX
XX PF 09-SEP-1994; 94WO-US010283.
XX XX
XX PR 10-SEP-1993; 93US-00119361.
XX PR 21-OCT-1993; 93US-00141324.
XX PR 24-JUN-1994; 94US-00265441.
XX XX
XX PA (UYGE-) UNIV GEORGIA RES FOUND INC.
XX XX
XX PI Travis J, Potempa J, Barr PJ, Pavloff N;
XX XX
XX DR WPI; 1995-123373/16.
XX DR N-PSDB; AAQ83484.
XX XX
XX PT DNA encoding Arg-gingipain proteins - used to develop prods. for
XX PT detection, treatment and prevention of periodontal disease.
XX PS Disclosure; Page 63-66; 89pp; English.
XX XX
XX CC A low mol.wt. arginine-specific gingipain (AG-1) and high mol.wt. AG (AG-
XX CC 2) were isolated from P. gingivalis strains H66 (ATCC 33277) and W50
XX CC (ATCC 53973). The sequences of the proteins were used to design PCR
XX CC primers and probes to isolate AG DNA. Lambda DASH and lambda ZAP
XX CC libraries were screened with a probe based on amino acids 11-22 of the AG
XX CC protein to obtain DNA encoding AG-1 (AAQ83484) and AG-2 (AAQ83489).
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 737 AA;
XX
XX Query Match 96.6%; Score 114; DB 2; Length 737;
XX Best Local Similarity 95.2%; Pred. No. 1.7e-08;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 FNGGISLANYTGHGSETAWGT 21
XX ||||| ||||| ||||| |||||
XX Db 426 FNGGISLVNYTGHGSETAWGT 446
XX
XX RESULT 15
XX AAQ34846
XX ID AAQ34846 standard; protein; 737 AA.
XX AC AAW34846;
XX DT 03-JUN-1998 (first entry)
XX XX
XX DE Arg-gingipain high molecular weight polypeptide sequence.
XX XX
XX KW Arg-specific gingipain protease; gingivalis; periodontal disease;
XX KW vaccine; infection.
XX XX
XX OS Porphyromonas gingivalis.
XX XX
XX PH Key Location/Qualifiers
XX FT Protein 1..227
XX FT /note= "precursor protein"
XX FT 228..737
XX FT /note= "mature Arg-gingipain"
XX FT

```

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XX PN WO9734629-A1.
XX XX
XX PD 25-SEP-1997.
XX XX
XX PF 21-MAR-1997; 97WO-US004635.
XX XX
XX PR 22-MAR-1996; 96US-0013945P.
XX XX
XX PA (UYGE-) UNIV GEORGIA RES FOUND INC.
XX PA (MORE-) MOREHOUSE SCHOOL MEDICINE.
XX PI Potempa J, Travis J, Genco C;
XX DR WPI; 1997-479993/44.
XX DR N-PSDB; AAT93873.
XX XX
XX PT Porphyromonas gingivalis Arg-specific gingipain protease peptide(s) -
XX PT useful for protecting animals and humans from gingivalis and periodontal
XX PT diseases.
XX PS Disclosure; Page 58-60; 95pp; English.
XX XX
XX CC The present sequence represents an arginine-specific protease of
XX CC Porphyromonas gingivalis. The following peptides, derived from Arg- and
XX CC Lys-specific high molecular weight proteases, offer protection against
XX CC infection: YTVVYRDGK IKEGLTATTE DDGATGNHE YCWEKYTAGS VSPKVC (I);
XX CC YTPVEKQNG RMIVIVAKKY (II); QLPFIFDVAC VNGDFLFSMP CFAEALMRAQ (III);
XX CC GEPNPQDVS NLTAATGQKQ VTLKWDASTK (IV); GNHEYCVKVK YTAGVSPKVC KDVTV (V);
XX CC RMFNYPFGR YTPVEKQNG (VI); TTAGFEDTYK RMFNYPFGR (VII); DYTVYVYRDG
XX CC TKIKEGLTAT TFEEDGVATG NMEYCVKVKY TAGVSPKVC (VIII); YTVVYRDGT KIKEGLTATTF
XX CC EEDG (IX); RDGKIKEGL TATTFEEDGV ATGN (X); KIKEGLTATT FEEDGVATGN HEY (XI)
XX CC ; KWDAPNGTNP PNP PNPENPN PGTTLSE (XII); and YTPVEKENG RMIVIVAKKY
XX CC (XIII). They are used in vaccines to protect animals, including humans,
XX CC from gingivitis and/or periodontal diseases
XX SQ Sequence 737 AA;
XX
XX Query Match 96.6%; Score 114; DB 2; Length 737;
XX Best Local Similarity 95.2%; Pred. No. 1.7e-08;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 FNGGISLANYTGHGSETAWGT 21
XX ||||| ||||| ||||| |||||
XX Db 426 FNGGISLVNYTGHGSETAWGT 446
XX
XX Search completed: August 25, 2006, 17:57:47
XX Job time : 216.372 secs

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OM protein - protein search, using sw model

Run on: August 25, 2006, 18:04:46 ; Search time 34.6744 Seconds
(without alignments)
53.012 Million cell updates/sec

Title: US-10-387-977-1

Perfect score: 118

Sequence: 1 FNGGISLANTYGHGSETAWGT 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
- 1: /EMC Celerra_SIDS3/ptodata/2/iaa/5 COMB.pep.*
 - 2: /EMC Celerra_SIDS3/ptodata/2/iaa/6 COMB.pep.*
 - 3: /EMC Celerra_SIDS3/ptodata/2/iaa/7 COMB.pep.*
 - 4: /EMC Celerra_SIDS3/ptodata/2/iaa/H COMB.pep.*
 - 5: /EMC Celerra_SIDS3/ptodata/2/iaa/PCTUS COMB.pep.*
 - 6: /EMC Celerra_SIDS3/ptodata/2/iaa/RE COMB.pep.*
 - 7: /EMC Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	118	100.0	1706	2	US-09-066-330-10
2	114	96.6	492	2	US-09-482-500A-2
3	114	96.6	507	2	US-09-482-500A-3
4	114	96.6	737	1	US-08-119-361-5
5	114	96.6	737	2	US-08-336-308A-4
6	114	96.6	737	2	US-08-822-324-4
7	114	96.6	737	2	US-09-490-931-4
8	114	96.6	1477	2	US-09-482-500A-1
9	114	96.6	1687	1	US-08-570-311-29
10	114	96.6	1704	2	US-08-336-308A-10
11	114	96.6	1704	2	US-08-822-324-6
12	114	96.6	1704	2	US-09-490-931-10
13	82	69.5	1732	1	US-08-570-311-10
14	82	69.5	1732	1	US-08-353-485-10
15	82	69.5	1732	2	US-09-066-330-11
16	75	63.6	942	1	US-08-141-324-14
17	75	63.6	942	1	US-08-541-902-14
18	75	63.6	1358	1	US-08-570-311-27
19	72	61.0	509	2	US-08-822-324-8
20	57	48.3	382	2	US-09-134-000C-3738
21	54	45.8	207	2	US-09-149-476-516
22	54	45.8	232	2	US-09-149-476-633
23	54	45.8	252	2	US-09-149-476-332
24	49.5	41.9	47	2	US-10-375-913-7
25	49.5	41.9	47	2	US-11-110-001-7
26	49.5	41.9	47	2	US-11-110-002-7

27	48	40.7	244	2	US-09-107-532A-5529	Sequence 5529, Ap
28	48	40.7	556	2	US-09-134-000C-5850	Sequence 5850, Ap
29	48	40.7	614	1	US-08-295-814E-12	Sequence 12, Appl
30	48	40.7	614	1	US-08-543-881-2	Sequence 2, Appl
31	48	40.7	614	1	US-08-291-299-2	Sequence 2, Appl
32	48	40.7	614	1	US-08-291-299-8	Sequence 8, Appl
33	48	40.7	614	2	US-09-343-361-12	Sequence 12, Appl
34	48	40.7	614	2	US-09-919-039-378	Sequence 378, Ap
35	48	40.7	614	5	PCT-US94-00119-2	Sequence 2, Appl
36	48	40.7	614	5	PCT-US95-10579-2	Sequence 2, Appl
37	48	40.7	614	5	PCT-US95-10579-8	Sequence 8, Appl
38	48	40.7	634	2	US-09-949-016-7681	Sequence 7681, Ap
39	48	40.7	1012	1	US-08-475-891A-4	Sequence 4, Appl
40	48	40.7	1025	1	US-08-567-375-4	Sequence 4, Appl
41	48	40.7	1025	1	US-08-587-680A-4	Sequence 4, Appl
42	48	40.7	1026	2	US-09-623-551-18	Sequence 18, Appl
43	47	39.8	932	2	US-09-248-796A-19128	Sequence 19128, A
44	45	38.1	243	2	US-09-328-352-7058	Sequence 7058, Ap
45	45	38.1	404	2	US-09-543-681A-6702	Sequence 6702, Ap

ALIGNMENTS

RESULT 1

US-09-066-330-10
; Sequence 10, Application US/09066330A
; Patent No. 6511666
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric C.
; APPLICANT: Bhogal, Peter S.
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE
; FILE REFERENCE: Reynolds
; CURRENT APPLICATION NUMBER: US/09/066,330A
; CURRENT FILING DATE: 1998-09-15
; EARLIER APPLICATION NUMBER: PN 6275
; EARLIER FILING DATE: 1995-10-30
; EARLIER APPLICATION NUMBER: PCT/AU96/00673
; EARLIER FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 10
; LENGTH: 1706
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-09-066-330-10

Query Match 100.0%; Score 118; DB 2; Length 1706;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNGGISLANTYGHGSETAWGT 21
Db 426 FNGGISLANTYGHGSETAWGT 446

RESULT 2

US-09-482-500A-2
; Sequence 2, Application US/09482500A
; Patent No. 6627193
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Imamura, Takahisa
; APPLICANT: Potempa, Jan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROL OF BLOOD COAGULATION
; FILE REFERENCE: 235.00160101
; CURRENT APPLICATION NUMBER: US/09/482,500A
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US 60/115,869
; PRIOR FILING DATE: 1999-01-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0

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; SEQ ID NO 2
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-09-482-500A-2

Query Match          96.6%; Score 114; DB 2; Length 492;
Best Local Similarity 95.2%; Pred. No. 1.7e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FNGGISLVNYTGHGSETAWGT 21
    ||||| ||||| ||||| |||||
Db 199 FNGGISLVNYTGHGSETAWGT 219

RESULT 3
US-09-482-500A-3
; Sequence 3, Application US/09482500A
; Patent No. 6627193
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Imamura, Takahisa
; APPLICANT: Potempa, Jan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROL OF BLOOD COAGULATION
; FILE REFERENCE: 235.00160101
; CURRENT APPLICATION NUMBER: US/09/482,500A
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US 60/115,869
; PRIOR FILING DATE: 1999-01-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-09-482-500A-3

Query Match          96.6%; Score 114; DB 2; Length 507;
Best Local Similarity 95.2%; Pred. No. 1.7e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FNGGISLVNYTGHGSETAWGT 21
    ||||| ||||| ||||| |||||
Db 199 FNGGISLVNYTGHGSETAWGT 219

RESULT 4
US-08-119-361-5
; Sequence 5, Application US/08119361
; Patent No. 5523390
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; TITLE OF INVENTION: Porphyromonas gingivalis Arginine-specific Proteinase
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: USA
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/119,361
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 424
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; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33878
; REFERENCE/DOCKET NUMBER: 21-93
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8089
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 737 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-119-361-5

Query Match          96.6%; Score 114; DB 1; Length 737;
Best Local Similarity 95.2%; Pred. No. 2.6e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FNGGISLVNYTGHGSETAWGT 21
    ||||| ||||| ||||| |||||
Db 426 FNGGISLVNYTGHGSETAWGT 446

RESULT 5
US-08-336-308A-4
; Sequence 4, Application US/08336308A
; Patent No. 6017532
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; TITLE OF INVENTION: Porphyromonas gingivalis
; TITLE OF INVENTION: Arginine-specific Proteinase Coding Sequences
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,308A
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/119,361
; FILING DATE: 10-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/265,441
; FILING DATE: 24-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 21-93C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 737 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-336-308A-4
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Query Match          96.6%; Score 114; DB 2; Length 737;
Best Local Similarity 95.2%; Pred. No. 2.6e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FNGGISLVNYTGHGSETAWGT 21
   ||||| ||||| ||||| |||||
Db 426 FNGGISLVNYTGHGSETAWGT 446

RESULT 6
US-08-822-324-4
; Sequence 4, Application US/08822324
; Patent No. 6129917
; GENERAL INFORMATION:
; APPLICANT: Potempa, Jan S.
; APPLICANT: Travis, James
; APPLICANT: Genco, Caroline A.
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS COMPRISING
; TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS PROTEINS AND/OR PEPTIDES AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,324
; FILING DATE: 21-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,945
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 103-95 WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 498-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 737 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-822-324-4

Query Match          96.6%; Score 114; DB 2; Length 737;
Best Local Similarity 95.2%; Pred. No. 2.6e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FNGGISLVNYTGHGSETAWGT 21
   ||||| ||||| ||||| |||||
Db 426 FNGGISLVNYTGHGSETAWGT 446

RESULT 7
US-09-490-931-4
; Sequence 4, Application US/09490931
; Patent No. 6274718
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine

; TITLE OF INVENTION: Porphyromonas gingivalis
; TITLE OF INVENTION: Arginine-specific Proteinase Coding Sequences
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,931
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/336,308
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 21-93C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 737 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-490-931-4

Query Match          96.6%; Score 114; DB 2; Length 737;
Best Local Similarity 95.2%; Pred. No. 2.6e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FNGGISLVNYTGHGSETAWGT 21
   ||||| ||||| ||||| |||||
Db 426 FNGGISLVNYTGHGSETAWGT 446

RESULT 8
US-09-482-500A-1
; Sequence 1, Application US/09482500A
; Patent No. 6627193
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Imamura, Takahisa
; APPLICANT: Potempa, Jan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROL OF BLOOD COAGULATION
; FILE REFERENCE: 235.00160101
; CURRENT APPLICATION NUMBER: US/09/482,500A
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US 60/115,869
; PRIOR FILING DATE: 1999-01-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1477
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-09-482-500A-1

Query Match          96.6%; Score 114; DB 2; Length 1477;
Best Local Similarity 95.2%; Pred. No. 5.7e-08;
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Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FNGGISLVNTGHSSETAWGT 21
Db 199 FNGGISLVNTGHSSETAWGT 219

RESULT 9

US-08-570-311-29
; Sequence 29, Application US/08570311
; Patent No. 5824791
; GENERAL INFORMATION:
; APPLICANT: Proguiske-Fox, Ann
; APPLICANT: Tumwasorn, Somying
; APPLICANT: Lepine, GUYLAINE
; APPLICANT: Han, Naiming
; APPLICANT: Lantz, Marilyn
; APPLICANT: Patti, Joseph
; TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
and Probes for the Detection of Periodontal Disease
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ted W. Whitlock
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570,311
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/353,485
; FILING DATE: 09-DEC-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/647,119
; FILING DATE: 25-JAN-1991
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/241,640
; FILING DATE: 08-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF15.C3
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1687 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-570-311-29

Query Match 96.6%; Score 114; DB 1; Length 1687;
Best Local Similarity 95.2%; Pred. No. 6.7e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FNGGISLVNTGHSSETAWGT 21
Db 407 FNGGISLVNTGHSSETAWGT 427

RESULT 10

US-08-336-308A-10
; Sequence 10, Application US/08336308A
; Patent No. 6017532
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; TITLE OF INVENTION: Porphyromonas gingivalis
; ARGinine-specific Proteinase Coding Sequences
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,308A
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/119,361
; FILING DATE: 10-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/265,441
; FILING DATE: 24-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 21-93C
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1704 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-336-308A-10

Query Match 96.6%; Score 114; DB 2; Length 1704;
Best Local Similarity 95.2%; Pred. No. 6.8e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FNGGISLVNTGHSSETAWGT 21
Db 426 FNGGISLVNTGHSSETAWGT 446

RESULT 11

US-08-822-324-6
; Sequence 6, Application US/08822324
; Patent No. 6129917
; GENERAL INFORMATION:
; APPLICANT: Potempa, Jan S.
; APPLICANT: Travis, James
; APPLICANT: Genco, Caroline A.
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS COMPRISING
PORPHYROMONAS GINGIVALIS PROTEINS AND/OR PEPTIDES AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder

```
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,324
; FILING DATE: 21-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,945
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 103-95 WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8089
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1704 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-822-324-6

Query Match          96.6%; Score 114; DB 2; Length 1704;
Best Local Similarity 95.2%; Pred. No. 6.8e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 FNGGISLVNYTGHGSETAWGT 21
Db 426 FNGGISLVNYTGHGSETAWGT 446

RESULT 13
US-08-570-311-10
; Sequence 10, Application US/08570311
; Patent No. 5824791
; GENERAL INFORMATION:
; APPLICANT: Proguiske-Fox, Ann
; APPLICANT: Tumwasorn, Somying
; APPLICANT: Lepine, Guylaine
; APPLICANT: Han, Naiming
; APPLICANT: Lantz, Marilyn
; APPLICANT: Patti, Joseph
; TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
; TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ted W. Whitlock
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570,311
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/353,485
; FILING DATE: 09-DEC-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/647,119
; FILING DATE: 25-JAN-1991
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/241,640
; FILING DATE: 08-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF15.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
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; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,931
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/336,308
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/265,441
; FILING DATE: 24-JUN-1994

Query Match          96.6%; Score 114; DB 2; Length 1704;
Best Local Similarity 95.2%; Pred. No. 6.8e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 FNGGISLVNYTGHGSETAWGT 21
Db 426 FNGGISLVNYTGHGSETAWGT 446

RESULT 12
US-09-490-931-10
; Sequence 10, Application US/09490931
; Patent No. 6274718
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; TITLE OF INVENTION: Porphyromonas gingivalis
; TITLE OF INVENTION: Arginine-specific Proteinase Coding Sequences
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,931
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/336,308
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/265,441
; FILING DATE: 24-JUN-1994
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1732 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-570-311-10

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Query Match          69.5%; Score 82; DB 1; Length 1732;
Best Local Similarity 77.8%; Pred. No. 0.0032;
Matches 14: Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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QY 2 NGGISLANYTGHGSETAW 19
|||:|||||
Db 433 NTGVSFANYTAHGSETAW 450

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RESULT 14
US-08-353-485-10
; Sequence 10, Application US/08353485
; Patent No. 5830710
; GENERAL INFORMATION:
; APPLICANT: Progulske-Fox, Ann
; APPLICANT: Tumwasorn, Somying
; APPLICANT: Lepine, Guylaine
; APPLICANT: Han, Naiming
; APPLICANT: Lantz, Marilyn
; APPLICANT: Patti, Joseph
; TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
; TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
;

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Query Match	69.5%;	Score 82;	DB 1;	Length 1732;
Best Local Similarity	77.8%;	Pred. No. 0.0032;		
Matches 14:	Conservative	1;	Mismatches	3;
			Indels	0;
			Gaps	0;

QY 2 NGGISLANYTGHGSETAW 19

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      | | | | | | | | | |
      | : | | | | | | | |
Db      433  NTGVSFANYTAHGETAW 450

      RESULT 15
      US-09-066-330-11
      ; Sequence 11, Application US/09066330A
      ; Patent No. 6511666
      ; GENERAL INFORMATION:
      ; APPLICANT: Reynolds, Eric C.
      ; APPLICANT: Bhogal, Peter S.
      ; APPLICANT: Slakeeshi, Nada
      ; TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE
      ; FILE REFERENCE: Reynolds
      ; CURRENT APPLICATION NUMBER: US/09/066.330A
      ; CURRENT FILING DATE: 1998-09-15
      ; EARLIER APPLICATION NUMBER: PN 6275
      ; EARLIER FILING DATE: 1995-10-30
      ; EARLIER APPLICATION NUMBER: PCT/AU96/00673
      ; EARLIER FILING DATE: 1996-10-30
      ; NUMBER OF SEQ ID NOS: 15
      ; SOFTWARE: PatentIn Ver. 2.0
      ; SEQ ID NO 11
      ; LENGTH: 1732
      ; TYPE: PRT
      ; ORGANISM: Porphyromonas gingivalis
      US-09-066-330-11

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Query Match      69.5%; Score 82; DB 2; Length 1732;
Best Local Similarity 77.8%; Pred. No. 0.0032;
Matches 14: Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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Qy 2 NGGISLANYTGHGETAW 19
||:|||||
pb 433 NTGVSFANYTAHGSETAW 450

Search completed: August 25, 2006, 18:06:29
Job time : 35.6744 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 25, 2006, 18:21:12 ; Search time 121.116 Seconds
(without alignments)
80.315 Million cell updates/sec

Title: US-10-387-977-1

Perfect score: 118

Sequence: 1 FNGGISLANYTGHGSETAWGT 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA Main:*

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3: /EMC_Celerra_SID33/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	118	100.0	491	4	US-10-387-977-100
3	118	100.0	507	4	US-10-387-977-99
4	118	100.0	736	4	US-10-387-977-105
5	118	100.0	1706	4	US-10-229-066-10
6	118	100.0	1706	5	US-10-915-002-186
7	118	100.0	1706	5	US-10-915-002-210
8	118	100.0	1706	5	US-10-915-002-221
9	118	100.0	1706	5	US-10-915-002-239
10	118	100.0	1706	6	US-11-052-554A-176
11	82	69.5	22	4	US-10-387-977-2
12	82	69.5	509	4	US-10-387-977-101
13	82	69.5	1731	5	US-10-915-002-176
14	82	69.5	1731	5	US-10-915-002-192
15	82	69.5	1731	5	US-10-915-002-211
16	82	69.5	1731	5	US-10-915-002-222
17	82	69.5	1732	4	US-10-229-066-11
18	58.5	49.6	450	4	US-10-369-493-8448
19	58.5	49.6	475	6	US-11-087-099-5183
20	58.5	49.6	475	6	US-11-188-298-15792
21	54	45.8	207	3	US-09-809-391-516
22	54	45.8	207	3	US-09-882-171-516
23	54	45.8	207	4	US-10-164-861-516
24	54	45.8	207	6	US-11-144-947-516
25	54	45.8	232	3	US-09-809-391-633
26	54	45.8	232	3	US-09-882-171-633
27	54	45.8	232	4	US-10-164-861-633

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28 54 45.8 232 6 US-11-144-947-633 Sequence 633, App
29 54 45.8 252 3 US-09-809-391-332 Sequence 332, App
30 54 45.8 252 3 US-09-882-171-332 Sequence 332, App
31 54 45.8 252 4 US-10-164-861-332 Sequence 332, App
32 54 45.8 252 6 US-11-144-947-332 Sequence 332, App
33 54 45.8 1123 5 US-10-915-002-245 Sequence 245, App
34 50 42.4 491 6 US-11-188-298-4899 Sequence 4899, App
35 50 42.4 817 4 US-10-437-963-114827 Sequence 114827, App
36 49.5 41.9 47 4 US-10-375-913-7 Sequence 7, Appli
37 49.5 41.9 47 6 US-11-110-001-7 Sequence 7, Appli
38 49.5 41.9 47 6 US-11-110-002-7 Sequence 7, Appli
39 49.5 41.9 47 6 US-11-235-009-7 Sequence 7, Appli
40 49.5 41.9 323 3 US-09-925-301-952 Sequence 952, App
41 49 41.5 132 4 US-10-425-115-324154 Sequence 324154,
42 48 40.7 263 6 US-11-096-568A-11199 Sequence 11199, A
43 48 40.7 351 6 US-11-096-568A-11198 Sequence 11198, A
44 48 40.7 416 4 US-10-369-493-20445 Sequence 20445, A
45 48 40.7 525 4 US-10-424-599-260318 Sequence 260318,

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ALIGNMENTS

RESULT 1

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US-10-387-977-1
; Sequence 1, Application US/10387977
; Publication No. US20040005276A1
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric Charles
; APPLICANT: O'Brien-Simpson, Neil Martin
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
; TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
; FILE REFERENCE: 529282000301
; CURRENT APPLICATION NUMBER: US/10/387,977
; CURRENT FILING DATE: 2003-07-18
; PRIOR FILING DATE: US 09/423,056
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/AU98/00311
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: AU PO 6528
; PRIOR FILING DATE: 1997-04-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-387-977-1

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Query Match 100.0%; Score 118; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 FNGGISLANYTGHGSETAWGT 21
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Db 1 FNGGISLANYTGHGSETAWGT 21

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RESULT 2

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US-10-387-977-100
; Sequence 100, Application US/10387977
; Publication No. US20040005276A1
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric Charles
; APPLICANT: O'Brien-Simpson, Neil Martin
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
; TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
; FILE REFERENCE: 529282000301
; CURRENT APPLICATION NUMBER: US/10/387,977

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; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 09/423,056
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/AU98/00311
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: AU PO 6528
; PRIOR FILING DATE: 1997-04-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-387-977-100

Query Match 100.0%; Score 118; DB 4; Length 491;
Best Local Similarity 100.0%; Pred. No. 3.8e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNGGISLANYTGHGSETAWGT 21
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Db 199 FNGGISLANYTGHGSETAWGT 219

RESULT 3

US-10-387-977-99
; Sequence 99, Application US/10387977
; Publication No. US20040005276A1
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric Charles
; APPLICANT: O'Brien-Simpson, Neil Martin
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
; TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
; FILE REFERENCE: 529282000301
; CURRENT APPLICATION NUMBER: US/10/387,977
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 09/423,056
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/AU98/00311
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: AU PO 6528
; PRIOR FILING DATE: 1997-04-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-387-977-99

Query Match 100.0%; Score 118; DB 4; Length 507;
Best Local Similarity 100.0%; Pred. No. 3.9e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNGGISLANYTGHGSETAWGT 21
|||||
Db 199 FNGGISLANYTGHGSETAWGT 219

RESULT 4

US-10-387-977-105
; Sequence 105, Application US/10387977
; Publication No. US20040005276A1
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric Charles
; APPLICANT: O'Brien-Simpson, Neil Martin
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
; TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
; FILE REFERENCE: 529282000301

; CURRENT APPLICATION NUMBER: US/10/387,977
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 09/423,056
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/AU98/00311
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: AU PO 6528
; PRIOR FILING DATE: 1997-04-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105
; LENGTH: 736
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-387-977-105

Query Match 100.0%; Score 118; DB 4; Length 736;
Best Local Similarity 100.0%; Pred. No. 5.8e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNGGISLANYTGHGSETAWGT 21
|||||
Db 428 FNGGISLANYTGHGSETAWGT 448

RESULT 5

US-10-229-066-10
; Sequence 10, Application US/10229066
; Publication No. US20030157637A1
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric C.
; APPLICANT: Bhogal, Peter S.
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE
; FILE REFERENCE: Reynolds
; CURRENT APPLICATION NUMBER: US/10/229,066
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US/09/066,330
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: PN 6275
; PRIOR FILING DATE: 1995-10-30
; PRIOR APPLICATION NUMBER: PCT/AU96/00673
; PRIOR FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1706
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-229-066-10

Query Match 100.0%; Score 118; DB 4; Length 1706;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNGGISLANYTGHGSETAWGT 21
|||||
Db 426 FNGGISLANYTGHGSETAWGT 446

RESULT 6

US-10-915-002-186
; Sequence 186, Application US/10915002
; Publication No. US20060078950A1
; GENERAL INFORMATION:
; APPLICANT: Progulskie-Fox, Ann
; APPLICANT: Hillman, Jeffrey D.
; APPLICANT: Handfield, Martin
; TITLE OF INVENTION: IDENTIFICATION OF PORPHYROMONAS GINGIVALIS VIRULENCE
; TITLE OF INVENTION: USE IN DIAGNOSIS ANTIGENS FOR USE IN THE DIAGNOSIS,
; TITLE OF INVENTION: PERIODONTAL DISEASES
; FILE REFERENCE: 02-042
; CURRENT APPLICATION NUMBER: US/10/915,002

Query Match	100.0%;	Score 118;	DB 5;	Length 1706;
Best Local Similarity	100.0%;	Pred. No. 1.4e-08;		

RESULT 11
US-10-387-977-2
: Sequence 2. Application US/10387977

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; Publication No. US20040005276A1
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric Charles
; APPLICANT: O'Brien-Simpson, Neil Martin
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
; TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
; FILE REFERENCE: 52928200301
; CURRENT APPLICATION NUMBER: US/10/387,977
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 09/423,056
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/AU98/00311
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: AU PO 6528
; PRIOR FILING DATE: 1997-04-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-387-977-2

Query Match          69.5%; Score 82; DB 4; Length 22;
Best Local Similarity 77.8%; Pred. No. 3.7e-05;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      2 NGGISLANYTGHGSETAW 19
Db      2 NTGVSFANYTAHGSETAW 19

RESULT 12
US-10-387-977-101
; Sequence 101, Application US/10387977
; Publication No. US20040005276A1
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric Charles
; APPLICANT: O'Brien-Simpson, Neil Martin
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
; TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
; FILE REFERENCE: 52928200301
; CURRENT APPLICATION NUMBER: US/10/387,977
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 09/423,056
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/AU98/00311
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: AU PO 6528
; PRIOR FILING DATE: 1997-04-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-387-977-101

Query Match          69.5%; Score 82; DB 4; Length 509;
Best Local Similarity 77.8%; Pred. No. 0.0011;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      2 NGGISLANYTGHGSETAW 19
Db      205 NTGVSFANYTAHGSETAW 222

RESULT 13
US-10-915-002-176
; Sequence 176, Application US/10915002
; Publication No. US20060078950A1
; GENERAL INFORMATION:
; APPLICANT: Proguiske-Fox, Ann
; APPLICANT: Hillman, Jeffrey D.
; APPLICANT: Handfield, Martin
; TITLE OF INVENTION: IDENTIFICATION OF PORPHYROMONAS GINGIVALIS VIRULENCE POLYNUCLEOTIDE
; TITLE OF INVENTION: USE IN DIAGNOSIS ANTIGENS FOR USE IN THE DIAGNOSIS, TREATMENT, A
; TITLE OF INVENTION: PERIODONTAL DISEASES
; FILE REFERENCE: 02-042
; CURRENT APPLICATION NUMBER: US/10/915,002
; CURRENT FILING DATE: 2004-08-10
; NUMBER OF SEQ ID NOS: 354
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 176
; LENGTH: 1731
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-915-002-176

Query Match          69.5%; Score 82; DB 5; Length 1731;
Best Local Similarity 77.8%; Pred. No. 0.0041;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      2 NGGISLANYTGHGSETAW 19
Db      433 NTGVSFANYTAHGSETAW 450

RESULT 14
US-10-915-002-192
; Sequence 192, Application US/10915002
; Publication No. US20060078950A1
; GENERAL INFORMATION:
; APPLICANT: Proguiske-Fox, Ann
; APPLICANT: Hillman, Jeffrey D.
; APPLICANT: Handfield, Martin
; TITLE OF INVENTION: IDENTIFICATION OF PORPHYROMONAS GINGIVALIS VIRULENCE POLYNUCLEOTIDE
; TITLE OF INVENTION: USE IN DIAGNOSIS ANTIGENS FOR USE IN THE DIAGNOSIS, TREATMENT, A
; TITLE OF INVENTION: PERIODONTAL DISEASES
; FILE REFERENCE: 02-042
; CURRENT APPLICATION NUMBER: US/10/915,002
; CURRENT FILING DATE: 2004-08-10
; NUMBER OF SEQ ID NOS: 354
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 192
; LENGTH: 1731
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-915-002-192

Query Match          69.5%; Score 82; DB 5; Length 1731;
Best Local Similarity 77.8%; Pred. No. 0.0041;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      2 NGGISLANYTGHGSETAW 19
Db      433 NTGVSFANYTAHGSETAW 450

RESULT 15
US-10-915-002-211
; Sequence 211, Application US/10915002
; Publication No. US20060078950A1
; GENERAL INFORMATION:
; APPLICANT: Proguiske-Fox, Ann
; APPLICANT: Hillman, Jeffrey D.
; APPLICANT: Handfield, Martin
; TITLE OF INVENTION: IDENTIFICATION OF PORPHYROMONAS GINGIVALIS VIRULENCE POLYNUCLEOTIDE
; TITLE OF INVENTION: USE IN DIAGNOSIS ANTIGENS FOR USE IN THE DIAGNOSIS, TREATMENT, A
; TITLE OF INVENTION: PERIODONTAL DISEASES
; FILE REFERENCE: 02-042
; CURRENT APPLICATION NUMBER: US/10/915,002
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; CURRENT FILING DATE: 2004-08-10
; NUMBER OF SEQ ID NOS: 354
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 211
; LENGTH: 1731
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-915-002-211
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Query Match      69.5%  Score 82;  DB 5;  Length 1731;
Best Local Similarity 77.8%  Pred. No. 0.0041;
Matches 14;  Conservative 1;  Mismatches 3;  Indels 0;  Gaps 0;
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Db     433  NTGVSFANYTAGGSETAW 450
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Search completed: August 25, 2006, 18:26:06
Job time : 122.116 secs
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 25, 2006, 18:22:07 ; Search time 20.0233 Seconds
(without alignments)
71.760 Million cell updates/sec

Title: US-10-387-977-1

Perfect score: 118

Sequence: 1 FNGGISLANYTHGSETAWG 21

Scoring table: BLOSUM62

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Searched: 247503 seqs, 68422524 residues

Total number of hits satisfying chosen parameters: 247503

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /EMC_Celerra_SID83/ptodata/2/pubpaa/US06_NEW_PUB.pdb:*
- 3: /EMC_Celerra_SID83/ptodata/2/pubpaa/US07_NEW_PUB.pdb:*
- 4: /EMC_Celerra_SID83/ptodata/2/pubpaa/US08_NEW_PUB.pdb:*
- 5: /EMC_Celerra_SID83/ptodata/2/pubpaa/PCT_NEW_PUB.pdb:*
- 6: /EMC_Celerra_SID83/ptodata/2/pubpaa/US10_NEW_PUB.pdb:*
- 7: /EMC_Celerra_SID83/ptodata/2/pubpaa/US11_NEW_PUB.pdb:*
- 8: /EMC_Celerra_SID83/ptodata/2/pubpaa/US60_NEW_PUB.pdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	48	40.7	263	7 US-11-056-355B-69319	Sequence 69319, A
2	48	40.7	351	7 US-11-056-355B-69318	Sequence 69318, A
3	48	40.7	614	7 US-11-300-928-62	Sequence 62, Appl
4	47	39.8	389	6 US-10-449-902-33007	Sequence 33007, A
5	46	39.0	948	6 US-10-449-902-44448	Sequence 44448, A
6	45.5	38.6	266	6 US-10-449-902-37409	Sequence 37409, A
7	45	38.1	506	6 US-10-953-349-10213	Sequence 10213, A
8	45	38.1	548	6 US-10-953-349-10212	Sequence 10212, A
9	45	38.1	563	6 US-10-449-902-46522	Sequence 46522, A
10	45	38.1	574	6 US-10-953-349-10211	Sequence 10211, A
11	44	37.3	151	6 US-10-449-902-38955	Sequence 38955, A
12	44	37.3	393	6 US-10-449-902-41675	Sequence 41675, A
13	44	37.3	751	7 US-11-330-403-8183	Sequence 8183, A
14	43	36.4	249	6 US-10-374-780A-1540	Sequence 1540, Ap
15	42	35.6	192	6 US-10-449-902-41740	Sequence 41740, A
16	42	35.6	301	7 US-11-056-355B-66160	Sequence 66160, A
17	42	35.6	312	6 US-10-953-349-278	Sequence 278, App
18	42	35.6	320	7 US-11-174-307B-3740	Sequence 3740, Ap
19	42	35.6	320	7 US-11-056-355B-66159	Sequence 66159, A
20	42	35.6	325	6 US-10-953-349-277	Sequence 277, App
21	42	35.6	408	6 US-10-953-349-276	Sequence 276, App
22	42	35.6	636	6 US-10-449-902-44935	Sequence 44935, A
23	42	35.6	661	7 US-11-056-355B-47185	Sequence 47185, A
24	42	35.6	680	7 US-11-056-355B-47184	Sequence 47184, A
25	42	35.6	730	6 US-10-449-902-51873	Sequence 51873, A

ALIGNMENTS

RESULT 1

US-11-056-355B-69319
; Sequence 69319, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:

; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 69319
; LENGTH: 263
; TYPE: prt
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(263)
; OTHER INFORMATION: Ceres Seq. ID no. 15222289
US-11-056-355B-69319

Query Match 40.7% ; Score 48; DB 7; Length 263;
Best Local Similarity 39.1% ; Pred No. 8.3;
Matches 9; Conservative 5; Mismatches 5; Indels 4; Gaps 1;

Qy 2 NGGISLAN----YTHGSETAWG 20
|||:| |||:|:|
Db 189 NGGVPLTRQGSLSYTGTYGTVGVG 211

RESULT 2

US-11-056-355B-69318
; Sequence 69318, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:

; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13

Sequence 47183, A
Sequence 45698, A
Sequence 1654, Ap
Sequence 30389, A
Sequence 47941, A
Sequence 7181, Ap
Sequence 7180, Ap
Sequence 3948, Ap
Sequence 37993, A
Sequence 82889, A
Sequence 82888, A
Sequence 82887, A
Sequence 122, App
Sequence 14014, A
Sequence 5058, Ap
Sequence 55224, A
Sequence 55228, A
Sequence 38064, A
Sequence 58732, A
Sequence 58731, A

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; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 69318
; LENGTH: 351
; TYPE: prt
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)-(351)
; OTHER INFORMATION: Ceres Seq. ID no. 15222288
US-11-056-355B-69318

Query Match      40.7%; Score 48; DB 7; Length 351;
Best Local Similarity 39.1%; Pred. No. 11;
Matches 9; Conservative 5; Mismatches 5; Indels 4; Gaps 1;

Qy      2  NNGISLAN-----YTHGSETAWG 20
Db      277  NNGVPLTRQGSlyTGYGTQIGY 299

RESULT 3
US-11-300-928-62
; Sequence 62, Application US/11300928
; Publication No. US20060166277A1
; GENERAL INFORMATION:
; APPLICANT: Karumanchi, S. Ananth
; APPLICANT: Sukhame, Vikas P.
; TITLE OF INVENTION: Nucleic Acids and Polypeptides Useful For Diagnosing and Treating
; TITLE OF INVENTION: Complications of Pregnancy
; FILE REFERENCE: 01948/108002
; CURRENT APPLICATION NUMBER: US/11/300,928
; CURRENT FILING DATE: 2005-12-15
; PRIOR APPLICATION NUMBER: US 60/636,275
; PRIOR FILING DATE: 2004-12-15
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 62
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-300-928-62

Query Match      40.7%; Score 48; DB 7; Length 614;
Best Local Similarity 53.3%; Pred. No. 20;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy      5  ISLANYTGHSSETAW 19
Db      94  VALGQYTSQGSVTAW 108

RESULT 4
US-10-449-902-33007
; Sequence 33007, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33007
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-37409
; Sequence 37409, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37409
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-37409
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; ORGANISM: Oryza sativa
US-10-449-902-33007

Query Match      39.8%; Score 47; DB 6; Length 389;
Best Local Similarity 42.9%; Pred. No. 18;
Matches 9; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

Qy      2  NNGISLAN--TGHGSETAWG 20
Db      17  SGGYGQNYRPGHGAASQWG 37

RESULT 5
US-10-449-902-44448
; Sequence 44448, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44448
; LENGTH: 948
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-44448

Query Match      39.0%; Score 46; DB 6; Length 948;
Best Local Similarity 58.3%; Pred. No. 64;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      10  YTHGHSSETAWGT 21
Db      133  YAGHGNEEDWAT 144

RESULT 6
US-10-449-902-37409
; Sequence 37409, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37409
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-37409

Query Match      38.6%; Score 45.5; DB 6; Length 266;
Best Local Similarity 50.0%; Pred. No. 20;
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Matches 9; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

Qy 3 GGISLANYTGHGSETAW 20
   ||:|:|:|:|:|
Db 179 GGSAPASY-GYGNSGWMG 195

RESULT 7
US-10-953-349-10213
; Sequence 10213, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10213
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-10213

Query Match 38.1%; Score 45; DB 6; Length 506;
Best Local Similarity 50.0%; Pred. No. 47;
Matches 8; Conservative 2; Mismatches 2; Indels 6; Gaps 0;

Qy 4 GISLANYTGHGSETAW 19
   ||:|:|:|:|
Db 123 GLSMENRANGSBEAW 138

RESULT 8
US-10-953-349-10212
; Sequence 10212, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10212
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-10212

Query Match 38.1%; Score 45; DB 6; Length 548;
Best Local Similarity 50.0%; Pred. No. 51;
Matches 8; Conservative 2; Mismatches 2; Indels 6; Gaps 0;

Qy 4 GISLANYTGHGSETAW 19
   ||:|:|:|:|
Db 165 GLSMENRANGSBEAW 180

RESULT 9
US-10-449-902-46522
; Sequence 46522, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
```

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; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46522
; LENGTH: 563
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-46522

Query Match 38.1%; Score 45; DB 6; Length 563;
Best Local Similarity 50.0%; Pred. No. 53;
Matches 10; Conservative 1; Mismatches 7; Indels 2; Gaps 1;

Qy 2 NG--GISLANYTGHGSETAW 19
   ||:|:|:|:|
Db 542 NGLAGYSLDGTSHGPQAAW 561

RESULT 10
US-10-953-349-10211
; Sequence 10211, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10211
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-10211

Query Match 38.1%; Score 45; DB 6; Length 574;
Best Local Similarity 50.0%; Pred. No. 54;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 4 GISLANYTGHGSETAW 19
   ||:|:|:|:|
Db 191 GLSMENRANGSBEAW 206

RESULT 11
US-10-449-902-38955
; Sequence 38955, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38955
; LENGTH: 151
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; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-38955

Query Match      37.3%; Score 44; DB 6; Length 151;
Best Local Similarity 53.3%; Pred. No. 19;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1  FNGGISLANYTGHS 15
         |||||: |||||
Db      108  FNGGFLAIVAGHAA 122

RESULT 12
US-10-449-902-41675
; Sequence 41675, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41675
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-41675

Query Match      37.3%; Score 44; DB 6; Length 393;
Best Local Similarity 50.0%; Pred. No. 51;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY      1  FNGGISLANYTGHS2TA 18
         |||||: |||||
Db      68  FSGSGGSRYGCGFSESA 85

RESULT 13
US-11-330-403-8183
; Sequence 8183, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 8183
; LENGTH: 751
; TYPE: PRT
; ORGANISM: ASPERGILLUS NIDULANS FGSC A4
US-11-330-403-8183

Query Match      37.3%; Score 44; DB 7; Length 751;
Best Local Similarity 42.9%; Pred. No. 1e+02;
Matches 9; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY      1  FNGGISLANYTGHS2TA 21
         |||||: |||||
Db      153  FNLAARLARYTGNQYADWAT 173

us-10-374-780A-1540
; Sequence 1540, Application US/10374780A
; Publication No. US20060162006A9
; GENERAL INFORMATION:
; APPLICANT: Sherman, Bradley K
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Heard, Jacqueline E
; APPLICANT: Haake, Volker
; APPLICANT: Creelman, Robert A
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Adam, Luc J
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddle, James
; APPLICANT: Broun, Pierre E
; APPLICANT: Pilgrim, Marsha L
; APPLICANT: Dubell III, Arnold T
; APPLICANT: Pineda, Omaira
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
; FILE REFERENCE: MBI-0047 CIP
; CURRENT APPLICATION NUMBER: US/10/374,780A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/837,944
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/934,455
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 10/225,066
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,067
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,068
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 2906
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1540
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Orthologous to GI322
US-10-374-780A-1540

Query Match      36.4%; Score 43; DB 6; Length 249;
Best Local Similarity 47.1%; Pred. No. 45;
Matches 8; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY      5  ISLANYTGHS2TA 21
         |||||: |||||
Db      31  LSLVNYIAANGEGAWNT 47

RESULT 15
US-10-449-902-41740
; Sequence 41740, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
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; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41740
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-41740

Query Match      35.6%; Score 42; DB 6; Length 192;
Best Local Similarity 40.0%; Pred. No. 49;
Matches 8; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY      2  NGGISLANYTGHGSETAWGT 21
      || | | | | | | | | | |
Db      50  NGNKGNGNGNGNGLNYWGT 69

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OM protein - protein search, using sw model

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(without alignments)
76.794 Million cell updates/sec

Title: US-10-387-977-1
Perfect score: 118
Sequence: 1 FNGGISLANYTGHSETAWGT 21

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118	100.0	21	24	US-09-423-056B-1 Sequence 1, Appli
2	118	100.0	21	24	US-09-423-056B-1 Sequence 1, Appli
3	118	100.0	21	33	US-10-387-977-1 Sequence 1, Appli
4	118	100.0	491	24	US-09-423-056B-100 Sequence 100, App
5	118	100.0	491	24	US-09-423-056B-100 Sequence 100, App
6	118	100.0	491	33	US-10-387-977-100 Sequence 100, App
7	118	100.0	507	24	US-09-423-056B-99 Sequence 99, Appl
8	118	100.0	507	24	US-09-423-056B-99 Sequence 99, Appl
9	118	100.0	507	33	US-10-387-977-99 Sequence 105, App
10	118	100.0	736	24	US-09-423-056B-105 Sequence 21158, A
11	118	100.0	736	27	US-09-791-537-21158 Sequence 105, App
12	118	100.0	736	33	US-10-387-977-105 Sequence 105, App
13	118	100.0	1526	27	US-09-791-537-49353 Sequence 49353, A
14	118	100.0	1706	27	US-09-791-537-100403 Sequence 100403,
15	118	100.0	1706	27	US-09-791-537-113656 Sequence 113656,
16	118	100.0	1706	32	US-10-229-066-10 Sequence 10, Appl
17	118	100.0	1706	32	US-10-915-002-186 Sequence 186, App
18	118	100.0	1706	39	US-10-915-002-210 Sequence 210, App
19	118	100.0	1706	39	US-10-915-002-221 Sequence 221, App
20	118	100.0	1706	39	US-10-915-002-239 Sequence 239, App
21	118	100.0	1706	40	US-11-052-554A-176 Sequence 176, App
22	118	100.0	1706	49	US-60-495-589-186 Sequence 186, App
23	118	100.0	1706	49	US-60-495-589-210 Sequence 210, App
24	118	100.0	1706	49	US-60-495-589-221 Sequence 221, App
25	118	100.0	1706	49	US-60-495-589-239 Sequence 239, App
26	114	96.6	394	25	US-09-543-696B-29 Sequence 29, Appl
27	114	96.6	435	27	US-09-791-537-49386 Sequence 49386, A
28	114	96.6	435	29	US-09-979-624-1 Sequence 1, Appli
29	114	96.6	492	25	US-09-543-696B-27 Sequence 27, Appl
30	114	96.6	492	25	US-09-543-696B-27 Sequence 27, Appl
31	114	96.6	508	25	US-09-543-696B-28 Sequence 28, Appl
32	114	96.6	508	25	US-09-543-696B-28 Sequence 28, Appl
33	114	96.6	736	25	US-09-543-696B-26 Sequence 26, Appl
34	114	96.6	736	25	US-09-543-696B-26 Sequence 26, Appl
35	114	96.6	736	27	US-09-791-537-55763 Sequence 55763, A
36	114	96.6	736	27	US-09-791-537-94999 Sequence 94999, A
37	114	96.6	737	1	PCT-US94-10283-4 Sequence 4, Appli
38	114	96.6	737	12	US-08-265-441-5 Sequence 5, Appli
39	114	96.6	737	25	US-09-543-696B-4 Sequence 4, Appli
40	114	96.6	737	25	US-09-543-696B-4 Sequence 4, Appli
41	114	96.6	737	29	US-09-927-018-4 Sequence 4, Appli
42	114	96.6	991	27	US-09-791-537-65556 Sequence 65556, A
43	114	96.6	1185	12	US-08-265-441-18 Sequence 18, Appl
44	114	96.6	1687	21	US-09-174-517-29 Sequence 29, Appl
45	114	96.6			

ALIGNMENTS

RESULT 1
US-09-423-056-1
; Sequence 1, Application US/09423056
; GENERAL INFORMATION:

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; APPLICANT: Reynolds, Eric C.
; APPLICANT: O'Brien-Simpson, Neil M.
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: Synthetic peptide constructs for the diagnosis and
; TITLE OF INVENTION: treatment of periodontitis associated with
; TITLE OF INVENTION: Porphyromonas gingivalis
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/423,056
; CURRENT FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/AU98/00311
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: PO 6528
; PRIOR FILING DATE: 1997-04-30
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-09-423-056-1

Query Match          100.0%; Score 118; DB 24; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNGGISLANYTGHGSETAWGT 21
Db 1 FNGGISLANYTGHGSETAWGT 21
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RESULT 2
US-09-423-056B-1
; Sequence 1, Application US/09423056B
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric Charles
; APPLICANT: O'Brien-Simpson, Neil Martin
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
; TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
; FILE REFERENCE: 529282000300
; CURRENT APPLICATION NUMBER: US/09/423,056B
; CURRENT FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/AU98/00311
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-09-423-056B-1

Query Match          100.0%; Score 118; DB 24; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 FNGGISLANYTGHGSETAWGT 21
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RESULT 3
US-10-387-977-1
; Sequence 1, Application US/10387977
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric Charles
; APPLICANT: O'Brien-Simpson, Neil Martin
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
; TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
; FILE REFERENCE: 529282000301
; CURRENT APPLICATION NUMBER: US/09/423,056B
; CURRENT FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/AU98/00311
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-09-423-056B-1

Query Match          100.0%; Score 118; DB 24; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNGGISLANYTGHGSETAWGT 21
Db 1 FNGGISLANYTGHGSETAWGT 21
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; CURRENT APPLICATION NUMBER: US/10/387,977
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 09/423,056
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/AU98/00311
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: AU PO 6528
; PRIOR FILING DATE: 1997-04-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-387-977-1

Query Match          100.0%; Score 118; DB 33; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 FNGGISLANYTGHGSETAWGT 21
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RESULT 4
US-09-423-056-100
; Sequence 100, Application US/09423056
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric C.
; APPLICANT: O'Brien-Simpson, Neil M.
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: Synthetic peptide constructs for the diagnosis and
; TITLE OF INVENTION: treatment of periodontitis associated with
; TITLE OF INVENTION: Porphyromonas gingivalis
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/423,056
; CURRENT FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/AU98/00311
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: PO 6528
; PRIOR FILING DATE: 1997-04-30
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 100
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-09-423-056-100

Query Match          100.0%; Score 118; DB 24; Length 491;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNGGISLANYTGHGSETAWGT 21
Db 199 FNGGISLANYTGHGSETAWGT 219
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RESULT 5
US-09-423-056B-100
; Sequence 100, Application US/09423056B
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric Charles
; APPLICANT: O'Brien-Simpson, Neil Martin
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
; TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
; FILE REFERENCE: 529282000300
; CURRENT APPLICATION NUMBER: US/09/423,056B
; CURRENT FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/AU98/00311
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; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
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; LENGTH: 491
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-09-423-056B-100

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Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 199 FNGGISLANYTGHGSETAWGT 219

RESULT 6
US-10-387-977-100
; Sequence 100, Application US/10387977
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric Charles
; APPLICANT: O'Brien-Simpson, Neil Martin
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
; FILE REFERENCE: 52928200301
; CURRENT APPLICATION NUMBER: US/10/387,977
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 09/423,056
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/AU98/00311
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: AU PO 6528
; PRIOR FILING DATE: 1997-04-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-387-977-100

Query Match      100.0%; Score 118; DB 33; Length 491;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNGGISLANYTGHGSETAWGT 21
Db 199 FNGGISLANYTGHGSETAWGT 219

RESULT 7
US-09-423-056B-99
; Sequence 99, Application US/09423056
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric C.
; APPLICANT: O'Brien-Simpson, Neil M.
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: Synthetic peptide constructs for the diagnosis and
; TITLE OF INVENTION: treatment of periodontitis associated with
; TITLE OF INVENTION: Porphyromonas gingivalis
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/423,056
; CURRENT FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/AU98/00311
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: PO 6528
; PRIOR FILING DATE: 1997-04-30
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
US-10-387-977-99

Query Match      100.0%; Score 118; DB 24; Length 507;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNGGISLANYTGHGSETAWGT 21
Db 199 FNGGISLANYTGHGSETAWGT 219

RESULT 8
US-09-423-056B-99
; Sequence 99, Application US/09423056B
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric Charles
; APPLICANT: O'Brien-Simpson, Neil Martin
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
; FILE REFERENCE: 52928200300
; CURRENT APPLICATION NUMBER: US/09/423,056B
; CURRENT FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/AU98/00311
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-09-423-056B-99

Query Match      100.0%; Score 118; DB 24; Length 507;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNGGISLANYTGHGSETAWGT 21
Db 199 FNGGISLANYTGHGSETAWGT 219

RESULT 9
US-10-387-977-99
; Sequence 99, Application US/10387977
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric Charles
; APPLICANT: O'Brien-Simpson, Neil Martin
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
; TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
; FILE REFERENCE: 52928200301
; CURRENT APPLICATION NUMBER: US/10/387,977
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 09/423,056
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/AU98/00311
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: AU PO 6528
; PRIOR FILING DATE: 1997-04-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-387-977-99
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Mon Aug 28 11:30:41 2006

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; Sequence 105, Application US/10387977
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric Charles
; APPLICANT: O'Brien-Simpson, Neil Martin
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
; TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
; FILE REFERENCE: 52928200301
; CURRENT APPLICATION NUMBER: US/10/387,977
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 09/423,056
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/AU98/00311
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: AU PO 6528
; PRIOR FILING DATE: 1997-04-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
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; LENGTH: 736
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
; US-10-387-977-105

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Best Local Similarity 100.0%; Pred. No. 1.9e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNGGISLANYTGHGSETAWGT 21
Db 199 FNGGISLANYTGHGSETAWGT 219

RESULT 10
US-09-423-056B-105
; Sequence 105, Application US/09423056B
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric Charles
; APPLICANT: O'Brien-Simpson, Neil Martin
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
; TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
; FILE REFERENCE: 52928200300
; CURRENT APPLICATION NUMBER: US/09/423,056B
; CURRENT FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/AU98/00311
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105
; LENGTH: 736
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
; US-09-423-056B-105

Query Match 100.0%; Score 118; DB 24; Length 736;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNGGISLANYTGHGSETAWGT 21
Db 428 FNGGISLANYTGHGSETAWGT 448

RESULT 11
US-09-791-537-21158
; Sequence 21158, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21158
; LENGTH: 736
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
; US-09-791-537-21158

Query Match 100.0%; Score 118; DB 27; Length 736;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNGGISLANYTGHGSETAWGT 21
Db 428 FNGGISLANYTGHGSETAWGT 448

RESULT 12
US-10-387-977-105
; Sequence 105, Application US/10387977
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric Charles
; APPLICANT: O'Brien-Simpson, Neil Martin
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
; TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
; FILE REFERENCE: 52928200301
; CURRENT APPLICATION NUMBER: US/10/387,977
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 09/423,056
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/AU98/00311
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: AU PO 6528
; PRIOR FILING DATE: 1997-04-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105
; LENGTH: 736
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
; US-10-387-977-105

Query Match 100.0%; Score 118; DB 33; Length 736;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNGGISLANYTGHGSETAWGT 21
Db 199 FNGGISLANYTGHGSETAWGT 219

RESULT 13
US-09-791-537-49353
; Sequence 49353, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 49353
; LENGTH: 1526
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
; US-09-791-537-49353

Query Match 100.0%; Score 118; DB 27; Length 1526;
Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNGGISLANYTGHGSETAWGT 21
Db 426 FNGGISLANYTGHGSETAWGT 446

RESULT 14
US-09-791-537-100403
; Sequence 100403, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210

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; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 100403
; LENGTH: 1706
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-09-791-537-100403

Query Match 100.0%; Score 118; DB 27; Length 1706;
Best Local Similarity 100.0%; Pred. No. 5.5e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNGGISLANYTGHGSETAWGT 21
|||||
Db 426 FNGGISLANYTGHGSETAWGT 446

RESULT 15

US-09-791-537-113656
; Sequence 113656, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 113656
; LENGTH: 1706
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-09-791-537-113656

Query Match 100.0%; Score 118; DB 27; Length 1706;
Best Local Similarity 100.0%; Pred. No. 5.5e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNGGISLANYTGHGSETAWGT 21
|||||
Db 426 FNGGISLANYTGHGSETAWGT 446

Search completed: August 25, 2006, 18:20:51
Job time : 418.558 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 25, 2006, 18:06:46 ; Search time 26.3721 Seconds
(without alignments)
68.789 Million cell updates/sec

Title: US-10-387-977-1

Perfect score: 118

Sequence: 1 FNGGISLANYTGHSETAWGT 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 363143 seqs, 86385820 residues

Total number of hits satisfying chosen parameters: 363143

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /EMC_Celerra_SID83/ptodata/2/paa/US06_NEW_COMB.pep.*
- 3: /EMC_Celerra_SID83/ptodata/2/paa/US07_NEW_COMB.pep.*
- 4: /EMC_Celerra_SID83/ptodata/2/paa/US08_NEW_COMB.pep.*
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- 8: /EMC_Celerra_SID83/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	118	100.0	1706	6	US-10-229-066A-21	Sequence 21, Appl
2	82	69.5	1732	6	US-10-229-066A-24	Sequence 24, Appl
3	60.5	51.3	433	1	PCT-US06-18535-26437	Sequence 26437, A
4	60.5	51.3	433	7	US-11-431-855-26437	Sequence 26437, A
5	53.5	45.3	468	1	PCT-US06-18535-26266	Sequence 26266, A
6	53.5	45.3	468	7	US-11-431-855-26266	Sequence 26266, A
7	50.5	42.8	471	1	PCT-US06-18535-26339	Sequence 26339, A
8	50.5	42.8	471	7	US-11-431-855-26339	Sequence 26339, A
9	50	42.4	491	1	PCT-US06-18535-19305	Sequence 19305, A
10	50	42.4	491	7	US-11-431-855-19305	Sequence 19305, A
11	48	40.7	614	7	US-11-431-708-3588	Sequence 3588, Ap
12	48	40.7	614	7	US-11-431-708-3590	Sequence 3590, Ap
13	48	40.7	614	7	US-11-431-708-3601	Sequence 3601, Ap
14	48	40.7	614	7	US-11-431-708-3609	Sequence 3609, Ap
15	48	40.7	614	7	US-11-431-708-3614	Sequence 3614, Ap
16	48	40.7	614	7	US-11-475-062-6827	Sequence 6827, Ap
17	48	40.7	614	7	US-11-475-062-6829	Sequence 6829, Ap
18	48	40.7	614	7	US-11-475-062-6840	Sequence 6840, Ap
19	48	40.7	614	7	US-11-475-062-6848	Sequence 6848, Ap
20	48	40.7	614	7	US-11-475-062-6853	Sequence 6853, Ap
21	44	37.3	1256	8	US-60-836-986-9889	Sequence 9889, Ap
22	43	36.4	90	7	US-11-366-965-1049	Sequence 1049, Ap
23	43	36.4	269	7	US-11-371-354-58591	Sequence 58591, A
24	43	36.4	269	8	US-60-836-986-22583	Sequence 22583, A
25	43	36.4	289	1	PCT-US06-18535-24456	Sequence 24456, A

ALIGNMENTS

RESULT 1

US-10-229-066A-21

; Sequence 21, Application US/10229066A

; GENERAL INFORMATION:

; APPLICANT: REYNOLDS, ERIC CHARLES

; APPLICANT: BHOGAL, PETER SINGH

; APPLICANT: SLAKESKI, NADA

; TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE

; FILE REFERENCE: 4137-20

; CURRENT APPLICATION NUMBER: US/10/229,066A

; CURRENT FILING DATE: 2002-08-28

; PRIOR APPLICATION NUMBER: 09/066,330

; PRIOR FILING DATE: 1998-09-15

; PRIOR APPLICATION NUMBER: PCT/AU96/00673

; PRIOR FILING DATE: 1996-10-30

; PRIOR APPLICATION NUMBER: AU PN 6275

; PRIOR FILING DATE: 1995-10-30

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn Ver. 3.3

; SEQ ID NO 21

; LENGTH: 1706

; TYPE: PRT

; ORGANISM: Porphyromonas gingivalis

US-10-229-066A-21

Query Match 100.0%; Score 118; DB 6; Length 1706;

Best Local Similarity 100.0%; Pred.No. 4.8e-10;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qv 1 FNGGISLANYTGHSETAWGT 21

|||||

Db 426 FNGGISLANYTGHSETAWGT 446

RESULT 2

US-10-229-066A-24

; Sequence 24, Application US/10229066A

; GENERAL INFORMATION:

; APPLICANT: REYNOLDS, ERIC CHARLES

; APPLICANT: BHOGAL, PETER SINGH

; APPLICANT: SLAKESKI, NADA

; TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE

; FILE REFERENCE: 4137-20

; CURRENT APPLICATION NUMBER: US/10/229,066A

; CURRENT FILING DATE: 2002-08-28

; PRIOR APPLICATION NUMBER: 09/066,330

; PRIOR FILING DATE: 1998-09-15

; PRIOR APPLICATION NUMBER: PCT/AU96/00673

; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: AU PN 6275
; PRIOR FILING DATE: 1995-10-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 24
; LENGTH: 1732
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-229-066A-24

Query Match 69.5%; Score 82; DB 6; Length 1732;
Best Local Similarity 77.8%; Pred. No. 0.00025;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NGGISLANYTGHGSETAW 19
Db 433 NTGVSFANYTAHGETAW 450
|:|:|||||:|||||

RESULT 3
PCT-US06-18535-26437
; Sequence 26437, Application PC/TUS0618535
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark et. al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; CURRENT APPLICATION NUMBER: PCT/US06/18535
; CURRENT FILING DATE: 2006-05-10
; NUMBER OF SEQ ID NOS: 33637
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26437
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Burkholderia cepacia R1808
PCT-US06-18535-26437

Query Match 51.3%; Score 60.5; DB 1; Length 433;
Best Local Similarity 57.1%; Pred. No. 0.16; Length 433;
Matches 12; Conservative 1; Mismatches 5; Indels 3; Gaps 1;

Qy 4 GISLANYTGHGS---ETAWGT 21
Db 164 GIGFANYTGHGFMKPGPWGT 184
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RESULT 4
US-11-431-855-26437
; Sequence 26437, Application US/11431855
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark et. al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53708)C
; CURRENT APPLICATION NUMBER: US/11/431,855
; CURRENT FILING DATE: 2006-05-10
; NUMBER OF SEQ ID NOS: 33637
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26437
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Burkholderia cepacia R1808
US-11-431-855-26437

Query Match 51.3%; Score 60.5; DB 7; Length 433;
Best Local Similarity 57.1%; Pred. No. 0.16;
Matches 12; Conservative 1; Mismatches 5; Indels 3; Gaps 1;

Qy 4 GISLANYTGHGS---ETAWGT 21
Db 164 GIGFANYTGHGFMKPGPWGT 184
||:|||||:|||||

RESULT 5

PCT-US06-18535-26266
; Sequence 26266, Application PC/TUS0618535
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark et. al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53708)A
; CURRENT APPLICATION NUMBER: PCT/US06/18535
; CURRENT FILING DATE: 2006-05-10
; NUMBER OF SEQ ID NOS: 33637
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26266
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Burkholderia cepacia R18194
PCT-US06-18535-26266

Query Match 45.3%; Score 53.5; DB 1; Length 468;
Best Local Similarity 47.6%; Pred. No. 2.2;
Matches 10; Conservative 2; Mismatches 6; Indels 3; Gaps 1;

Qy 4 GISLANYTGHGS---ETAWGT 21
Db 199 GVGFPANYTAHGGFMKPGPWGT 219
|:|:|||||:|||||

RESULT 6
US-11-431-855-26266
; Sequence 26266, Application US/11431855
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark et. al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53708)C
; CURRENT APPLICATION NUMBER: US/11/431,855
; CURRENT FILING DATE: 2006-05-10
; NUMBER OF SEQ ID NOS: 33637
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26266
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Burkholderia cepacia R18194
US-11-431-855-26266

Query Match 45.3%; Score 53.5; DB 7; Length 468;
Best Local Similarity 47.6%; Pred. No. 2.2;
Matches 10; Conservative 2; Mismatches 6; Indels 3; Gaps 1;

Qy 4 GISLANYTGHGS---ETAWGT 21
Db 199 GVGFPANYTAHGGFMKPGPWGT 219
|:|:|||||:|||||

RESULT 7
PCT-US06-18535-26339
; Sequence 26339, Application PC/TUS0618535
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark et. al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53708)A
; CURRENT APPLICATION NUMBER: PCT/US06/18535
; CURRENT FILING DATE: 2006-05-10
; NUMBER OF SEQ ID NOS: 33637
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26339
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Burkholderia cepacia R18194
PCT-US06-18535-26339

Query Match 42.8%; Score 50.5; DB 1; Length 471;
Best Local Similarity 50.0%; Pred. No. 6.5;
Matches 10; Conservative 1; Mismatches 6; Indels 3; Gaps 1;

Qy 4 GISLANYTGHGS---ETAWGT 20

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Db      189 GIGFANYTAHGGFPKGVWG 208
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      || ||||| || : ||

RESULT 8
US-11-431-855-26339
; Sequence 26339, Application US/11431855
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark et. al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53708)C
; CURRENT APPLICATION NUMBER: US/11/431,855
; CURRENT FILING DATE: 2006-05-10
; NUMBER OF SEQ ID NOS: 33637
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26339
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Burkholderia cepacia R18194
US-11-431-855-26339

Query Match      42.8%; Score 50.5; DB 7; Length 471;
Best Local Similarity 50.0%; Pred. No. 6.5;
Matches 10; Conservative 1; Mismatches 6; Indels 3; Gaps 1;

Qy      4 GISLANYTGHGS---ETAWG 20
      || ||||| || : ||
      || ||||| || : ||

Db      189 GIGFANYTAHGGFPKGVWG 208
      || ||||| || : ||
      || ||||| || : ||

RESULT 9
PCT-US06-18535-19305
; Sequence 19305, Application PC/TUS0618535
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark et. al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53708)A
; CURRENT APPLICATION NUMBER: PCT/US06/18535
; CURRENT FILING DATE: 2006-05-10
; NUMBER OF SEQ ID NOS: 33637
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19305
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Bacteroides thetaiotaomicron VPI-5482
PCT-US06-18535-19305

Query Match      42.4%; Score 50; DB 1; Length 491;
Best Local Similarity 69.2%; Pred. No. 8.2;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      9 NYTGHGSETAWGT 21
      || ||||| || : ||
      || ||||| || : ||

Db      476 NWTGHGGETKSGT 488
      || ||||| || : ||
      || ||||| || : ||

RESULT 10
US-11-431-855-19305
; Sequence 19305, Application US/11431855
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark et. al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53708)C
; CURRENT APPLICATION NUMBER: US/11/431,855
; CURRENT FILING DATE: 2006-05-10
; NUMBER OF SEQ ID NOS: 33637
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19305
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Bacteroides thetaiotaomicron VPI-5482
US-11-431-855-19305

Query Match      42.4%; Score 50; DB 7; Length 491;
Best Local Similarity 69.2%; Pred. No. 8.2;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      9 NYTGHGSETAWGT 21
      || ||||| || : ||
      || ||||| || : ||

Db      476 NWTGHGGETKSGT 488
      || ||||| || : ||
      || ||||| || : ||

RESULT 11
US-11-431-708-3588
; Sequence 3588, Application US/11431708
; GENERAL INFORMATION:
; APPLICANT: RUBEN, Steven
; TITLE OF INVENTION: BREAST DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001599-ORD
; CURRENT APPLICATION NUMBER: US/11/431,708
; CURRENT FILING DATE: 2006-05-11
; NUMBER OF SEQ ID NOS: 8544
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3588
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-431-708-3588

Query Match      40.7%; Score 48; DB 7; Length 614;
Best Local Similarity 53.3%; Pred. No. 21;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy      5 ISLANYTGHGSETAW 19
      : || ||||| || : ||
      : || ||||| || : ||

Db      94 VALGQYTSQGSVTAW 108
      : || ||||| || : ||
      : || ||||| || : ||

RESULT 12
US-11-431-708-3590
; Sequence 3590, Application US/11431708
; GENERAL INFORMATION:
; APPLICANT: RUBEN, Steven
; TITLE OF INVENTION: BREAST DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001599-ORD
; CURRENT APPLICATION NUMBER: US/11/431,708
; CURRENT FILING DATE: 2006-05-11
; NUMBER OF SEQ ID NOS: 8544
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3590
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-431-708-3590

Query Match      40.7%; Score 48; DB 7; Length 614;
Best Local Similarity 53.3%; Pred. No. 21;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy      5 ISLANYTGHGSETAW 19
      : || ||||| || : ||
      : || ||||| || : ||

Db      94 VALGQYTSQGSVTAW 108
      : || ||||| || : ||
      : || ||||| || : ||

RESULT 13
US-11-431-708-3601
; Sequence 3601, Application US/11431708
; GENERAL INFORMATION:
; APPLICANT: RUBEN, Steven
; TITLE OF INVENTION: BREAST DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001599-ORD
; CURRENT APPLICATION NUMBER: US/11/431,708
; CURRENT FILING DATE: 2006-05-11
; NUMBER OF SEQ ID NOS: 8544
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3601
US-11-431-708-3601
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; LENGTH: 614
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-431-708-3601

Query Match      40.7%; Score 48; DB 7; Length 614;
Best Local Similarity 53.3%; Pred. No. 21;
Matches      8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      5 ISLANYTGHGSETAW 19
Db      94 VALGQYTSQGSVTAW 108

RESULT 14
US-11-431-708-3609
; Sequence 3609, Application US/11431708
; GENERAL INFORMATION:
; APPLICANT: RUBEN, Steven
; TITLE OF INVENTION: BREAST DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001599-ORD
; CURRENT APPLICATION NUMBER: US/11/431,708
; CURRENT FILING DATE: 2006-05-11
; NUMBER OF SEQ ID NOS: 8544
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3609
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-431-708-3609

Query Match      40.7%; Score 48; DB 7; Length 614;
Best Local Similarity 53.3%; Pred. No. 21;
Matches      8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      5 ISLANYTGHGSETAW 19
Db      94 VALGQYTSQGSVTAW 108

RESULT 15
US-11-431-708-3614
; Sequence 3614, Application US/11431708
; GENERAL INFORMATION:
; APPLICANT: RUBEN, Steven
; TITLE OF INVENTION: BREAST DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001599-ORD
; CURRENT APPLICATION NUMBER: US/11/431,708
; CURRENT FILING DATE: 2006-05-11
; NUMBER OF SEQ ID NOS: 8544
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3614
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-431-708-3614

Query Match      40.7%; Score 48; DB 7; Length 614;
Best Local Similarity 53.3%; Pred. No. 21;
Matches      8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      5 ISLANYTGHGSETAW 19
Db      94 VALGQYTSQGSVTAW 108

Search completed: August 25, 2006, 18:21:51
Job time : 27.3721 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 25, 2006, 17:58:43 ; Search time 23.4419 Seconds
(without alignments)
86.194 Million cell updates/sec

Title: US-10-387-977-1
Perfect score: 118
Sequence: 1 FNGGISLVNTGHGSETAWGT 21
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	114	96.6	991	2 I40229	arginyl endopeptidase
3	114	96.6	1704	2 A55426	gingipain R (EC 3.1.1.1)
4	82	69.5	1732	2 T30836	lysine-specific cy
5	53	44.9	234	2 S41406	arginine-specific
6	49.5	41.9	542	2 I39540	chitinase (EC 3.2.1.1)
7	48	40.7	612	2 T10727	protein kinase Xa2
8	48	40.7	614	2 S68236	betaine/GABA trans
9	48	40.7	614	2 A41757	betaine transport
10	48	40.7	677	2 A27286	levanase (EC 3.2.1.1)
11	48	40.7	813	2 T04313	protein kinase Xa2
12	48	40.7	996	2 T10725	protein kinase Xa2
13	48	40.7	1025	1 A57676	protein kinase Xa2
14	47	39.8	61	2 G83651	hypothetical prote
15	47	39.8	294	2 AE2695	conserved hypothet
16	47	39.8	294	2 E97477	hypothetical prote
17	46	39.0	404	2 E82012	sodium/glutamate s
18	46	39.0	404	2 F81240	sodium/glutamate s
19	46	39.0	1002	2 T09438	toXR-activated lip
20	46	39.0	1013	2 B82276	ToXR-activated gen
21	46	39.0	2136	2 B84651	hypothetical prote
22	45.5	38.6	760	2 B44817	probable membrane
23	45.5	38.6	760	2 B85589	hypothetical prote
24	45.5	38.6	760	2 C90739	hypothetical prote
25	45	38.1	130	2 S65682	elkp protein - Sta
26	45	38.1	212	2 T22437	hypothetical prote
27	45	38.1	248	2 C75140	hypothetical prote
28	45	38.1	307	2 AB2029	ribokinase [impor
29	45	38.1	548	2 T49948	hypothetical prote

30	45	38.1	1736	2 T00391	hypothetical prote
31	45	38.1	4639	1 A54794	dynain heavy chain
32	44.5	37.7	287	2 S65765	chitinase (EC 3.2.1.1)
33	44.5	37.7	328	2 AE0301	conserved hypothet
34	44	37.3	289	2 S23402	sperm surface prot
35	44	37.3	458	2 E70145	aminopeptidase I (
36	44	37.3	465	2 B69768	probable acid-CoA
37	44	37.3	614	2 A43390	gamma-aminobutyric
38	44	37.3	793	2 S59067	penton long fiber
39	44	37.3	2871	2 A55567	fibrillin I - bovi
40	43.5	36.9	281	2 S18245	xyIF protein - Pse
41	43.5	36.9	555	2 AC0210	pectate disacchari
42	43	36.4	169	2 F72532	hypothetical prote
43	43	36.4	205	2 A37329	antigen 5 - paper
44	43	36.4	254	2 D35957	probable 2-deoxy-D
45	43	36.4	301	2 B84533	hypothetical prote

ALIGNMENTS

RESULT 1

S49763

gingipain R (EC 3.4.22.37) precursor - Porphyromonas gingivalis (fragment)

C;Species: Porphyromonas gingivalis

C;Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004

C;Accession: S49763

R;Aduse-Opoku, J.; Muir, J.; Slaney, J. M.; Rangarajan, M.; Curtis, M. A.

Submitted to the EMBL Data Library, November 1994

A;Description: Cloning, sequence analysis and expression in Escherichia coli of prpR1 of

A;Reference number: S49763

A;Accession: S49763

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1526 <ADU>

A;Cross-references: UNIPROT:Q51838; UNIPARC:UPI0000179912; EMBL:X82680

C;Genetics:

A;Gene: prpR1

C;Keywords: cysteine proteinase; hydrolase

Query Match 100.0%; Score 118; DB 2; Length 1526;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNGGISLVNTGHGSETAWGT 21
|||||
DB 426 FNGGISLVNTGHGSETAWGT 446

RESULT 2

I40229

arginyl endopeptidase - Porphyromonas gingivalis

C;Species: Porphyromonas gingivalis

C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004

C;Accession: I40229

R;Okamoto, K.; Misumi, Y.; Kadowaki, T.; Yoneda, M.; Yamamoto, K.; Ikehara, Y.

Arch. Biochem. Biophys. 316, 917-925, 1995

A;Title: Structural characterization of argingipain, a novel arginine-specific cysteine

A;Reference number: I40229; MUID:95168884; PMID:7864651

A;Accession: I40229

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-991 <RES>

A;Cross-references: UNIPROT:P28784; UNIPARC:UPI000012829F; GB:D26470; NID:9927644; PIDN:

Query Match 96.6%; Score 114; DB 2; Length 991;
Best Local Similarity 95.2%; Pred. No. 3.7e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FNGGISLVNTGHGSETAWGT 21
|||||
DB 426 FNGGISLVNTGHGSETAWGT 446

RESULT 7

Tl0727
protein kinase Xa21 (EC 2.7.1.1-) D, receptor type - long-staminate rice
C:Species: Oryza longistaminata (long-staminate rice)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: Tl0727
R;Song, W.Y.; Pi, L.Y.; Wang, G.L.; Gardner, J.; Holsten, T.; Ronald, P.C.
Plant Cell 9, 1279-1287, 1997
A>Title: Evolution of the rice Xa21 disease resistance gene family.
A;Reference number: Z15276; MUID:97432142; PMID:9286106
A:Accession: Tl0727
A;Status: preliminary; translated from GB/EMBL/DDBB
A:Molecule type: DNA
A;Residues: 1-612 <SON>
A;Cross-references: UNIPROT:O24437; UNIPARC:UPI000009D7E7; EMBL:U72726; NID:G2586078; PID:
A;Experimental source: strain IRBB21
C:Genetics:
A;Map position: 11
C;Keywords: phosphotransferase

Query Match	40.7%;	Score 48;	DB 2;	Length 612;
Best Local Similarity	47.6%;	Pred. No. 25;		
Matches 10;	Conservative 2;	Mismatches 7;	Indels 2;	Gaps 1;

Qy 1 FNGGISLA--NYTGHGSETAW 19
 : || || | | | | | | | |
Dd 45 YQGQSGLASWNTSGHGQHCTW 65

RESULT 8

S68236
betaine/GABA transport protein BGT-1 - human
C:Species: Homo sapiens (man)
C>Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S68236; I56522
R;Rasola, A.; Galietta, L.J.V.; Barone, V.; Romeo, G.; Bagnasco, S.
FEBS Lett. 373, 229-233, 1995
A>Title: Molecular cloning and functional characterization of a GABA/betaine transporter
A;Reference number: S68236; MUID:96033979; PMID:7589472
A:Accession: S68236
A;Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A;Residues: 1-614 <RAS>
A;Cross-references: UNIPROT:P48065; UNIPARC:UPI0000161F4B; EMBL:U27699; NID:g881474; PID:
R;Borden, L.A.; Smith, K.E.; Gustafson, E.L.; Brancheck, T.A.; Weinshank, R.L.
J. Neurochem. 64, 977-984, 1995
A>Title: Cloning and expression of a betaine/GABA transporter from human brain.
A;Reference number: I56522; MUID:95165166; PMID:7861179
A:Accession: I56522
A;Status: preliminary; translated from GB/EMBL/DDBB
A:Molecule type: mRNA
A;Residues: 1-9,'Y',11-570,'QL',573-614 <RES>
A;Cross-references: UNIPARC:UPI00001354A9; GB:L42300; NID:g808695; PIDN:AAA66574.1; PID:
C:Genetics:
A;Gene: BGT-1
A;Map position: 12p13
C;Superfamily: gamma-aminobutyric acid transporter
C;Keywords: glycoprotein; phosphoprotein; transmembrane protein
F;45-65/Domain: transmembrane #status predicted <TM1>
F;72-92/Domain: transmembrane #status predicted <TM2>
F;116-137/Domain: transmembrane #status predicted <TM3>
F;213-232/Domain: transmembrane #status predicted <TM4>
F;238-260/Domain: transmembrane #status predicted <TM5>
F;287-307/Domain: transmembrane #status predicted <TM6>
F;321-340/Domain: transmembrane #status predicted <TM7>
F;373-393/Domain: transmembrane #status predicted <TM8>
F;423-440/Domain: transmembrane #status predicted <TM9>
F;456-476/Domain: transmembrane #status predicted <TM10>
F;496-517/Domain: transmembrane #status predicted <TM11>
F;538-559/Domain: transmembrane #status predicted <TM12>
F;40,235/Binding site: phosphate (Thr) (covalent) #status predicted
F;171,183/Binding site: carbohydtrate (Asn) (covalent) #status predicted

F:418/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 40.7%; Score 48; DB 2; Length 614;
Best Local Similarity 53.3%; Pred. No. 25;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5 ISLANVTGHGSETAW 19
::||| ||| ||| |||
DB 94 VALGQVTSQGSVTAW 108

RESULT 9
A41757
betaine transport protein, renal - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: A41757
R:Yamauchi, A.; Uchida, S.; Kwon, H.M.; Preston, A.S.; Robey, R.B.; Garcia-Perez, A.; B
J. Biol. Chem. 267, 649-652, 1992
A:Title: Cloning of a Na(+)- and Cl(-)-dependent betaine transporter that is regulated b
A:Reference number: A41757; MUID:92112724; PMID:1370453
A:Accession: A41757
A:Molecule type: mRNA
A:Residues: 1-614 <YAM>
A:Cross-references: UNIPROT:P27799; UNIPARC:UPI00001354A8; GB:M80403; NID:g164031; PIDN:
C:Superfamily: gamma-aminobutyric acid transporter
C:Keywords: membrane protein

Query Match 40.7%; Score 48; DB 2; Length 614;
Best Local Similarity 53.3%; Pred. No. 25;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5 ISLANVTGHGSETAW 19
::||| ||| ||| |||
DB 94 VALGQVTSQGSVTAW 108

RESULT 10
A27286
levanase (EC 3.2.1.65) precursor - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C:Accession: A27286; S06353; S11402; A69703
R:Schoengenderfer, K.; Schwab, H.; Lafferty, R.M.
Nucleic Acids Res. 15, 9606, 1987
A:Title: Nucleotide sequence of a cloned 2.5 kb PstI-EcoRI Bacillus subtilis DNA fragmen
A:Reference number: A27286; MUID:98067786; PMID:3120151
A:Accession: A27286
A:Molecule type: DNA
A:Residues: 1-677 <SCH>
A:Cross-references: UNIPROT:P05656; UNIPARC:UPI0000165952; GB:Y00485; NID:g40124; PIDN:C
R:Martin, I.; Debarbouille, M.; Ferrari, E.; Klier, A.; Rapoport, G.
Mol. Gen. Genet. 208, 177-184, 1987
A:Title: Characterization of the levanase gene of Bacillus subtilis which shows homology
A:Reference number: S06353; MUID:87286401; PMID:3112519
A:Accession: S06353
A:Molecule type: DNA
A:Residues: 1-657, 'Q', 659-677 <MAR>
A:Cross-references: UNIPARC:UPI00000607F3; EMBL:X05649
R:Martin-Verstraete, I.; Debarbouille, M.; Klier, A.; Rapoport, G.
J. Mol. Biol. 214, 657-671, 1990
A:Title: Levanase operon of Bacillus subtilis includes a fructose-specific phosphotransf
A:Reference number: S11398; MUID:90355183; PMID:2117666
A:Accession: S11402
A:Molecule type: DNA
A:Residues: 1-10 <MA2>
A:Cross-references: UNIPARC:UPI00001658BE; GB:X56098; NID:g39977; PIDN:CAA3981.1; PID:G
R:Kunst, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iesh, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono S.; Hullo, M.F.

Matches 10; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

Qy 1 FNGGISLA--NYTGHSETAW 19
: ||||| | : |||||
Db 45 YQGGQSLASWNTSGHGQCTW 65

RESULT 14

G83651
hypothetical protein BH0015 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: G83651
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: G83651
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-61 <STO>
A;Cross-references: UNIPROT:Q9KGP2; UNIPARC:UPI000000C377B; GB:AP001507; GB:BA000004; NID
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH0015

Query Match 39.8%; Score 47; DB 2; Length 61;
Best Local Similarity 52.9%; Pred. No. 2.9;
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 3 GGISLANYTGHSETAW 19
|| : |||||
Db 42 GGRLLSTNWTGHPSEQHW 58

RESULT 15

AE2695
conserved hypothetical protein Atu0965 [imported] - Agrobacterium tumefaciens (strain C58)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AE2695
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
erage, G.; Gillet, W.; Grant, C.; Guenthrner, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AE2695
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-294 <EUR>
A;Cross-references: UNIPROT:Q8UGS0; UNIPARC:UPI000000D19C5; GB:AE008688; PIDN:AAL41979.1;
C;Genetics:
A;Gene: Atu0965
A;Map position: circular chromosome

Query Match 39.8%; Score 47; DB 2; Length 294;
Best Local Similarity 53.3%; Pred. No. 16;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 4 GISLANYTGHSETA 18
| : | : |||||
Db 161 GVDLTRFTGHGSVAA 175

Search completed: August 25, 2006, 18:05:18
Job time : 27.4419 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 25, 2006, 17:50:25 ; Search time 188.512 Seconds
(without alignments)
103.046 Million cell updates/sec

Title: US-10-387-977-1
Perfect score: 118
Sequence: 1 FNGGISLANYTHGHSETAMGT 21

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	118	100.0	736	1	CPG2_PORGI	P95493 porphyromon
2	118	100.0	1706	2	Q51838_PORGI	Q51838 porphyromon
3	118	100.0	1706	2	Q51839_PORGI	Q51839 porphyromon
4	118	100.0	1706	2	Q7MTE2_PORGI	Q7MTE2 porphyromon
5	114	96.6	736	2	Q51844_PORGI	Q51844 porphyromon
6	114	96.6	991	1	CPGI_PORGI	P28784 porphyromon
7	114	96.6	1687	2	Q9R9B7_PORGI	Q9R9B7 porphyromon
8	114	96.6	1704	2	Q51816_PORGI	Q51816 porphyromon
9	100.5	85.2	422	2	Q51818_PORGI	Q51818 porphyromon
10	82	69.5	1358	2	Q6Q4T4_PORGI	Q6Q4T4 porphyromon
11	82	69.5	1732	2	Q07442_PORGI	Q07442 porphyromon
12	82	69.5	1732	2	Q52050_PORGI	Q52050 porphyromon
13	82	69.5	1732	2	Q51817_PORGI	Q51817 porphyromon
14	75	63.6	1358	2	P96967_PORGI	P96967 porphyromon
15	75	63.6	1723	2	P72194_PORGI	P72194 porphyromon
16	75	63.6	1723	2	P72197_PORGI	P72197 porphyromon
17	60.5	51.3	459	2	Q4BEX8_BURVI	Q4BEX8 burkholderi
18	58.5	49.6	475	2	Q3RT78_RALME	Q3RT78 ralstonia m
19	57	48.3	559	2	Q2PJ92_ENTFA	Q2PJ92 enterococcu
20	57	48.3	559	2	Q839T9_ENTFA	Q839T9 enterococcu
21	55	46.6	527	2	Q52PM7_9CAUD	Q52PM7 xanthomonas
22	54.5	46.2	468	2	Q44296_9BURK	Q44296 burkholderi
23	54.5	46.2	468	2	Q4LK93_9BURK	Q4LK93 burkholderi
24	54	45.8	1123	2	Q7MXX2_PORGI	Q7MXX2 porphyromon
25	54	45.8	1357	2	Q220E1_9BACT	Q220E1 uncultured
26	53.5	45.3	468	2	Q39DM3_BURS3	Q39DM3 burkholderi
27	53	44.9	418	2	Q7VD37_PROMA	Q7VD37 prochloroco
28	52	44.1	157	2	Q93SL6_STRTR	Q93SL6 streptococc
29	52	44.1	357	2	Q3B616_PELUD	Q3B616 pelodictyon
30	52	44.1	408	2	Q8Y1V4_RALSO	Q8Y1V4 ralstonia s
31	51	43.2	156	2	Q47AY8_DECAR	Q47AY8 dechloromon

32 51 43.2 444 2 Q4H890_9DEIO Q4H890 deinococcus

33 51 43.2 1090 2 Q9HJG1_THEAC Q9HJG1 thermoplasm

34 51 43.2 1148 2 Q2PY26_9BACT Q2PY26 uncultured

35 50.5 42.8 471 2 Q39LI4_BURS3 Q39LI4 burkholderi

36 50 42.4 434 2 Q35NH4_9BRAD Q35NH4 bradyrhizob

37 50 42.4 491 2 Q8A8E5_BACTN Q8A8E5 bacteroides

38 50 42.4 495 2 Q5LI05_BACFN Q5LI05 bacteroides

39 50 42.4 526 2 Q6MS69_MYCMS Q6MS69 mycoplasma

40 50 42.4 884 2 Q3E1V9_CHLAU Q3E1V9 chloroflexu

41 50 42.4 926 2 Q4AIR5_9CHLB Q4AIR5 chlorobium

42 50 42.4 1037 2 Q2R2D5_ORYSA Q2R2D5 oryza sativ

43 50 42.4 3032 2 Q60XP7_CAEBR Q60XP7 caenorhabdi

44 49.5 41.9 302 2 Q5TPA7_ANOGA Q5TPA7 anopheles g

45 49.5 41.9 407 2 Q7Q1Q0_ANOGA Q7Q1Q0 anopheles g

ALIGNMENTS

RESULT 1

CPG2_PORGI ID_CPG2_PORGI STANDARD; PRT; 736 AA.

AC P95493; O33441; PRT; 736 AA.

DT 15-DEC-1998, integrated into UniProtKB/Swiss-Prot.

DT 03-OCT-2003, sequence version 2.

DT 07-MAR-2006, entry version 53.

DE Gingipain R2 precursor (EC 3.4.22.37) (Gingipain 2) (Arg-gingipain) (RGP-2).

DE Name=rgpB; Synonyms=prtR11, rgp2; OrderedLocusNames=PG0506;

OS Porphyromonas gingivalis (Bacteroides gingivalis).

OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;

OC Porphyromonadaceae; Porphyromonas.

OX NCBI_TaxID=837;

RN [1]

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND PROTEIN SEQUENCE OF 230-651.

RC STRAIN=HG66;

RX MEDLINE=98370998; PubMed=9705298; DOI=10.1074/jbc.273.34.21648;

RA Potempa J., Mikolajczyk-Pawlinska J., Brassell D., Nelson D.,

RA Thøgersen I.B., Enghild J.J., Travis J.

RT "Comparative properties of two cysteine proteinases (gingipains R), the products of two related but individual genes of Porphyromonas gingivalis.";

RT J. Biol. Chem. 273:21648-21657 (1998).

RN [2]

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].

RC STRAIN=W50;

RX MEDLINE=98304082; PubMed=9639929;

RA Slakeski N., Bhogal P.S., O'Brien-Simpson N.M., Reynolds E.C.;

RT "Characterization of a second cell-associated Arg-specific cysteine proteinase of Porphyromonas gingivalis and identification of an adhesin-binding motif involved in association of the prtR and prtK proteinases and adhesins into large complexes.";

RT Microbiology 144:1583-1592 (1998).

RN [3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=W83;

RX MEDLINE=22829867; PubMed=12949112;

DOI=10.1128/JB.185.18.5591-5601.2003;

RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,

RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,

RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,

RA Granger D., Tetelin H., Dong H., Galvin J.L., Duncan M.J.,

RA Dewhirst F.E., Fraser C.M.;

RT "Complete genome sequence of the oral pathogenic bacterium Porphyromonas gingivalis strain W83.";

RT J. Bacteriol. 185:5591-5601 (2003).

RN [4]

RP ENZYME REGULATION.

RX PubMed=11179305; DOI=10.1128/IAI.69.3.1402-1408.2001;

RA Gusman H., Travis J., Helmerhorst E.J., Potempa J., Troxler R.F.,

RA Oppenheim F.G.;

RT "Salivary histatin 5 is an inhibitor of both host and bacterial enzymes implicated in periodontal disease.";

RL Infect. Immun. 69:1402-1408(2001).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RX MEDLINE=99452753; PubMed=10523290; DOI=10.1093/emboj/18.20.5453;
RA Eichinger A., Beisel H.-G., Jacob U., Huber R., Medrano F.-J.,
RA Banbula A., Potempa J., Travis J., Bode W.;
RT "Crystal structure of gingipain R: an Arg-specific bacterial cysteine
RT proteinase with a caspase-like fold.";
RL EMBL J. 18:5453-5462(1999).
CC -1- FUNCTION: Thiol protease which is believed to participate in
CC intracellular degradation and turnover of proteins. Its
CC proteolytic activity is a major factor in both periodontal tissue
CC destruction and in bacterial host defense mechanisms. Activates
CC complement C3 and C5 (By similarity).
CC -1- CATALYTIC ACTIVITY: Hydrolysis of proteins and small molecule
CC substrates, with a preference for Arg in P1.
CC -1- ENZYME REGULATION: Inhibited by human histatin-3 1/24 (histatin-
CC 5).
CC -1- SIMILARITY: Belongs to the peptidase C25 family.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL: AF007124; AAC26371.1; -; Genomic DNA.
DR EMBL: AF007124; AAC26371.1; -; Genomic DNA.
DR EMBL: AE015924; AA065700.1; -; Genomic DNA.
DR PDB: 1CVR; X-ray; A=230-664.
DR MEROPS: C25.003; -.
DR GenomeReviews; AE015924_GR; PG0506.
DR TIGR; PG0506; -.
DR BioCyc; PGIN242619; PG0506-MONOMER; -.
DR InterPro; IPR001769; Peptidase_C25.
DR InterPro; IPR005536; Peptidase_C25_C.
DR InterPro; IPR012600; Propeptide_C25.
DR Pfam; PF01364; Peptidase_C25; 1.
DR Pfam; PF03785; Peptidase_C25_C; 1.
DR Pfam; PF08126; Propeptide_C25; 1.
KW 3D-structure; Calcium; Complete proteome; Direct protein sequencing;
KW Hydrolase; Protease; Signal; Thiol protease; Virulence; Zymogen.
FT SIGNAL 1 24 By similarity.
FT PROPEP 25 229
FT CHAIN 230 736 /FTid=PRO_0000026535.
FT ACT SITE 440 440 Gingipain_R2.
FT ACT SITE 473 473 /FTid=PRO_0000026536.
FT CONFLICT 58 58 Proton donor.
FT CONFLICT 246 246 Nucleophile.
FT CONFLICT 251 251 G -> D (in Ref. 1).
FT CONFLICT 251 251 P -> A (in Ref. 1).
FT CONFLICT 254 254 E -> G (in Ref. 1).
FT CONFLICT 254 254 E -> K (in Ref. 1).
FT CONFLICT 398 398 I -> V (in Ref. 1).
FT CONFLICT 435 435 A -> V (in Ref. 1).
FT CONFLICT 480 480 YNV -> FSM (in Ref. 1).
FT CONFLICT 510 510 N -> D (in Ref. 1).
FT CONFLICT 512 512 S -> Y (in Ref. 1).
FT CONFLICT 515 515 S -> P (in Ref. 1).
FT CONFLICT 560 560 K -> N (in Ref. 1).
FT CONFLICT 582 582 K -> E (in Ref. 1).
FT TURN 237 238
FT STRAND 240 245
FT STRAND 247 252
FT HELIX 254 262
FT TURN 263 264
FT STRAND 266 271
FT STRAND 272 275
FT STRAND 277 278
FT HELIX 281 283
FT STRAND 294 294
FT TURN 295 296
FT STRAND 299 306
FT TURN 308 310
FT STRAND 311 311
FT STRAND 314 316

FT TURN 317 317
FT STRAND 319 322
FT HELIX 323 326
FT STRAND 329 333
FT STRAND 336 342
FT STRAND 345 346
FT HELIX 347 362
FT STRAND 363 363
FT TURN 366 367
FT TURN 369 372
FT STRAND 373 378
FT STRAND 380 380
FT STRAND 382 382
FT TURN 384 385
FT STRAND 386 386
FT STRAND 387 389
FT HELIX 391 391
FT STRAND 392 406
FT TURN 407 407
FT STRAND 409 418
FT HELIX 421 430
FT STRAND 433 439
FT STRAND 441 441
FT STRAND 443 446
FT TURN 447 449
FT STRAND 452 452
FT TURN 453 455
FT HELIX 456 458
FT TURN 462 463
FT STRAND 467 474
FT TURN 475 476
FT TURN 478 479
FT STRAND 480 482
FT HELIX 485 491
FT STRAND 493 494
FT TURN 495 496
FT STRAND 497 498
FT STRAND 500 500
FT STRAND 502 509
FT STRAND 513 514
FT HELIX 515 527
FT TURN 528 529
FT STRAND 531 531
FT TURN 532 533
FT STRAND 538 538
FT HELIX 539 564
FT STRAND 565 569
FT TURN 571 572
FT STRAND 574 574
FT STRAND 578 578
FT STRAND 581 581
FT STRAND 585 586
FT STRAND 589 592
FT TURN 593 594
FT STRAND 596 604
FT TURN 605 606
FT STRAND 608 613
FT TURN 614 615
FT STRAND 616 622
FT STRAND 624 624
FT TURN 625 626
FT STRAND 627 631
FT STRAND 633 634
FT TURN 637 638
FT STRAND 640 647
FT TURN 649 650
FT STRAND 651 651
FT STRAND 654 661
SQ SEQUENCE 736 AA; 80967 MW; C848DD3FAB420833 CRC64;

Query Match 100.0%; Score 118; DB 1; Length 736;
Best Local Similarity 100.0%; Pred. No. 2.7e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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Qy      1  FNGGISLANYTGHGSETAWGT 21
Db      428 FNGGISLANYTGHGSETAWGT 448

RESULT 2
Q51838_PORGI
ID      Q51838_PORGI      PRELIMINARY;      PRT;      1706 AA.
AC      Q51838;
DT      01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT      01-MAY-1997, sequence version 2.
DT      07-FEB-2006, entry version 26.
DE      Protease precursor.
GN      Name=prp1;
OS      Porphyromonas gingivalis (Bacteroides gingivalis).
OC      Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC      Porphyromonadaceae; Porphyromonas.
OX      NCBI_TaxID=837;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=W50;
RX      MEDLINE=96071894; PubMed=7591131;
RA      Aduse-Opoku J., Muir J., Slaney J.M., Rangarajan M., Curtis M.A.;
RT      "Characterization, genetic analysis, and expression of a protease
RT      antigen (Prp1) of Porphyromonas gingivalis W50.";
RL      Infect. Immun. 63:4744-4754(1995).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=W50;
RX      MEDLINE=96071894; PubMed=7591131;
RA      Aduse-Opoku J., Muir J., Slaney J.M., Rangarajan M., Curtis M.A.;
RT      "The prp1 and the pr2 arginine-specific protease genes of
RT      porphyromonas gingivalis W50 produce five biochemically distinct
RT      enzymes.";
RL      Mol. Microbiol. 23:0-0(1997).
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
CC      EMBL; X82680; CAA57997.1; -; Genomic_DNA.
DR      PR1; S49763; S49763.
DR      HSSP; P95493; 1CVR.
DR      SMR; Q51838; 228-655.
DR      GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR      GO; GO:0009405; P:pathogenesis; IEA.
DR      GO; GO:0006508; P:proteolysis; IEA.
DR      GO; GO:0006508; P:proteolysis; IEA.
DR      InterPro; IPR011628; Cleaved_adhesin.
DR      InterPro; IPR000977; DNA_ligase.
DR      InterPro; IPR000977; DNA_ligase.
DR      InterPro; IPR001769; Peptidase_C25.
DR      InterPro; IPR005536; Peptidase_C25.
DR      InterPro; IPR012600; Propeptide_C25.
DR      Pfam; PF07675; Cleaved_Adhesin; 2.
DR      Pfam; PF01364; Peptidase_C25; 1.
DR      Pfam; PF03785; Peptidase_C25; 1.
DR      Pfam; PF08126; Propeptide_C25; 1.
DR      PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN_1.
KW      Protease; Signal.
FT      SIGNAL      1      23      Potential.
FT      CHAIN      228      719      alpha-protease.
FT      CHAIN      720      1262      beta-adhesin.
SQ      SEQUENCE      1706 AA; 185706 MW; 0856DCD87FDA8CDD CRC64;

Query Match      100.0%; Score 118; DB 2; Length 1706;
Best Local Similarity 100.0%; Pred. NO. 6.9e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  FNGGISLANYTGHGSETAWGT 21
Db      426 FNGGISLANYTGHGSETAWGT 446

RESULT 3
Q51839_PORGI
ID      Q51839_PORGI      PRELIMINARY;      PRT;      1706 AA.
AC      Q51839;
DT      01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT      07-FEB-2006, entry version 27.
DE      Arginine-specific thiol protease precursor.
GN      Name=prtr;
OS      Porphyromonas gingivalis (Bacteroides gingivalis).
OC      Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC      Porphyromonadaceae; Porphyromonas.
OX      NCBI_TaxID=837;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=W50;
RX      MEDLINE=95160709; PubMed=7857299;
RA      Kirsbaum L., Sotiropoulos C., Jackson C., Cleal S., Slakeski N.,
RA      Reynolds E.C.;
RT      "Complete nucleotide sequence of a gene prtr of Porphyromonas
RT      gingivalis W50 encoding a 132 kDa protein that contains an arginine-
RT      specific thiol endopeptidase domain and a haemagglutinin domain.";
RL      Biochem. Biophys. Res. Commun. 207:424-431(1995).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=W50;
RX      MEDLINE=96311339; PubMed=8713096; DOI=10.1006/bbrc.1996.1073;
RA      Slakeski N., Cleal S.M., Reynolds E.C.;
RT      "Characterization of a Porphyromonas gingivalis gene prtr that encodes
RT      an arginine-specific thiol proteinase and multiple adhesins.";
RL      Biochem. Biophys. Res. Commun. 224:605-610(1996).
RN      [3]
RP      NUCLEOTIDE SEQUENCE OF 212-455.
RC      STRAIN=W50;
RA      Reynolds E.;
RL      Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
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CC      -----
CC      EMBL; L26341; AAC18876.1; -; Genomic_DNA.
DR      HSSP; P95493; 1CVR.
DR      SMR; Q51839; 228-655.
DR      GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR      GO; GO:0009405; P:pathogenesis; IEA.
DR      GO; GO:0006508; P:proteolysis; IEA.
DR      InterPro; IPR011628; Cleaved_adhesin.
DR      InterPro; IPR000977; DNA_ligase.
DR      InterPro; IPR001769; Peptidase_C25.
DR      InterPro; IPR005536; Peptidase_C25.
DR      InterPro; IPR012600; Propeptide_C25.
DR      Pfam; PF07675; Cleaved_Adhesin; 2.
DR      Pfam; PF01364; Peptidase_C25; 1.
DR      Pfam; PF03785; Peptidase_C25; 1.
DR      Pfam; PF08126; Propeptide_C25; 1.
DR      PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN_1.
KW      Protease; Signal.
FT      SIGNAL      1      23      Potential.
FT      CHAIN      228      1706      arginine-specific thiol protease.
FT      CHAIN      1706 AA; 185627 MW; E8BDF07C9813B844 CRC64;

Query Match      100.0%; Score 118; DB 2; Length 1706;
Best Local Similarity 100.0%; Pred. NO. 6.9e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  FNGGISLANYTGHGSETAWGT 21
Db      426 FNGGISLANYTGHGSETAWGT 446

RESULT 4
Q7MTE2_PORGI
ID      Q7MTE2_PORGI      PRELIMINARY;      PRT;      1706 AA.
AC      Q7MTE2;
DT      15-DEC-2003, integrated into UniProtKB/TrEMBL.

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15-DEC-2003, sequence version 1.
 DT 07-FEB-2006, entry version 12.
 DE Hemagglutinin protein HAgE.
 OS Porphyromonas gingivalis (Bacteroides gingivalis).
 OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
 OC Porphyromonadaceae; Porphyromonas.
 NCBI_TaxID=837;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=W83;
 RX MEDLINE=22829867; PubMed=12949112;
 DOI=10.1128/JB.185.18.5591-5601.2003;
 RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
 RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
 RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
 RA Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
 RA Dewhirst F.E., Fraser C.M.;
 RT "Complete genome sequence of the oral pathogenic bacterium
 RT Porphyromonas gingivalis strain W83.";
 RJ J. Bacteriol. 185:5591-5601(2003).
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 CC
 CC EMBL: AR015924; AAO66991.1; -; Genomic_DNA.
 DR HSSP: P95493; 1CVR.
 DR SMR: Q7MTE2; 228-655.
 DR TIGR: PG2024;
 DR Biocyc: PGIN242619:PG2024-MONOMER;
 DR GO: GO:0008234; P:cysteine-type peptidase activity; IEA.
 DR GO: GO:0009405; P:pathogenesis; IEA.
 DR GO: GO:0006508; P:proteolysis; IEA.
 DR InterPro: IPR011628; Cleaved adhesin.
 DR InterPro: IPR000977; DNA_ligase.
 DR InterPro: IPR001769; Peptidase_C25.
 DR InterPro: IPR005536; Peptidase_C25_C.
 DR InterPro: IPR012600; Propeptide_C25.
 DR Pfam: PF07675; Cleaved Adhesin_2.
 DR Pfam: PF01364; Peptidase_C25_1.
 DR Pfam: PF03785; Peptidase_C25_C; 1.
 DR Pfam: PF08126; Propeptide_C25; 1.
 DR PROSITE: PS00697; DNA_LIGASE_A1; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 1706 AA; 185673 MW; 6FE9B83AA98A2815 CRC64;
 Query Match 100.0%; Score 118; DB 2; Length 1706;
 Best Local Similarity 100.0%; Pred. No. 6.9e-09;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FNGGISLVNYTGHGSETAWGT 21
 DB 426 FNGGISLVNYTGHGSETAWGT 446
 RESULT 5
 Q51844_PORGI PRELIMINARY; PRT; 736 AA.
 AC Q51844;
 DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
 DT 01-NOV-1996, sequence version 1.
 DT 07-FEB-2006, entry version 25.
 DE Arginine-specific cysteine proteinase (Arg-gingipain).
 OS Porphyromonas gingivalis (Bacteroides gingivalis).
 OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
 OC Porphyromonadaceae; Porphyromonas.
 NCBI_TaxID=837;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC33277;
 RX MEDLINE=96007508; PubMed=7559528; DOI=10.1074/jbc.270.40.23619;
 RA Nakayama K., Kadowaki T., Okamoto K., Yamamoto K.;
 RT "Construction and characterization of arginine-specific cysteine
 RT proteinase (Arg-gingipain)-deficient mutants of Porphyromonas
 RT gingivalis. Evidence for significant contribution of Arg-gingipain to
 RT virulence.";
 RJ J. Biol. Chem. 270:23619-23626(1995).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC33277;
 RX MEDLINE=97276476; PubMed=9130229;
 RA Nakayama K.;
 RT "Domain-specific rearrangement between the two Arg-gingipain-encoding
 RT genes in Porphyromonas gingivalis: possible involvement of
 RT nonreciprocal recombination.";
 RJ Microbiol. Immunol. 41:185-196(1997).
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 CC
 CC EMBL: D64081; BAA10963.1; -; Genomic_DNA.
 DR HSSP: P95493; 1CVR.
 DR SMR: Q51844; 230-661.
 DR GO: GO:0008234; P:cysteine-type peptidase activity; IEA.
 DR GO: GO:0006508; P:proteolysis; IEA.
 DR InterPro: IPR001769; Peptidase_C25.
 DR InterPro: IPR005536; Peptidase_C25_C.
 DR InterPro: IPR012600; Propeptide_C25.
 DR Pfam: PF01364; Peptidase_C25; 1.
 DR Pfam: PF03785; Peptidase_C25_C; 1.
 DR Pfam: PF08126; Propeptide_C25; 1.
 DR SEQUENCE 736 AA; 81004 MW; 5BB9C40E0BB4798 CRC64;
 Query Match 96.6%; Score 114; DB 2; Length 736;
 Best Local Similarity 95.2%; Pred. No. 1.1e-08;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FNGGISLVNYTGHGSETAWGT 21
 DB 428 FNGGISLVNYTGHGSETAWGT 448
 RESULT 6
 CPGL_PORGI STANDARD; PRT; 991 AA.
 ID CPGL_PORGI
 AC P28784; Q45168;
 DT 01-DEC-1992, integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1997, sequence version 2.
 DT 07-FEB-2006, entry version 47.
 DE Gingipain R1 precursor (EC 3.4.22.37) (Gingipain 1) (Arg-gingipain)
 DE (RGP-1).
 GN Name=rgpA; Synonyms=rgp1;
 OS Porphyromonas gingivalis (Bacteroides gingivalis).
 OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
 OC Porphyromonadaceae; Porphyromonas.
 NCBI_TaxID=837;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND PROTEIN SEQUENCE OF 228-290 AND
 RP 517-541.
 RC STRAIN=381;
 RX MEDLINE=95168894; PubMed=7864651; DOI=10.1006/abbi.1995.1123;
 RA Okamoto K., Misumi Y., Kadowaki T., Yoneda M., Yamamoto K.,
 RA Ikehara Y.;
 RT "Structural characterization of argingipain, a novel arginine-specific
 RT cysteine proteinase as a major periodontal pathogenic factor from
 RT Porphyromonas gingivalis.";
 RJ Arch. Biochem. Biophys. 316:917-925(1995).
 CC -!- FUNCTION: Thiol protease which is believed to participate in

DR	GO; GO:0009405; P:pathogenesis; IEA.
DR	GO; GO:0006508; P:proteolysis; IEA.
DR	InterPro; IPR011628; Cleaved_adhesin.
DR	InterPro; IPR000977; DNA_ligase.
DR	InterPro; IPR001769; Peptidase_C25.
DR	InterPro; IPR005536; Peptidase_C25_C.
DR	InterPro; IPR012600; Propeptide_C25.
DR	Pfam; PF07675; Cleaved_Adhesin; 2.
DR	Pfam; PF01364; Peptidase_C25; 1.
DR	Pfam; PF03785; Peptidase_C25_C; 1.
DR	Pfam; PF08126; Propeptide_C25; 1.
DR	PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN_1.
KW	Protease.
SQ	SEQUENCE 1687 AA; 183703 MW; D085B516A399FE70 CR664;
	Query Match 96.6%; Score 114; DB 2; Length 1687;
	Best Local Similarity 95.2%; Pred. No. 2.9e-08;
	Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps
Qy	1 FNGGISLANYTGHGSETAWGT 21
Db	407 FNGGISLVNVTGHGSETAWGT 427
RESULT 8	
ID	Q51816 PORGI PRELIMINARY; PRT; 1704 AA.
AC	Q51816;
DT	01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT	01-NOV-1996, sequence version 1.
DT	07-FEB-2006, entry version 25.
DE	Arg-gingipain-1 proteinase.
OS	Porphyromonas gingivalis (Bacteroides gingivalis).
OC	Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC	Porphyromonadaceae; Porphyromonas.
OX	NCBI_TaxID=837;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RX	MEDLINE=95138080; PubMed=7836351; DOI=10.1074/jbc.270.3.1007;
RA	Pavloff N., Potempa J., Pike R.N., Prochazka V., Kiefer M.C.,
RA	Travis J., Barr P.J.;
RT	"Molecular cloning and structural characterization of the Arg-
RT	gingipain proteinase of Porphyromonas gingivalis. Biosynthesis as a
RT	proteinase-adhesin polypeptide.";
RL	J. Biol. Chem. 270:1007-1010(1995).
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ENBL; U15282; AAA69539.1; -; Genomic_DNA.	
PIR; A55426; A55426.	
HSP; P95493; ICVR.	
SWR; Q51816; 228-635.	
GO; GO:0008234; F:cysteine-type peptidase activity; IEA.	
GO; GO:0009405; P:pathogenesis; IEA.	
GO; GO:0006508; P:proteolysis; IEA.	
InterPro; IPR011628; Cleaved_adhesin.	
InterPro; IPR000977; DNA_ligase.	
InterPro; IPR001769; Peptidase_C25.	
InterPro; IPR005536; Peptidase_C25_C.	
InterPro; IPR012600; Propeptide_C25.	
Pfam; PF07675; Cleaved_Adhesin; 2.	
Pfam; PF01364; Peptidase_C25; 1.	
Pfam; PF03785; Peptidase_C25_C; 1.	
Pfam; PF08126; Propeptide_C25; 1.	
PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN_1.	
CHAIN 228 719	mature 50-kDa cysteine proteinase
FT	gingipain.
FT	SEQUENCE 1704 AA; 185437 MW; 6A34B40131C2A676 CR664;
	Query Match 96.6%; Score 114; DB 2; Length 1704;
	Best Local Similarity 95.2%; Pred. No. 2.9e-08;
	Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps

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QY      1  FNGGISLANYTGHGSETAWGT 21
DB      426  FNGGISLVNYTGHGSETAWGT 446

RESULT 9
Q51818 PORGI
ID  Q51818_PORGI  PRELIMINARY;  PRT;  422 AA.
AC  Q51818
DT  01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT  01-NOV-1996, sequence version 1.
DT  07-FEB-2006, entry version 21.
DE  Cysteine proteinase alpha-gingipain.
GN  Name:cpgr;
OS  Porphyromonas gingivalis (Bacteroides gingivalis).
OC  Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC  Porphyromonadaceae; Porphyromonas.
OX  NCBI_TaxID=837;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=ATCC 33277;
RA  Garbia S.E., Shah H.N.;
RT  "Molecular analysis of surface-associated enzymes of Porphyromonas
RT  gingivalis.";
RL  Clin. Infect. Dis. 0:0-0(0).
[2]
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=ATCC 33277;
RA  Garbia S.E.;
RT  Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
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CC  -----
DR  EMBL; X85186; CAA59469.1; -; Genomic_DNA.
DR  HSSP; P95493; 1CVR.
DR  SMR; Q51818; 5-422.
DR  GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR  GO; GO:0006508; P:proteolysis; IEA.
DR  InterPro; IPR001769; Peptidase_C25.
DR  InterPro; IPR005536; Peptidase_C25_C.
DR  Pfam; PF01364; Peptidase_C25; 1.
DR  Pfam; PF03785; Peptidase_C25_C; 1.
SQ  SEQUENCE 422 AA; 46280 MW; 773F18E28B4D4761 CRC64;

Query Match      85.2%; Score 100.5; DB 2; Length 422;
Best Local Similarity 86.4%; Pred. No. 7.9e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY      1  FNGGISLANYT-GHGSETAWGT 21
DB      202  FNGGISLVNYTAGHGSdTAWGT 223

RESULT 10
Q604T4 PORGI
ID  Q604T4_PORGI  PRELIMINARY;  PRT;  1358 AA.
AC  Q604T4;
DT  05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT  05-JUL-2004, sequence version 1.
DT  07-FEB-2006, entry version 9.
DE  Lys-gingipain (Fragment).
GN  Name:kgp;
OS  Porphyromonas gingivalis (Bacteroides gingivalis).
OC  Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC  Porphyromonadaceae; Porphyromonas.
OX  NCBI_TaxID=837;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=W83variant;
RX  PubMed=15297553; DOI=10.1128/JCM.42.8.3873-3876.2004;
RA  Nadkarni M.A., Nguyen K.A., Chapple C.C., DeCarlo A.A., Jacques N.A.,

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RA  Hunter N.;
RT  "Distribution of Porphyromonas gingivalis Biotypes Defined by Alleles
RT  of the kgp (lys-gingipain) Gene.";
RL  J. Clin. Microbiol. 42:3873-3876(2004).
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CC  -----
DR  EMBL; AY59244; AAS68176.1; -; Genomic_DNA.
DR  GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR  GO; GO:0009405; P:pathogenesis; IEA.
DR  GO; GO:0006508; P:proteolysis; IEA.
DR  InterPro; IPR011628; Cleaved_adhesin.
DR  InterPro; IPR001769; Peptidase_C25.
DR  InterPro; IPR005536; Peptidase_C25_C.
DR  Pfam; PF07675; Cleaved Adhesin; 3.
DR  Pfam; PF01364; Peptidase_C25; 1.
DR  Pfam; PF03785; Peptidase_C25_C; 1.
FT  NON_TER 1
FT  NON_TER 1358
SQ  SEQUENCE 1358 AA; 146666 MW; 4B6A5D52729BFECB CRC64;

Query Match      69.5%; Score 82; DB 2; Length 1358;
Best Local Similarity 77.8%; Pred. No. 0.0023;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2  NGGISLANYTGHGSETAW 19
DB      80  NTGVSFANYTAGSETAW 97

RESULT 11
O07442 PORGI
ID  O07442_PORGI  PRELIMINARY;  PRT;  1732 AA.
AC  O07442;
DT  01-JUL-1997, integrated into UniProtKB/TrEMBL.
DT  01-JUL-1997, sequence version 1.
DT  07-FEB-2006, entry version 27.
DE  Lysine-specific cysteine proteinase.
GN  Name:prtk;
OS  Porphyromonas gingivalis (Bacteroides gingivalis).
OC  Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC  Porphyromonadaceae; Porphyromonas.
OX  NCBI_TaxID=837;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=W50;
RX  MEDLINE=99235907; PubMed=10219167;
RX  DOI=10.1034/j.1399-302X.1999.140203.x;
RA  Slakeski N., Cleal S.M., Bhogal P.S., Reynolds E.C.;
RT  "Characterization of a Porphyromonas gingivalis gene prtk that encodes
RT  a lysine-specific cysteine proteinase and three sequence-related
RT  adhesins.";
RL  Oral Microbiol. Immunol. 14:92-97(1999).
CC  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC  Distributed under the Creative Commons Attribution-NoDerivs License
CC  -----
DR  EMBL; U75366; AAB60809.1; -; Genomic_DNA.
DR  MEROPS; C25.002; -.
DR  GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR  GO; GO:0009405; P:pathogenesis; IEA.
DR  GO; GO:0006508; P:proteolysis; IEA.
DR  InterPro; IPR011628; Cleaved_adhesin.
DR  InterPro; IPR000977; DNA_ligase.
DR  InterPro; IPR001769; Peptidase_C25.
DR  InterPro; IPR005536; Peptidase_C25_C.
DR  Pfam; PF07675; Cleaved Adhesin; 3.
DR  Pfam; PF01364; Peptidase_C25; 1.
DR  Pfam; PF03785; Peptidase_C25_C; 1.
DR  PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN 1.
SQ  SEQUENCE 1732 AA; 187915 MW; 45D5B9137791703 CRC64;

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Query Match          69.5%; Score 82; DB 2; Length 1732;
Best Local Similarity 77.8%; Pred. No. 0.003;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 NGGISLANYTGHGSETAW 19
    | | | | | | | | | |
Db 433 NTGVSFANYTAHGETAW 450

RESULT 12
ID O52050_PORGI PRELIMINARY; PRT; 1732 AA.
AC O52050;
DT 01-JUN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JUN-1998, sequence version 1.
DE 07-FEB-2006, entry version 25.
DE Lysine specific cysteine protease.
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroidetes (Class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=W83;
RX MEDLINE=98298016; PubMed=9632563;
RA Lewis J.P., Macrina F.L.;
RT "TS195, an insertion sequence-like element associated with protease
  genes in Porphyromonas gingivalis.";
RL Infect. Immun. 66:3035-3042(1998).
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DB EMBL; AF017059; AAC26523.1; -; Genomic_DNA.
DR MEROPS; C25.002; -.
DR GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR011628; Cleaved adhesin.
DR InterPro; IPR000977; DNA_ligase.
DR InterPro; IPR001769; Peptidase_C25.
DR Pfam; PF01364; Cleaved Adhesin; 3.
DR Pfam; PF03785; Peptidase_C25_C; 1.
DR PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN_1.
KW Protease.
SQ SEQUENCE 1732 AA; 187932 MW; B2337463D5CB5EAS CRC64;

Query Match          69.5%; Score 82; DB 2; Length 1732;
Best Local Similarity 77.8%; Pred. No. 0.003;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 NGGISLANYTGHGSETAW 19
    | | | | | | | | | |
Db 433 NTGVSFANYTAHGETAW 450

RESULT 13
ID O51817_PORGI PRELIMINARY; PRT; 1732 AA.
AC O51817;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DE 07-FEB-2006, entry version 28.
DE Porphyropain.
GN Name=prtP;
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroidetes (Class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP NUCLEOTIDE SEQUENCE.
```

```
RC STRAIN=W12;
RX MEDLINE=96213011; PubMed=8631659;
RA Barkocy-Gallagher G.A., Han N., Patti J.M., Whitlock J.,
RA Progulskie-Fox A., Lantz M.S.;
RT "Analysis of the prtP gene encoding porphypain, a cysteine proteinase
  of Porphyromonas gingivalis.";
RL J. Bacteriol. 178:2734-2741(1996).
CC -----
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CC -----
DB EMBL; U42210; AAB06565.1; -; Genomic_DNA.
DR PIR; T30836; T30836.
DR MEROPS; C25.002; -.
DR GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR011628; Cleaved adhesin.
DR InterPro; IPR000977; DNA_ligase.
DR InterPro; IPR001769; Peptidase_C25.
DR InterPro; IPR005536; Peptidase_C25_C.
DR Pfam; PF07675; Cleaved Adhesin; 3.
DR Pfam; PF01364; Peptidase_C25_C; 1.
DR Pfam; PF03785; Peptidase_C25_C; 1.
DR PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN_1.
SQ SEQUENCE 1732 AA; 187875 MW; 654271DBEF7BCAE4 CRC64;

Query Match          69.5%; Score 82; DB 2; Length 1732;
Best Local Similarity 77.8%; Pred. No. 0.003;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 NGGISLANYTGHGSETAW 19
    | | | | | | | | | |
Db 433 NTGVSFANYTAHGETAW 450

RESULT 14
ID P36967_PORGI PRELIMINARY; PRT; 1358 AA.
AC P36967;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1997, sequence version 1.
DT 07-FEB-2006, entry version 27.
DE Hemagglutinin.
GN Name=hagD;
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroidetes (Class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=381;
RA Han N., Lepine G., Whitlock J., Wojciechowski L., Progulskie-Fox A.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DB EMBL; U68468; AAB49691.1; -; Genomic_DNA.
DR MEROPS; C25.002; -.
DR GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR011628; Cleaved adhesin.
DR InterPro; IPR000977; DNA_ligase.
DR InterPro; IPR001769; Peptidase_C25.
DR InterPro; IPR005536; Peptidase_C25_C.
DR Pfam; PF07675; Cleaved Adhesin; 3.
DR Pfam; PF01364; Peptidase_C25_C; 1.
DR Pfam; PF03785; Peptidase_C25_C; 1.
DR PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN_1.
SQ SEQUENCE 1358 AA; 147102 MW; 47FCA0B25B06DED8 CRC64;
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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 25, 2006, 17:49:50 ; Search time 225.628 Seconds
(without alignments)
44.581 Million cell updates/sec

Title: US-10-387-977-2

Perfect score: 121

Sequence: 1 LNTGVSFANYAHGSETAWADP 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_8.*

1: geneseqp1990s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*
9: geneseqp2005s.*
10: geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	121	100.0	22	2	AAW83071	Peptide f
2	121	100.0	506	2	AAW83126	AAW83126 PtlIIR48
3	121	100.0	1731	9	ADZ10439	Adz10439 P. gingiv
4	121	100.0	1731	9	ADZ10409	Adz10409 P. gingiv
5	121	100.0	1731	9	ADZ10393	Adz10393 P. gingiv
6	121	100.0	1731	9	ADZ10428	Adz10428 P. gingiv
7	121	100.0	1732	2	AAR96029	Aar96029 P. gingiv
8	121	100.0	1732	2	AAW24787	AAW24787 PtlR anti
9	121	100.0	1732	2	AAW69487	AAW69487 Haemagglu
10	114	94.2	509	9	ADV16839	Adv16839 Human cys
11	114	94.2	1358	2	AAR96032	Aar96032 P. gingiv
12	114	94.2	1358	2	AAW69494	AAW69494 Haemagglu
13	114	94.2	1723	9	ADV16837	Adv16837 Human cys
14	110	90.9	509	2	AAW34847	AAW34847 Lys-gingi
15	110	90.9	970	2	AAR72458	Aar72458 Porphyrom
16	82	67.8	21	2	AAW83070	AAW83070 Peptide f
17	82	67.8	493	2	AAW83125	AAW83125 PtlIIR50
18	82	67.8	507	2	AAW83124	AAW83124 PtlIIR45
19	82	67.8	1706	2	AAW24786	AAW24786 PtlR anti
20	82	67.8	1706	9	ADZ10438	Adz10438 P. gingiv
21	82	67.8	1706	9	ADZ10403	Adz10403 P. gingiv
22	82	67.8	1706	9	ADZ10427	Adz10427 P. gingiv
23	82	67.8	1706	9	ADZ10456	Adz10456 P. gingiv

ALIGNMENTS

RESULT 1

AAW83071 ID AAW83071 standard; peptide; 22 AA.

XX AC AAW83071;

XX XX 03-MAR-1999 (first entry)

XX DE Peptide from the 300kDa complex of cysteine proteinases and adhesins.

XX KW 300 kD multiprotein complex; cysteine proteinase; adhesin;
KW virulence factor; immune response; P. gingivalis infection;
KW periodontal disease; passive immunisation; subgingival plaque.

XX OS Synthetic.

XX OS Porphyromonas gingivalis.

XX XX WO9849192-A1.

XX PN 05-NOV-1998.

XX PD 30-APR-1998; 98WO-AU000311.

XX PF 30-APR-1997; 97AU-00006528.

XX PR (UYME) UNIV MELBOURNE.

XX PA (VICT-) VICTORIAN DAIRY IND AUTHORITY.

XX PA (CSLC-) CSL LTD.

XX PI Reynolds EC, Obrien-Simpson NM, Slakeski N;

XX XX WPI; 1999-024043/02.

XX DR Immunogenic composition containing new Porphyromonas gingivalis peptides
XX PT - and related antibodies, useful for treatment, prevention and diagnosis
XX PT of periodontal disease.
XX XX Claim 1; Page 49; 70pp; English.

XX CC Peptides AAW83070-122 are derived from the 300 kD multiprotein complex of
XX CC cysteine proteinases and adhesins. The 300kDa multiprotein complex is the
XX CC major virulence factor of Porphyromonas gingivalis. The specification
XX CC describes a composition for raising an immune response against P.
XX CC gingivalis which contains at least one of the present peptides. The
XX CC products are used to treat and prevent P. gingivalis infection
XX CC (periodontal disease). Antibodies are used for passive immunisation, and

CC as diagnostic reagents for P. gingivalis in subgingival plaque. The
 CC peptides are used to detect P. gingivalis specific antibodies in serum

XX
 SQ Sequence 22 AA;
 Query Match 100.0%; Score 121; DB 2; Length 22;
 Best Local Similarity 100.0%; Pred. No. 7.6e-12;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNTGVSPANTAHGSETAWADP 22
 |||||
 Db 1 LNTGVSPANTAHGSETAWADP 22
 |||||

RESULT 2

AAW83126

ID AAW83126 standard; protein; 506 AA.

XX AAW83126;

XX 03-MAR-1999 (first entry)

XX PrtIIK48 Lysine specific proteinase fragment.

XX 300 kD multiprotein complex; cysteine proteinase; adhesin;
 KW virulence factor; immune response; P. gingivalis infection;
 KW periodontal disease; passive immunisation; subgingival plaque.

XX Porphyromonas gingivalis.

XX WO9849192-A1.

XX 05-NOV-1998.

XX 30-APR-1998; 98WO-AU000311.

XX 30-APR-1997; 97AU-00006528.

XX (UTME) UNIV MELBOURNE.

PA (VICT-) VICTORIAN DAIRY IND AUTHORITY.

PA (CSLC-) CSL LTD.

XX Reynolds EC, O'Brien-Simpson NM, Slakeski N;

XX WPI; 1999-024043/02.

XX Immunogenic composition containing new Porphyromonas gingivalis peptides
 PT - and related antibodies, useful for treatment, prevention and diagnosis
 PT of periodontal disease.

XX Example 1; Fig 8; 70pp; English.

XX The present sequence represents a fragment of the PrtIIK48 lysine
 CC specific proteinase of Porphyromonas gingivalis. The specification
 CC describes peptides derived from the 300 kD multiprotein complex of
 CC cysteine proteinases and adhesins. The 300kDa multiprotein complex is the
 CC major virulence factor of P. gingivalis. The specification describes a
 CC composition for raising an immune response against P. gingivalis which
 CC contains at least one of the present peptides. The products are used to
 CC treat and prevent P. gingivalis infection (periodontal disease).

CC Antibodies are used for passive immunisation, and as diagnostic reagents
 CC for P. gingivalis in subgingival plaque. The peptides are used to detect
 CC P. gingivalis specific antibodies in serum

XX Sequence 506 AA;

Query Match 100.0%; Score 121; DB 2; Length 506;

Best Local Similarity 100.0%; Pred. No. 3.4e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTGVSPANTAHGSETAWADP 22

|||||

Db 204 LNTGVSPANTAHGSETAWADP 225

RESULT 3

ADZ10439

ID ADZ10439 standard; protein; 1731 AA.

XX ADZ10439;

XX 16-JUN-2005 (first entry)

XX P. gingivalis lysine-specific cysteine protease SEQ ID 222.

XX Vaccine; enzyme; therapy; diagnosis; periodontal disease;
 KW antiinflammatory; mouth disease; gingivitis; inflammation; mouth disease;
 KW endocarditis; cardiac; cardiovascular disease; inflammation;
 KW bacterial urinary tract infection; antibacterial; uropathic;
 KW genitourinary disease; infection; osteomyelitis; osteopathic;
 KW musculoskeletal disease; antigen.

XX Porphyromonas gingivalis.

XX WO2005019249-A2.

XX 03-MAR-2005.

XX 10-AUG-2004; 2004WO-US025778.

XX 15-AUG-2003; 2003US-0495589P.

XX (UYFL) UNIV FLORIDA.

XX Progulskes-Fox A, Hillman JD, Handfield M;

XX WPI; 2005-214225/22.

XX N-PSDB; ADZ10270.

XX New isolated immunogenic polypeptide, useful for diagnosing, treating,
 PT preventing, or ameliorating diseases and infections caused by
 PT Porphyromonas gingivalis e.g. localized prepubertal periodontitis.

XX Claim 1; SEQ ID NO 222; 73pp; English.

XX The invention relates to an isolated immunogenic Porphyromonas gingivalis
 CC polypeptide (I) comprising (a) a polypeptide at least about 5 contiguous
 CC amino acids of an amino acid sequence appearing as ADZ10384 - ADZ10443,
 CC ADZ10445 - ADZ10478 or ADZ10480-ADZ10571 (b) the polypeptide of (a) and
 CC a heterologous polypeptide or (c) an amino acid sequence selected from
 CC ADZ10384 - ADZ10443, ADZ10445 - ADZ10478 or ADZ10480-ADZ10571. Also
 CC included are an isolated polynucleotide (comprising a sequence that
 CC encodes (I) (a), (b) or (c)), an expression control sequence operably
 CC linked to the polynucleotide above (or the polynucleotide above and a
 CC heterologous polynucleotide), an expression vector comprising the
 CC polynucleotide, a host cell comprising the expression vector, an antibody
 CC (antibody fragment, or single-chain antibody) that specifically binds to
 CC the polypeptide, a composition comprising the antibody (antibody
 CC fragment, or single-chain antibody) and a pharmaceutical carrier,
 CC treating or preventing a disease/infection caused by Porphyromonas
 CC gingivalis, a composition comprising the isolated immunogenic polypeptide
 CC (or the polynucleotide) and a pharmaceutical carrier, eliciting an immune
 CC response in an animal, detecting the presence of a first P. gingivalis
 CC polynucleotide in a test sample, detecting the presence of P.
 CC gingivalis antibody in a test sample, detecting the presence of P.
 CC gingivalis (or a P. gingivalis polypeptide) in a test sample, detecting
 CC P. gingivalis infection in a subject and detecting P. gingivalis in a
 CC subject. The immunogenic polypeptide is useful for the diagnosis, caused
 CC treatment, prevention, and amelioration of diseases and infections caused
 CC by P. gingivalis. It is useful for treating or preventing localized
 CC prepubertal periodontitis, generalized prepubertal periodontitis,
 CC localized juvenile periodontitis, generalized juvenile periodontitis,
 CC rapidly progressive adult periodontitis, refractory adult periodontitis,
 CC endocarditis, thyroid gland abscess, urinary tract infection, brain
 CC abscess, or vertebral osteomyelitis. The present sequence is a P.
 CC gingivalis immunogenic protein of the invention.


```

XX
SQ      Sequence 1731 AA;
Query Match      100.0%; Score 121; DB 9; Length 1731;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNTGVSFANYTAHGETAWADP 22
      |||||
Db      432 LNTGVSFANYTAHGETAWADP 453

RESULT 4
ADZ10409
ID      ADZ10409 standard; protein; 1731 AA.
XX
AC      ADZ10409;
XX
DT      16-JUN-2005 (first entry)
XX
DE      P. gingivalis lysine-specific cysteine proteinase SEQ ID 192.
XX
KW      Vaccine; enzyme; therapy; diagnosis; periodontal disease;
KW      antiinflammatory; mouth disease; gingivitis; inflammation; mouth disease;
KW      endocarditis; cardiant; cardiovascular disease; inflammation;
KW      bacterial urinary tract infection; antibacterial; uropathic;
KW      genitourinary disease; infection; osteomyelitis; osteopathic;
KW      musculoskeletal disease; antigen.
XX
OS      Porphyromonas gingivalis.
XX
PN      WO2005019249-A2.
XX
PD      03-MAR-2005.
XX
PF      10-AUG-2004; 2004WO-US025778.
XX
PR      15-AUG-2003; 2003US-0495589P.
XX      (UYFL ) UNIV FLORIDA.
XX
PI      Progulske-Fox A, Hillman JD, Handfield M;
XX
DR      WPI; 2005-214225/22.
XX      N-PSDB; ADZ10240.
XX
PT      New isolated immunogenic polypeptide, useful for diagnosing, treating,
PT      preventing, or ameliorating diseases and infections caused by
PT      Porphyromonas gingivalis e.g. localized prepubertal periodontitis.
XX
PS      Claim 1; SEQ ID NO 192; 73pp; English.
XX
CC      The invention relates to an isolated immunogenic Porphyromonas gingivalis
CC      polypeptide (I) comprising (a) a polypeptide at least about 5 contiguous
CC      amino acids of an amino acid sequence appearing as ADZ10384 - ADZ10443,
CC      ADZ10445 - ADZ10478 or ADZ10480-ADZ10571, (b) the polypeptide of (a) and
CC      a heterologous polypeptide or (c) an amino acid sequence selected from
CC      ADZ10384 - ADZ10443, ADZ10445 - ADZ10478 or ADZ10480-ADZ10571. Also
CC      included are an isolated polynucleotide (comprising a sequence that
CC      encodes (I) (a), (b) or (c)), an expression control sequence operably
CC      linked to the polynucleotide above (or the polynucleotide above and a
CC      heterologous polynucleotide), an expression vector comprising the
CC      polynucleotide, a host cell comprising the expression vector, an antibody
CC      (antibody fragment, or single-chain antibody) that specifically binds to
CC      the polypeptide, a composition comprising the antibody (antibody
CC      fragment, or single-chain antibody) and a pharmaceutical carrier,
CC      treating or preventing a disease/infection caused by Porphyromonas
CC      gingivalis, a composition comprising the isolated immunogenic polypeptide
CC      (or the polynucleotide) and a pharmaceutical carrier, eliciting an immune
CC      response in an animal, detecting the presence of a first P. gingivalis
CC      polynucleotide in a test sample, detecting the presence of a P.
CC      gingivalis antibody in a test sample, detecting the presence of P.
CC      gingivalis (or a P. gingivalis polypeptide) in a test sample, detecting

```

```

CC      P. gingivalis infection in a subject and detecting P. gingivalis in a
CC      subject. The immunogenic polypeptide is useful for the diagnosis,
CC      treatment, prevention, and amelioration of diseases and infections caused
CC      by P. gingivalis . It is useful for treating or preventing localized
CC      prepubertal periodontitis, generalized prepubertal periodontitis,
CC      localized juvenile periodontitis, generalized juvenile periodontitis,
CC      rapidly progressive adult periodontitis, refractory adult periodontitis,
CC      endocarditis, thyroid gland abscess, urinary tract infection, brain
CC      abscess, or vertebral osteomyelitis. The present sequence is a P.
CC      gingivalis immunogenic protein of the invention.
XX
SQ      Sequence 1731 AA;
Query Match      100.0%; Score 121; DB 9; Length 1731;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNTGVSFANYTAHGETAWADP 22
      |||||
Db      432 LNTGVSFANYTAHGETAWADP 453

RESULT 5
ADZ10393
ID      ADZ10393 standard; protein; 1731 AA.
XX
AC      ADZ10393;
XX
DT      16-JUN-2005 (first entry)
XX
DE      P. gingivalis lysine-specific cysteine proteinase SEQ ID 176.
XX
KW      Vaccine; enzyme; therapy; diagnosis; periodontal disease;
KW      antiinflammatory; mouth disease; gingivitis; inflammation; mouth disease;
KW      endocarditis; cardiant; cardiovascular disease; inflammation;
KW      bacterial urinary tract infection; antibacterial; uropathic;
KW      genitourinary disease; infection; osteomyelitis; osteopathic;
KW      musculoskeletal disease; antigen.
XX
OS      Porphyromonas gingivalis.
XX
PN      WO2005019249-A2.
XX
PD      03-MAR-2005.
XX
PF      10-AUG-2004; 2004WO-US025778.
XX
PR      15-AUG-2003; 2003US-0495589P.
XX      (UYFL ) UNIV FLORIDA.
XX
PI      Progulske-Fox A, Hillman JD, Handfield M;
XX
DR      WPI; 2005-214225/22.
XX      N-PSDB; ADZ10228.
XX
PT      New isolated immunogenic polypeptide, useful for diagnosing, treating,
PT      preventing, or ameliorating diseases and infections caused by
PT      Porphyromonas gingivalis e.g. localized prepubertal periodontitis.
XX
PS      Claim 1; SEQ ID NO 176; 73pp; English.
XX
CC      The invention relates to an isolated immunogenic Porphyromonas gingivalis
CC      polypeptide (I) comprising (a) a polypeptide at least about 5 contiguous
CC      amino acids of an amino acid sequence appearing as ADZ10384 - ADZ10443,
CC      ADZ10445 - ADZ10478 or ADZ10480-ADZ10571, (b) the polypeptide of (a) and
CC      a heterologous polypeptide or (c) an amino acid sequence selected from
CC      ADZ10384 - ADZ10443, ADZ10445 - ADZ10478 or ADZ10480-ADZ10571. Also
CC      included are an isolated polynucleotide (comprising a sequence that
CC      encodes (I) (a), (b) or (c)), an expression control sequence operably
CC      linked to the polynucleotide above (or the polynucleotide above and a
CC      heterologous polynucleotide), an expression vector comprising the
CC      polynucleotide, a host cell comprising the expression vector, an antibody

```

CC (antibody fragment, or single-chain antibody) that specifically binds to
 CC the polypeptide, a composition comprising the antibody (antibody
 CC fragment, or single-chain antibody) and a pharmaceutical carrier,
 CC treating or preventing a disease/infection caused by Porphyromonas
 CC gingivalis, a composition comprising the isolated immunogenic polypeptide
 CC (or the polynucleotide) and a pharmaceutical carrier, eliciting an immune
 CC response in an animal, detecting the presence of a first P. gingivalis
 CC polynucleotide in a test sample, detecting the presence of a P.
 CC gingivalis antibody in a test sample, detecting the presence of P.
 CC gingivalis (or a P. gingivalis polypeptide) in a test sample, detecting
 CC P. gingivalis infection in a subject and detecting P. gingivalis in a
 CC subject. The immunogenic polypeptide is useful for the diagnosis,
 CC treatment, prevention, and amelioration of diseases and infections caused
 CC by P. gingivalis. It is useful for treating or preventing localized
 CC prepubertal periodontitis, generalized prepubertal periodontitis,
 CC localized juvenile periodontitis, generalized juvenile periodontitis,
 CC rapidly progressive adult periodontitis, refractory adult periodontitis,
 CC endocarditis, thyroid gland abscess, urinary tract infection, brain
 CC abscess, or vertebral osteomyelitis. The present sequence is a P.
 CC gingivalis immunogenic protein of the invention.

XX SQ Sequence 1731 AA;

Query Match 100.0%; Score 121; DB 9; Length 1731;
 Best Local Similarity 100.0%; Pred. No. 1.5e-09;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTGVSFANYTAHGETAWADP 22
 |||||
 Db 432 LNTGVSFANYTAHGETAWADP 453

RESULT 6

ID ADZ10428 standard; protein; 1731 AA.

XX AC ADZ10428;

DT 16-JUN-2005 (first entry)

DE P. gingivalis lysine-specific cysteine protease SEQ ID 211.

XX Vaccine; enzyme; therapy; diagnosis; periodontal disease;
 KW antiinflammatory; mouth disease; gingivitis; inflammation; mouth disease;
 KW endocarditis; cardiac; cardiovascular disease; inflammation;
 KW bacterial urinary tract infection; antibacterial; uropathic;
 KW genitourinary disease; infection; osteomyelitis; osteopathic;
 KW musculoskeletal disease; antigen.

XX OS Porphyromonas gingivalis.

XX PN WO2005019249-A2.

XX PD 03-MAR-2005.

XX PF 10-AUG-2004; 2004WO-US025778.

XX PR 15-AUG-2003; 2003US-0495589P.

XX PA (UYFL) UNIV FLORIDA.

XX PI Progulske-Fox A, Hillman JD, Handfield M;

XX DR WPI: 2005-214225/22.

XX DR N-PSDB; ADZ10256.

XX New isolated immunogenic polypeptide, useful for diagnosing, treating,
 PT preventing, or ameliorating diseases and infections caused by
 PT Porphyromonas gingivalis e.g. localized prepubertal periodontitis.

XX PS Claim 1; SEQ ID NO 211; 73pp; English.

XX The invention relates to an isolated immunogenic Porphyromonas gingivalis

CC polypeptide (I) comprising (a) a polypeptide at least about 5 contiguous
 CC amino acids of an amino acid sequence appearing as ADZ10384 - ADZ10443,
 CC ADZ10445 - ADZ10478 or ADZ10480-ADZ10571, (b) the polypeptide of (a) and
 CC a heterologous polypeptide or (c) an amino acid sequence selected from
 CC ADZ10384 - ADZ10443, ADZ10445 - ADZ10478 or ADZ10480-ADZ10571. Also
 CC included are an isolated polynucleotide (comprising a sequence operably
 CC encoded (i) (a), (b) or (c)), an expression control sequence above and a
 CC heterologous polynucleotide), an expression vector comprising the
 CC polynucleotide, a host cell comprising the expression vector, an antibody
 CC (antibody fragment, or single-chain antibody) that specifically binds to
 CC the polypeptide, a composition comprising the antibody (antibody
 CC fragment, or single-chain antibody) and a pharmaceutical carrier,
 CC treating or preventing a disease/infection caused by Porphyromonas
 CC gingivalis, a composition comprising the isolated immunogenic polypeptide
 CC (or the polynucleotide) and a pharmaceutical carrier, eliciting an immune
 CC response in an animal, detecting the presence of a first P. gingivalis
 CC polynucleotide in a test sample, detecting the presence of a P.
 CC gingivalis antibody in a test sample, detecting the presence of P.
 CC gingivalis (or a P. gingivalis polypeptide) in a test sample, detecting
 CC P. gingivalis infection in a subject and detecting P. gingivalis in a
 CC subject. The immunogenic polypeptide is useful for the diagnosis,
 CC treatment, prevention, and amelioration of diseases and infections caused
 CC by P. gingivalis. It is useful for treating or preventing localized
 CC prepubertal periodontitis, generalized prepubertal periodontitis,
 CC localized juvenile periodontitis, generalized juvenile periodontitis,
 CC rapidly progressive adult periodontitis, refractory adult periodontitis,
 CC endocarditis, thyroid gland abscess, urinary tract infection, brain
 CC abscess, or vertebral osteomyelitis. The present sequence is a P.
 CC gingivalis immunogenic protein of the invention.

XX SQ Sequence 1731 AA;

Query Match 100.0%; Score 121; DB 9; Length 1731;
 Best Local Similarity 100.0%; Pred. No. 1.5e-09;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTGVSFANYTAHGETAWADP 22
 |||||
 Db 432 LNTGVSFANYTAHGETAWADP 453

RESULT 7

AAR96029

ID AAR96029 standard; protein; 1732 AA.

XX AC AAR96029;

XX 16-OCT-2003 (revised)

DT 04-SEP-1996 (first entry)

XX P. gingivalis porphyain.

XX Porphyain; haemagglutinin; periodontal disease; vaccine; antibody.

XX OS Porphyromonas gingivalis; strain W12.

XX Key Location/Qualifiers

FT Region 688..708
 FT /note= "Pro-Asn repeat region type 1"
 FT Region 887..952
 FT /note= "Pro-Asn repeat region type 2"
 FT Region 946..967
 FT /note= "Pro-Asn repeat region type 1"
 FT Region 985..1006
 FT /note= "Pro-Asn repeat region type 3"
 FT Region 1041..1100
 FT /note= "Pro-Asn repeat region type 4"
 FT Region 1341..1405
 FT /note= "Pro-Asn repeat region type 2"
 FT Region 1430..1451
 FT /note= "Pro-Asn repeat region type 3"
 FT Region 1488..1547


```

OS Porphyromonas gingivalis.
XX US5824791-A.
XX 20-OCT-1998.
XX 11-DEC-1995; 95US-00570311.
XX PF 08-SEP-1988; 88US-00241640.
XX PR 25-JAN-1991; 91US-00647119.
XX PR 09-DEC-1994; 94US-00353485.
XX (UYFL ) UNIV FLORIDA.
XX (UABR-) UAB RES FOUND.
XX Patti JM, Han N, Lantz M, Tumwasorn S, Progulske-Fox A, Lepine G;
XX WPI; 1998-582627/49.
XX DR N-PSDB; AAV58874.
XX Isolated Porphyromonas gingivalis genes - encoding haemagglutinin and/or
XX protease poly:peptide(s)).
XX Claim 1; Col 69-84; 101pp; English.
XX This sequence is encoded by a Porphyromonas gingivalis gene of the
XX invention. This sequence represents the prtP haemagglutinin protein. The
XX polypeptides are used to produce antibodies to organisms associated with
XX periodontal disease. The antibodies are also used in purification and
XX identification procedures. The genes and polypeptides are used as
XX vaccines against periodontal disease
XX SQ Sequence 1732 AA;

Query Match 100.0%; Score 121; DB 2; Length 1732;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNTGVSFANYTAHGSETAWADP 22
| | | | | | | | | | | | | | | | | |
Db 432 LNTGVSFANYTAHGSETAWADP 453

RESULT 10
ADV16839
ID ADV16839 standard; protein; 509 AA.
XX AC ADV16839;
XX DT 24-FEB-2005 (first entry)
XX DE Human cysteine protease related protein, SEQ ID 4.
XX KW selectable marker; periodontal disease; angina; antiangiinal;
XX KW cardiovascular disease; diabetes; antidiabetic; cysteine protease;
XX KW enzyme.
XX OS Homo sapiens.
XX PN WO2004106541-A1.
XX PD 09-DEC-2004.
XX PF 31-MAY-2004; 2004WO-JP007867.
XX PR 30-MAY-2003; 2003JP-00154070.
XX (KYUS-) KYUSHU TLO CO LTD.
XX Yamamoto K;
XX WPI; 2005-021305/02.
XX

PT Novel periodontal disease marker for detecting periodontal disease,
PT comprising cysteine protease derived from Porphyromonas gingivalis,
PT useful for detecting periodontal disease, in saliva.
XX Claim 5; SEQ ID NO 4; 44pp; Japanese.
XX The invention relates to a novel periodontal disease marker for detecting
XX periodontal disease. The marker comprises a cysteine protease derived
XX from a Porphyromonas gingivalis microbe. The invention further comprises:
XX a periodontal disease ward appearance kit, comprising a sampling tool,
XX periodontal disease marker, synthetic substrate, buffer, and a reducing
XX agent. The periodontal disease marker is useful for detecting and
XX diagnosing periodontal disease from saliva. The periodontal disease
XX marker provides reliable and convenient detection of periodontal disease,
XX and provides simultaneous detection of angina and diabetes. This sequence
XX represents a human cysteine protease related protein of the invention.
XX SQ Sequence 509 AA;

Query Match 94.2%; Score 114; DB 9; Length 509;
Best Local Similarity 90.9%; Pred. No. 4.4e-09;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LNTGVSFANYTAHGSETAWADP 22
| | | | | | | | | | | | | | | | | |
Db 204 LNTGVGFANYTAHGSETSWADP 225

RESULT 11
AAR96032
ID AAR96032 standard; protein; 1358 AA.
XX AC AAR96032;
XX DT 16-OCT-2003 (revised)
XX DT 04-SEP-1996 (first entry)
XX DE P. gingivalis hagD haemagglutinin.
XX KW Haemagglutinin; hagD; periodontal disease; vaccine; antibody.
XX OS Porphyromonas gingivalis; strain FDC381.
XX PN WO9617936-A2.
XX PD 13-JUN-1996.
XX PF 11-DEC-1995; 95WO-US016108.
XX PR 09-DEC-1994; 94US-00353485.
XX (UYFL ) UNIV FLORIDA.
XX (UABR-) UAB RES FOUND.
XX Progulske-Fox A, Tumwasorn S, Lepine G, Han N, Lantz M, Patti JM;
XX WPI; 1996-287181/29.
XX DR N-PSDB; AAT30655.
XX Porphyromonas gingivalis genes and proteins - used in the detection and
XX vaccination against periodontal disease.
XX Claim 5; Page 125-129; 153pp; English.
XX P. gingivalis 381 haemagglutinin hagD (AAR96032) was identified as the
XX product of the second open reading frame of the hagD gene (AAR30655)
XX derived from P. gingivalis 318 genomic DNA. A first open reading frame
XX coded for hagD protease (see also AAR96031). The protease and
XX haemagglutinin can be obtd. from transformed host cells and used in
XX vaccines to protect humans or animals against periodontal disease.
XX Expression in Salmonella cells allows prodn. of live vaccines. The
XX haemagglutinin and protease can also be used to detect the presence of
XX anti-P. gingivalis antibodies and to raise monoclonal antibodies for

```

CC diagnostic appln. (Updated on 16-OCT-2003 to standardise OS field)

XX SQ Sequence 1358 AA;

Query Match 94.2%; Score 114; DB 2; Length 1358;
Best Local Similarity 90.9%; Pred. No. 1.4e-08;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNTGVSPFANYTAHGETAWADP 22
||||| ||||| ||||| ||||| |||||
Db 67 LNTGVGFANYTAHGETSWADP 88

RESULT 12
AAW69494
ID AAW69494 standard; protein; 1358 AA.

XX AC AAW69494;

XX DT 22-DEC-1998 (first entry)

XX DE Haemagglutinin protein hagD.

XX KW Haemagglutinin protein; periodontal disease; vaccine; hagD.

XX OS Porphyromonas gingivalis.

XX PN US824791-A.

XX PD 20-OCT-1998.

XX PF 11-DEC-1995; 95US-00570311.

XX PR 08-SEP-1988; 88US-00241640.

XX PR 25-JAN-1991; 91US-00647119.

XX PR 09-DEC-1994; 94US-00353485.

XX PA (UYFL) UNIV FLORIDA.

XX PA (UABR-) UAB RES FOUND.

XX PI Patti JM, Han N, Lantz M, Tunwasorn S, Progulske-Fox A, Lepine G;

XX DR N-PSDB; AAV58880.

XX PT Isolated Porphyromonas gingivalis genes - encoding haemagglutinin and/or

XX PS Claim 1; Col 145-158; 101pp; English.

XX CC This sequence is encoded by a Porphyromonas gingivalis gene of the
invention. This sequence represents the hagD haemagglutinin protein. The
polypeptides are used to produce antibodies to organisms associated with
periodontal disease. The antibodies are also used in purification and
identification procedures. The genes and polypeptides are used as
vaccines against periodontal disease

XX SQ Sequence 1358 AA;

Query Match 94.2%; Score 114; DB 2; Length 1358;
Best Local Similarity 90.9%; Pred. No. 1.4e-08;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNTGVSPFANYTAHGETAWADP 22
||||| ||||| ||||| ||||| |||||
Db 67 LNTGVGFANYTAHGETSWADP 88

RESULT 13

ID ADV16837 standard; protein; 1723 AA.

XX AC ADV16837;

XX DT

XX 24-FEB-2005 (first entry)

XX DE Human cysteine protease Arg-gingipain protein, rgpB.

XX KW selectable marker; periodontal disease; angina; antianginal;

XX KW cardiovascular disease; diabetes; antidiabetic; cysteine protease;

XX OS Homo sapiens.

XX PN WO2004106541-A1.

XX PD 09-DEC-2004.

XX PF 31-MAY-2004; 2004WO-JP007867.

XX PR 30-MAY-2003; 2003JP-00154070.

XX PA (KYUS-) KYUSHU TLO CO LTD.

XX PI Yamamoto K;

XX DR WPI; 2005-021305/02.

XX PT Novel periodontal disease marker for detecting periodontal disease,

XX PT comprising cysteine protease derived from Porphyromonas gingivalis,

XX PT useful for detecting periodontal disease, in saliva.

XX PS Claim 4; SEQ ID NO 2; 44pp; Japanese.

XX CC The invention relates to a novel periodontal disease marker for detecting
periodontal disease. The marker comprises a cysteine protease derived
from a Porphyromonas gingivalis microbe. The invention further comprises:
a periodontal disease ward appearance kit, comprising a sampling tool,
periodontal disease marker, synthetic substrate, buffer, and a reducing
agent. The periodontal disease marker is useful for detecting and
diagnosing periodontal disease from saliva. The periodontal disease
marker provides reliable and convenient detection of periodontal disease,
and provides simultaneous detection of angina and diabetes. This sequence
represents a cysteine protease human Arg-gingipain (rgp) protein of the
invention.

XX SQ Sequence 1723 AA;

Query Match 94.2%; Score 114; DB 9; Length 1723;
Best Local Similarity 90.9%; Pred. No. 1.9e-08;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNTGVSPFANYTAHGETAWADP 22

Db 432 LNTGVGFANYTAHGETSWADP 453

RESULT 14

AAW34847

ID AAW34847 standard; protein; 509 AA.

XX AC AAW34847;

XX DT 03-JUN-1998 (first entry)

XX DE Lys-gingipain high molecular weight prepolyprotein sequence.

XX KW Arg-specific gingipain protease; gingivalis; periodontal disease;

XX KW vaccine; infection.

XX OS Porphyromonas gingivalis.

XX PN WO9734629-A1.

XX PD 25-SEP-1997.

XX XX

PF 21-MAR-1997; 97WO-US004635.
XX
PR 22-MAR-1996; 96US-0013945P.
XX
XX (UYGE-) UNIV GEORGIA RES FOUND INC.
PA (MORE-) MOREHOUSE SCHOOL MEDICINE.
XX
XX Potempa J, Travis J, Genco C;
XX
XX WPI; 1997-479993/44.
DR N-PSDB; AAT93874.
XX
XX Porphyromonas gingivalis Arg-specific gingipain protease peptide(s) -
PT useful for protecting animals and humans from gingivalis and periodontal
PT diseases.
XX
XX Disclosure; Page 76-78; 95pp; English.
XX
XX The present sequence represents a lysine-specific protease of
CC Porphyromonas gingivalis. The following peptides, derived from Arg- and
CC Lys-specific high molecular weight proteases, offer protection against
CC infection: YTYTVRDGK IKEGLTATTE DDGVTGNHE YCWEKVTAGS VSPKVC (I);
CC YTPVEKQNG RMIVIVAKKY (II); QLPFIDFVAC VNGDFLFSMP CFAELMRAQ (III);
CC GSPNYPQPS NLTATQGGK VTLKWDAPSTK (IV); GNHEYCEVK YTAGVSPKVC KDVTV (V);
CC RMFMNYPEGR YTPVEKQNG (VI); TFAGPETYK RMFMNYPEGR (VII); YTYTVYRDG
CC TKIKEGLTAT TPEEDGVTG NMEYCVCKY TAGVSPKVC (VIII); YTYTVYRDGT KIKEGLTATTF
CC EDG (IX); RGTGKKEGL TATTFEEDGV ATGN (X); KIKEGLTATTFEEDGVATGN HEY (XI)
CC ; KWDAPNGTPN PNPN PNPN FTITLSE (XII); and YTPVEKQNG RMIVIVAKKY
CC (XIII). They are used in vaccines to protect animals, including humans,
CC from gingivitis and/or periodontal diseases
XX
XX Sequence 509 AA;
SQ

Query Match 90.9%; Score 110; DB 2; Length 509;
Best Local Similarity 86.4%; Pred. No. 1.9e-08;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Oy 1 LNTGVSPFANYTAHGETAWADP 22
Db 204 LNTGVGFANYTVHGETSWADP 225

RESULT 15
AAR72458
ID AAR72458 standard; protein; 970 AA.
XX
AC AAR72458;
XX
DT 19-DEC-1995 (first entry)
XX
XX Porphyromonas gingivalis lysine-gingipain protein complex.
DE
XX Lysine-gingipain protein complex; amidolytic; proteolytic;
KW lysine specific proteinase; modulator identification; periodontitis;
KW therapy monitoring.
XX
XX Porphyromonas gingivalis.
OS
XX Key Location/Qualifiers
FH Peptide 1..228
FT Peptide /label= sig_peptide
FT Peptide 229..970
FT /label= mat_peptide
XX
XX WO9511298-A1.
PN
XX 27-APR-1995.
PD
XX 21-OCT-1994; 94WO-US012094.
PF
XX 21-OCT-1993; 93US-00141324.
PR
XX (UYGE-) UNIV GEORGIA RES FOUND INC.
PA

XX Travis J, Potempa JS, Barr P, Pavloff N, Pike RN;
PI
XX WPI; 1995-170220/22.
DR N-PSDB; AAQ88141.
XX
XX Lys-gingipain complex prepn with amidolytic and proteolytic specificity -
PT for cleavage of an amide bond with Lysine contributing the carboxyl gp.
XX
XX Claim 2; Page 53-57; 75pp; English.
XX
XX AAQ88141 encodes AAR72458 the Porphyromonas gingivalis lysine-gingipain
CC protein complex (LGPC). The LGPC has amidolytic and proteolytic
CC specificity for an amide bond, where lysine contributes the carboxyl gp.,
CC i.e. a lysine specific protease. LGPC can be used to identify agents that
CC modulate the effect of LGPC on animals, and also for monitoring the
CC exposure of an animal to LGPC. Such a method can be used to monitor the
CC progress of a therapy designed to lessen the symptoms of periodontitis
XX
XX Sequence 970 AA;
SQ

Query Match 90.9%; Score 110; DB 2; Length 970;
Best Local Similarity 86.4%; Pred. No. 4.1e-08;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Oy 1 LNTGVSPFANYTAHGETAWADP 22
Db 432 LNTGVGFANYTVHGETSWADP 453

Search completed: August 25, 2006, 17:57:46
Job time : 231.628 secs

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OM protein - protein search, using sw model

Run on: August 25, 2006, 18:04:46 ; Search time 36.3256 Seconds
(without alignments)
53.012 Million cell updates/sec

Title: US-10-387-977-2

Perfect score: 121

Sequence: 1 LNTGVSFANYAHGSETAWADP 22

Scoring table: BLOSUM62

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Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	121	100.0	1732	1	US-08-570-311-10 Sequence 10, Appl
2	121	100.0	1732	1	US-08-570-311-10 Sequence 10, Appl
3	121	100.0	1732	1	US-08-570-311-10 Sequence 10, Appl
4	114	94.2	1732	1	US-08-570-311-10 Sequence 10, Appl
5	114	94.2	1732	1	US-08-570-311-10 Sequence 10, Appl
6	114	94.2	1732	1	US-08-570-311-10 Sequence 10, Appl
7	110	90.9	1732	1	US-08-570-311-10 Sequence 10, Appl
8	82	67.8	1732	1	US-08-570-311-10 Sequence 10, Appl
9	78	64.5	1732	1	US-08-570-311-10 Sequence 10, Appl
10	78	64.5	1732	1	US-08-570-311-10 Sequence 10, Appl
11	78	64.5	1732	1	US-08-570-311-10 Sequence 10, Appl
12	78	64.5	1732	1	US-08-570-311-10 Sequence 10, Appl
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16	78	64.5	1732	1	US-08-570-311-10 Sequence 10, Appl
17	78	64.5	1732	1	US-08-570-311-10 Sequence 10, Appl
18	78	64.5	1732	1	US-08-570-311-10 Sequence 10, Appl
19	78	64.5	1732	1	US-08-570-311-10 Sequence 10, Appl
20	46	38.0	321	1	US-10-152-886-21 Sequence 21, Appl
21	46	38.0	321	1	US-10-152-886-21 Sequence 21, Appl
22	46	38.0	321	1	US-10-152-886-21 Sequence 21, Appl
23	46	38.0	321	1	US-10-152-886-21 Sequence 21, Appl
24	46	38.0	321	1	US-10-152-886-21 Sequence 21, Appl
25	46	38.0	321	1	US-10-152-886-21 Sequence 21, Appl
26	46	38.0	321	1	US-10-152-886-21 Sequence 21, Appl

27 46 38.0 361 2 US-09-503-444A-22 Sequence 22, Appl
28 46 38.0 503 1 US-07-946-497-2 Sequence 2, Appl
29 46 38.0 503 1 US-08-483-322-2 Sequence 2, Appl
30 46 38.0 503 1 US-08-478-882-2 Sequence 2, Appl
31 46 38.0 589 2 US-09-740-041-2 Sequence 2, Appl
32 46 38.0 614 1 US-08-295-814E-12 Sequence 12, Appl
33 46 38.0 614 1 US-08-543-881-2 Sequence 2, Appl
34 46 38.0 614 1 US-08-291-299-2 Sequence 2, Appl
35 46 38.0 614 1 US-08-291-299-2 Sequence 2, Appl
36 46 38.0 614 2 US-09-343-361-12 Sequence 8, Appl
37 46 38.0 614 2 US-09-919-039-378 Sequence 378, App
38 46 38.0 614 5 PCT-US94-00119-2 Sequence 2, Appl
39 46 38.0 614 5 PCT-US95-10579-2 Sequence 2, Appl
40 46 38.0 634 2 PCT-US95-10579-8 Sequence 8, Appl
41 46 38.0 634 2 US-09-543-681A-7681 Sequence 7681, Ap
42 46 38.0 954 2 US-09-351-150A-17 Sequence 17, Appl
43 46 38.0 954 2 US-09-482-273-251 Sequence 251, App
44 45 37.2 191 2 US-09-482-273-161 Sequence 161, App
45 45 37.2 191 2 US-09-482-273-161 Sequence 161, App

ALIGNMENTS

RESULT 1
US-08-570-311-10
; Sequence 10, Application US/08570311
; Patent No. 5824791
; GENERAL INFORMATION:
; APPLICANT: Progulsk-Fox, Ann
; APPLICANT: Tumwasorn, Somying
; APPLICANT: Lepine, Guylaine
; APPLICANT: Han, Naiming
; APPLICANT: Lantz, Marilyn
; APPLICANT: Patti, Joseph
; TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Ted W. Whitlock
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570,311
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/353,485
; FILING DATE: 09-DEC-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/647,119
; FILING DATE: 25-JAN-1991
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/241,640
; FILING DATE: 08-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF15.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1732 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-570-311-10

Query Match 100.0%; Score 121; DB 1; Length 1732;
Best Local Similarity 100.0%; Pred. No. 5.7e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTGVSPFANYTAHGETAWADP 22
DB 432 LNTGVSPFANYTAHGETAWADP 453

RESULT 2
US-08-353-485-10
; Sequence 10, Application US/08353485
; Patent No. 5830710
; GENERAL INFORMATION:
; APPLICANT: Proguiske-Fox, Ann
; APPLICANT: Tumwasorn, Somying
; APPLICANT: Lepine, Guylaine
; APPLICANT: Han, Naiming
; APPLICANT: Lantz, Marilyn
; APPLICANT: Patti, Joseph
; TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ted W. Whitlock
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,485
; FILING DATE: 09-DEC-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/647,119
; FILING DATE: 25-JAN-1991
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/241,640
; FILING DATE: 08-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF15.C2
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1732 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-353-485-10

Query Match 100.0%; Score 121; DB 1; Length 1732;
Best Local Similarity 100.0%; Pred. No. 5.7e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTGVSPFANYTAHGETAWADP 22

DB 432 LNTGVSPFANYTAHGETAWADP 453

RESULT 3
US-09-066-330-11
; Sequence 11, Application US/09066330A
; Patent No. 6511666
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric C.
; APPLICANT: Bhogal, Peter S.
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE
; FILE REFERENCE: Reynolds
; CURRENT APPLICATION NUMBER: US/09/066,330A
; CURRENT FILING DATE: 1998-09-15
; EARLIER APPLICATION NUMBER: EN 6275
; EARLIER FILING DATE: 1995-10-30
; EARLIER APPLICATION NUMBER: PCT/AU96/00673
; EARLIER FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 1732
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
; US-09-066-330-11

Query Match 100.0%; Score 121; DB 2; Length 1732;
Best Local Similarity 100.0%; Pred. No. 5.7e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTGVSPFANYTAHGETAWADP 22
DB 432 LNTGVSPFANYTAHGETAWADP 453

RESULT 4
US-08-141-324-14
; Sequence 14, Application US/08141324
; Patent No. 5475097
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; APPLICANT: Pike, Robert N.
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,324
; FILING DATE: 21-OCT-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 44-93
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8089


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; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 942 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
; US-08-141-324-14
;
Query Match          94.2%; Score 114; DB 1; Length 942;
Best Local Similarity 90.9%; Pred. No. 3.4e-09;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

;
; 1 LNTGVSFANYTAHGETAWADP 22
; 432 LNTGVGFANYTAHGETSWADP 453
;
Db
;
RESULT 5
US-08-541-902-14
; Sequence 14, Application US/08541902
; Patent No. 5707620
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; APPLICANT: Pike, Robert N.
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,902
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,324
; FILING DATE: 21-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 44-93
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8089
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 942 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
; US-08-541-902-14
;
Query Match          94.2%; Score 114; DB 1; Length 942;
Best Local Similarity 90.9%; Pred. No. 3.4e-09;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

;
; 1 LNTGVSFANYTAHGETAWADP 22
; 432 LNTGVGFANYTAHGETSWADP 453
;
Db
;
RESULT 6
US-08-570-311-27
; Sequence 27, Application US/08570311
; Patent No. 5824791
; GENERAL INFORMATION:
; APPLICANT: Progulske-Fox, Ann
; APPLICANT: Tumwasorn, Somying
; APPLICANT: Lepine, Guylaine
; APPLICANT: Han, Naiming
; APPLICANT: Lantz, Marilyn
; APPLICANT: Patti, Joseph
; TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
; TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ted W. Whitlock
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570,311
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/647,119
; FILING DATE: 25-JAN-1991
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/241,640
; FILING DATE: 08-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF15.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1358 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
; US-08-570-311-27
;
Query Match          94.2%; Score 114; DB 1; Length 1358;
Best Local Similarity 90.9%; Pred. No. 5.3e-09;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

;
; 1 LNTGVSFANYTAHGETAWADP 22
; 67 LNTGVGFANYTAHGETSWADP 88
;
Db
;
RESULT 7
US-08-822-324-8
; Sequence 8, Application US/08822324
; Patent No. 612917
; GENERAL INFORMATION:
; APPLICANT: Potempa, Jan S.
; APPLICANT: Travis, James
; APPLICANT: Genco, Caroline A.

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;; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS COMPRISING
;; TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS PROTEINS AND/OR PEPTIDES AND
;; TITLE OF INVENTION: METHODS
;; NUMBER OF SEQUENCES: 24
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
;; STREET: 5370 Manhattan Circle, Suite 201
;; CITY: Boulder
;; STATE: CO
;; COUNTRY: US
;; ZIP: 80303
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/822,324
;; FILING DATE: 21-MAR-1997
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/013,945
;; FILING DATE: 22-MAR-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ferber, Donna M.
;; REGISTRATION NUMBER: 33,878
;; REFERENCE/DOCKET NUMBER: 103-95 WO
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (303) 488-8080
;; TELEFAX: (303) 499-8089
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 509 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-822-324-8

Query Match 90.9%; Score 110; DB 2; Length 509;
Best Local Similarity 86.4%; Pred. No. 7e-09;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LNTGVSFANYTAHGETAWDP 22
Db 204 LNTGVGFANYTVHGETSWADP 225

RESULT 8
US-09-066-330-10
; Sequence 10, Application US/09066330A
; Patent No. 6511666
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric C.
; APPLICANT: Bhogal, Peter S.
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE
; FILE REFERENCE: Reynolds
; CURRENT APPLICATION NUMBER: US/09/066,330A
; CURRENT FILING DATE: 1998-09-15
; EARLIER APPLICATION NUMBER: PN 6275
; EARLIER FILING DATE: 1995-10-30
; EARLIER APPLICATION NUMBER: PCT/AU96/00673
; EARLIER FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1706
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-09-066-330-10

Query Match 67.8%; Score 82; DB 2; Length 1706;
Best Local Similarity 77.8%; Pred. No. 0.0007;

Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 2 NTGVSFANYTAHGETAW 19
Db 427 NGGISLVNYTGHGETAW 444

RESULT 9
US-09-482-500A-2
; Sequence 2, Application US/09482500A
; Patent No. 6627193
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Imamura, Takahisa
; APPLICANT: Potempa, Jan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROL OF BLOOD COAGULATION
; FILE REFERENCE: 235.00160101
; CURRENT APPLICATION NUMBER: US/09/482,500A
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US 60/115,869
; PRIOR FILING DATE: 1999-01-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-09-482-500A-2

Query Match 64.5%; Score 78; DB 2; Length 492;
Best Local Similarity 72.2%; Pred. No. 0.00067;
Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 NTGVSFANYTAHGETAW 19
Db 200 NGGISLVNYTGHGETAW 217

RESULT 10
US-09-482-500A-3
; Sequence 3, Application US/09482500A
; Patent No. 6627193
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Imamura, Takahisa
; APPLICANT: Potempa, Jan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROL OF BLOOD COAGULATION
; FILE REFERENCE: 235.00160101
; CURRENT APPLICATION NUMBER: US/09/482,500A
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US 60/115,869
; PRIOR FILING DATE: 1999-01-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-09-482-500A-3

Query Match 64.5%; Score 78; DB 2; Length 507;
Best Local Similarity 72.2%; Pred. No. 0.0007;
Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 NTGVSFANYTAHGETAW 19
Db 200 NGGISLVNYTGHGETAW 217

RESULT 11
US-08-119-361-5
; Sequence 5, Application US/08119361
; Patent No. 5523390

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;
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; TITLE OF INVENTION: Porphyromonas gingivalis Arginine-specific Proteinase
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: USA
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 10-SEP-1993
; APPLICATION NUMBER: US/08/119,361
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33878
; REFERENCE/DOCKET NUMBER: 21-93
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8089
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 737 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-119-361-5

Query Match 64.5%; Score 78; DB 1; Length 737;
Best Local Similarity 72.2%; Pred. No. 0.0011;
Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 NTGVSFANYTAHGSETAW 19
| | | | | | | | | |
Db 427 NGGISLVNYTGHGSETAW 444

RESULT 12
US-08-336-308A-4
; Sequence 4, Application US/08336308A
; Patent No. 6017532
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; TITLE OF INVENTION: Porphyromonas gingivalis
; TITLE OF INVENTION: Arginine-specific Proteinase Coding Sequences
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,308A
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; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/119,361
; FILING DATE: 10-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/265,441
; FILING DATE: 24-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 21-93C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 737 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-336-308A-4

Query Match 64.5%; Score 78; DB 2; Length 737;
Best Local Similarity 72.2%; Pred. No. 0.0011;
Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 NTGVSFANYTAHGSETAW 19
| | | | | | | | | |
Db 427 NGGISLVNYTGHGSETAW 444

RESULT 13
US-08-822-324-4
; Sequence 4, Application US/08822324
; Patent No. 6129917
; GENERAL INFORMATION:
; APPLICANT: Potempa, Jan S.
; APPLICANT: Travis, James
; APPLICANT: Genco, Caroline A.
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS COMPRISING
; TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS PROTEINS AND/OR PEPTIDES AND
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,324
; FILING DATE: 21-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,945
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 103-95 WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 488-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 737 amino acids
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-822-324-4

Query Match 64.5%; Score 78; DB 2; Length 737;
Best Local Similarity 72.2%; Pred. No. 0.0011;
Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 NTGVSFANYTAHGSETAW 19
Db 427 NGGISLVNYTGHGSETAW 444

RESULT 14

US-09-490-931-4
; Sequence 4, Application US/09490931
; Patent No. 6274718

GENERAL INFORMATION:

; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; TITLE OF INVENTION: Porphyromonas gingivalis
; TITLE OF INVENTION: Arginine-specific Proteinase Coding Sequences
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS: 16

; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: 16
; APPLICATION NUMBER: US/09/490,931
; FILING DATE:
; CLASSIFICATION:

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/336,308
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/265,441
; FILING DATE: 24-JUN-1994
; ATTORNEY/AGENT INFORMATION:

; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 21-93C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089

INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 737 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-490-931-4

Query Match 64.5%; Score 78; DB 2; Length 737;
Best Local Similarity 72.2%; Pred. No. 0.0011;
Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 NTGVSFANYTAHGSETAW 19
Db 427 NGGISLVNYTGHGSETAW 444

RESULT 15

US-09-482-500A-1
; Sequence 1, Application US/09482500A
; Patent No. 6627193
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Imamura, Takahisa
; APPLICANT: Potempa, Jan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROL OF BLOOD COAGULATION
; FILE REFERENCE: 235.00160101
; CURRENT APPLICATION NUMBER: US/09/482,500A
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US 60/115,869
; PRIOR FILING DATE: 1999-01-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1477
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-09-482-500A-1

Query Match 64.5%; Score 78; DB 2; Length 1477;
Best Local Similarity 72.2%; Pred. No. 0.0025;
Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 NTGVSFANYTAHGSETAW 19
Db 200 NGGISLVNYTGHGSETAW 217

Search completed: August 25, 2006, 18:06:28
Job time : 38.3256 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 25, 2006, 18:21:12 ; Search time 126.884 Seconds
(without alignments)
80.315 Million cell updates/sec

Title: US-10-387-977-2

Perfect score: 121

Sequence: 1 LNTGVSPANTAHGSETAWADP 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /EMC_Celerra_SID33/ptodata/2/pubpaa/US07_PUBCOMB.psp.*
- 2: /EMC_Celerra_SID33/ptodata/2/pubpaa/US08_PUBCOMB.psp.*
- 3: /EMC_Celerra_SID33/ptodata/2/pubpaa/US09_PUBCOMB.psp.*
- 4: /EMC_Celerra_SID33/ptodata/2/pubpaa/US10A_PUBCOMB.psp.*
- 5: /EMC_Celerra_SID33/ptodata/2/pubpaa/US10B_PUBCOMB.psp.*
- 6: /EMC_Celerra_SID33/ptodata/2/pubpaa/US11_PUBCOMB.psp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	121	100.0	22	4	US-10-387-977-2
2	121	100.0	509	4	Sequence 2, Appli
3	121	100.0	1731	5	Sequence 101, App
4	121	100.0	1731	5	Sequence 176, App
5	121	100.0	1731	5	Sequence 192, App
6	121	100.0	1731	5	Sequence 211, App
7	121	100.0	1731	5	Sequence 222, App
8	82	67.8	21	4	Sequence 11, Appli
9	82	67.8	491	4	Sequence 100, Appl
10	82	67.8	507	4	Sequence 99, Appl
11	82	67.8	736	4	Sequence 105, App
12	82	67.8	1706	4	Sequence 106, App
13	82	67.8	1706	5	Sequence 186, App
14	82	67.8	1706	5	Sequence 210, App
15	82	67.8	1706	5	Sequence 221, App
16	82	67.8	1706	5	Sequence 239, App
17	82	67.8	1706	6	Sequence 276, App
18	55	45.5	1123	5	Sequence 245, App
19	50	41.3	230	4	Sequence 189940
20	50	41.3	450	4	Sequence 8448, Ap
21	50	41.3	453	5	Sequence 43923, A
22	50	41.3	475	6	Sequence 5183, Ap
23	50	41.3	475	6	Sequence 15792, A
24	50	41.3	878	4	Sequence 155762
25	50	41.3	1528	4	Sequence 146309
26	50	41.3	1843	4	Sequence 117317
27	50	41.3	3041	4	Sequence 202715

28	49	40.5	1534	4	US-10-437-963-189652	Sequence 189652,
29	48.5	40.1	731	4	US-10-437-963-189840	Sequence 189840,
30	48	39.7	444	5	US-10-481-265-9	Sequence 9, Appli
31	48	39.7	1686	4	US-10-437-963-181004	Sequence 181004,
32	47.5	39.3	445	4	US-10-081-872-116	Sequence 116, App
33	47.5	39.3	445	4	US-10-385-305-116	Sequence 116, App
34	47.5	39.3	463	4	US-10-081-872-318	Sequence 318, App
35	47.5	39.3	463	4	US-10-385-305-318	Sequence 318, App
36	47.5	39.3	464	4	US-10-081-872-126	Sequence 126, App
37	47.5	39.3	464	4	US-10-105-733-9	Sequence 9, Appli
38	47.5	39.3	464	4	US-10-081-739A-9	Sequence 9, Appli
39	47.5	39.3	464	4	US-10-385-305-126	Sequence 126, App
40	47.5	39.3	464	5	US-10-489-510-9	Sequence 9, Appli
41	47.5	39.3	471	4	US-10-081-872-112	Sequence 112, App
42	47.5	39.3	471	4	US-10-385-305-112	Sequence 112, App
43	47	38.8	321	4	US-10-424-599-239193	Sequence 239193,
44	47	38.8	359	5	US-10-450-763-54188	Sequence 54188, A
45	47	38.8	499	4	US-10-274-694-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-10-387-977-2
; Sequence 2, Application US/10387977
; Publication No. US20040005276A1
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric Charles
; APPLICANT: O'Brien-Simpson, Neil Martin
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
; TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
; FILE REFERENCE: 52928200301
; CURRENT APPLICATION NUMBER: US/10/387,977
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 09/423,056
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/AU98/00311
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: AU PO 6528
; PRIOR FILING DATE: 1997-04-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-387-977-2

Query Match 100.0%; Score 121; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTGVSPANTAHGSETAWADP 22
|||||
Db 1 LNTGVSPANTAHGSETAWADP 22
|||||

RESULT 2

US-10-387-977-101
; Sequence 101, Application US/10387977
; Publication No. US20040005276A1
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric Charles
; APPLICANT: O'Brien-Simpson, Neil Martin
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
; TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
; FILE REFERENCE: 52928200301
; CURRENT APPLICATION NUMBER: US/10/387,977

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; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 09/423,056
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/AU98/00311
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: AU PO 6528
; PRIOR FILING DATE: 1997-04-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
; US-10-387-977-101

Query Match      100.0%; Score 121; DB 4; Length 509;
Best Local Similarity 100.0%; Pred. No. 7.7e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTGVSFANYTAHGETAWADP 22
Db 204 LNTGVSFANYTAHGETAWADP 225

RESULT 3
US-10-915-002-176
; Sequence 176, Application US/10915002
; Publication No. US20060078950A1
; GENERAL INFORMATION:
; APPLICANT: Progulske-Fox, Ann
; APPLICANT: Hillman, Jeffrey D.
; APPLICANT: Handfield, Martin
; TITLE OF INVENTION: IDENTIFICATION OF PORPHYROMONAS GINGIVALIS VIRULENCE POLYNUCLEOTIDE
; TITLE OF INVENTION: USE IN DIAGNOSIS ANTIGENS FOR USE IN THE DIAGNOSIS, TREATMENT, A
; TITLE OF INVENTION: PERIODONTAL DISEASES
; FILE REFERENCE: 02-042
; CURRENT APPLICATION NUMBER: US/10/915,002
; CURRENT FILING DATE: 2004-08-10
; NUMBER OF SEQ ID NOS: 354
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 176
; LENGTH: 1731
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
; US-10-915-002-176

Query Match      100.0%; Score 121; DB 5; Length 1731;
Best Local Similarity 100.0%; Pred. No. 2.9e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTGVSFANYTAHGETAWADP 22
Db 432 LNTGVSFANYTAHGETAWADP 453

RESULT 4
US-10-915-002-192
; Sequence 192, Application US/10915002
; Publication No. US20060078950A1
; GENERAL INFORMATION:
; APPLICANT: Progulske-Fox, Ann
; APPLICANT: Hillman, Jeffrey D.
; APPLICANT: Handfield, Martin
; TITLE OF INVENTION: IDENTIFICATION OF PORPHYROMONAS GINGIVALIS VIRULENCE POLYNUCLEOTIDE
; TITLE OF INVENTION: USE IN DIAGNOSIS ANTIGENS FOR USE IN THE DIAGNOSIS, TREATMENT, A
; TITLE OF INVENTION: PERIODONTAL DISEASES
; FILE REFERENCE: 02-042
; CURRENT APPLICATION NUMBER: US/10/915,002
; CURRENT FILING DATE: 2004-08-10
; NUMBER OF SEQ ID NOS: 354
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 192
; LENGTH: 1731
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; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
; US-10-915-002-192

Query Match      100.0%; Score 121; DB 5; Length 1731;
Best Local Similarity 100.0%; Pred. No. 2.9e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTGVSFANYTAHGETAWADP 22
Db 432 LNTGVSFANYTAHGETAWADP 453

RESULT 5
US-10-915-002-211
; Sequence 211, Application US/10915002
; Publication No. US20060078950A1
; GENERAL INFORMATION:
; APPLICANT: Progulske-Fox, Ann
; APPLICANT: Hillman, Jeffrey D.
; APPLICANT: Handfield, Martin
; TITLE OF INVENTION: IDENTIFICATION OF PORPHYROMONAS GINGIVALIS VIRULENCE POLYNUCLEOTIDE
; TITLE OF INVENTION: USE IN DIAGNOSIS ANTIGENS FOR USE IN THE DIAGNOSIS, TREATMENT, A
; TITLE OF INVENTION: PERIODONTAL DISEASES
; FILE REFERENCE: 02-042
; CURRENT APPLICATION NUMBER: US/10/915,002
; CURRENT FILING DATE: 2004-08-10
; NUMBER OF SEQ ID NOS: 354
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 211
; LENGTH: 1731
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
; US-10-915-002-211

Query Match      100.0%; Score 121; DB 5; Length 1731;
Best Local Similarity 100.0%; Pred. No. 2.9e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTGVSFANYTAHGETAWADP 22
Db 432 LNTGVSFANYTAHGETAWADP 453

RESULT 6
US-10-915-002-222
; Sequence 222, Application US/10915002
; Publication No. US20060078950A1
; GENERAL INFORMATION:
; APPLICANT: Progulske-Fox, Ann
; APPLICANT: Hillman, Jeffrey D.
; APPLICANT: Handfield, Martin
; TITLE OF INVENTION: IDENTIFICATION OF PORPHYROMONAS GINGIVALIS VIRULENCE POLYNUCLEOTIDE
; TITLE OF INVENTION: USE IN DIAGNOSIS ANTIGENS FOR USE IN THE DIAGNOSIS, TREATMENT, A
; TITLE OF INVENTION: PERIODONTAL DISEASES
; FILE REFERENCE: 02-042
; CURRENT APPLICATION NUMBER: US/10/915,002
; CURRENT FILING DATE: 2004-08-10
; NUMBER OF SEQ ID NOS: 354
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 222
; LENGTH: 1731
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
; US-10-915-002-222

Query Match      100.0%; Score 121; DB 5; Length 1731;
Best Local Similarity 100.0%; Pred. No. 2.9e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTGVSFANYTAHGETAWADP 22
Db 432 LNTGVSFANYTAHGETAWADP 453
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RESULT 7
US-10-387-977-1066-11
; Sequence 11, Application US/10229066
; Publication No. US20040005276A1
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric C.
; APPLICANT: Bhogal, Peter S.
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE
; FILE REFERENCE: Reynolds
; CURRENT APPLICATION NUMBER: US/10/229,066
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US/09/066,330
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: PN 6275
; PRIOR FILING DATE: 1995-10-30
; PRIOR APPLICATION NUMBER: PCT/AU96/00673
; PRIOR FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 11
; LENGTH: 1732
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-229-066-11

Query Match          100.0%; Score 121; DB 4; Length 1732;
Best Local Similarity 100.0%; Pred. No. 2.9e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNTGVSFANYTAHGSETAWDP 22
        |||||
Db       432 LNTGVSFANYTAHGSETAWDP 453

RESULT 8
US-10-387-977-1
; Sequence 1, Application US/10387977
; Publication No. US20040005276A1
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric Charles
; APPLICANT: O'Brien-Simpson, Neil Martin
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
; FILE REFERENCE: 529282000301
; CURRENT APPLICATION NUMBER: US/10/387,977
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 09/423,056
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/AU98/00311
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: AU PO 6528
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-387-977-1

Query Match          67.8%; Score 82; DB 4; Length 21;
Best Local Similarity 77.8%; Pred. No. 2.4e-05;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 NTGVSFANYTAHGSETAW 19
        |.:|:|||||
Db       2 NGGISLANYTGHGSETAW 19

RESULT 9
US-10-387-977-100
; Sequence 100, Application US/10387977
; Publication No. US20040005276A1
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric Charles
; APPLICANT: O'Brien-Simpson, Neil Martin
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
; FILE REFERENCE: 529282000301
; CURRENT APPLICATION NUMBER: US/10/387,977
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 09/423,056
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/AU98/00311
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: AU PO 6528
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 100
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-387-977-100

Query Match          67.8%; Score 82; DB 4; Length 491;
Best Local Similarity 77.8%; Pred. No. 0.00072;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 NTGVSFANYTAHGSETAW 19
        |.:|:|||||
Db       200 NGGISLANYTGHGSETAW 217

RESULT 10
US-10-387-977-99
; Sequence 99, Application US/10387977
; Publication No. US20040005276A1
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric Charles
; APPLICANT: O'Brien-Simpson, Neil Martin
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
; FILE REFERENCE: 529282000301
; CURRENT APPLICATION NUMBER: US/10/387,977
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 09/423,056
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/AU98/00311
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: AU PO 6528
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 99
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-387-977-99

Query Match          67.8%; Score 82; DB 4; Length 507;
Best Local Similarity 77.8%; Pred. No. 0.00074;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 NTGVSFANYTAHGSETAW 19
        |.:|:|||||
Db       200 NGGISLANYTGHGSETAW 217
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; TITLE OF INVENTION: PERIODONTAL DISEASES
; FILE REFERENCE: 02-042
; CURRENT APPLICATION NUMBER: US/10/915,002
; CURRENT FILING DATE: 2004-08-10
; NUMBER OF SEQ ID NOS: 354
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 221
; LENGTH: 1706
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-915-002-221

Query Match          67.8%; Score 82; DB 5; Length 1706;
Best Local Similarity 77.8%; Pred. No. 0.0028;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 NTGVSPFANYTAHGGSETAW 19
      |.:|:|:|:|:|:|:|:|:|
Db      427 NGGISLANYTGHGGSETAW 444

Search completed: August 25, 2006, 18:26:05
Job time : 129.884 secs
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; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54345
; LENGTH: 731
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-54345

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Query Match      40.1%; Score 48.5; DB 6; Length 731;
Best Local Similarity 45.5%; Pred. No. 16;
Matches 10; Conservative 5; Mismatches 4; Indels 3; Gaps 1;
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Qy      4  GVSFANYTAHGSET--AWADP 22
          |::| | | | |::| | |
Db      16 GLSYDGYTDHGSQSDYFRFADP 37

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RESULT 3
US-10-449-902-54740
; Sequence 54740, Application US/10449902
; Publication No. US20060123505A1

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; GENERAL INFORMATION:
;
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-Oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
;
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

```

```

: FILE ORIGINATOR: TOSHIBA-YI-US
: FILE REFERENCE: MOR-A020SYI-US
: CURRENT APPLICATION NUMBER: US/10/449,902
: CURRENT FILING DATE: 2003-05-29
: PRIOR APPLICATION NUMBER: JP 2002-203269
: PRIOR FILING DATE: 2002-05-30
: PRIOR APPLICATION NUMBER: JP 2002-383870
: PRIOR FILING DATE: 2002-12-11
: NUMBER OF SEQ ID NOS: 56791
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 54740
: LENGTH: 731
: TYPE: PRT
: ORGANISM: Orvza sativa
:

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Query Match 40.1%; Score 48.5; DB 6; Length 731;
Best Local Similarity 45.5%; Pred.No.16;
Matches 10; Conservative 5; Mismatches 4; Indels 3; Gaps 1

QY 4 GVSFANYTAHGSET--AWADP 22
|:|:| | | | | :| |
pb 16 GLSYDGYTDHGSODPYRFADP 37

RESULT 4
US-11-327-689-22
; Sequence 22, Application US/11327689
; Publication No. US20060177854A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.

WOLFF, ROGER K.
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York

```
,  
,  
, COUNTRY: USA  
,  
ZIP: 10036-2811  
,  
COMPUTER READABLE FORM:  
,  
MEDIUM TYPE: Floppy disk  
,  
COMPUTER: IBM PC compatible  
,  
OPERATING SYSTEM: Windows 95  
,  
SOFTWARE: FastSeq for Windows Version 2.0.b  
,  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/11/327,689  
FILING DATE: 05-Jan-2006  
CLASSIFICATION: <Unknown>  
,
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, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US/09/497,957
, FILING DATE: 04-FEB-2000
, APPLICATION NUMBER: US/08/834,497
, FILING DATE: 04-APR-1997
, APPLICATION NUMBER: US 08/652,265
, FILING DATE: 23-MAY-1996
, APPLICATION NUMBER: US 08/632,673
, FILING DATE: 16-APR-1996
, APPLICATION NUMBER: US 08/630,912
, FILING DATE: 04-APR-1996
,
```

ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELECOMMUNICATION INFORMATION:

```

1 TELEPHONE: 650-493-4935
2
3 TELEFAX: 650-493-5556
4
5 TRLEX: 66141 PENNTE
6
7 INFORMATION FOR SEQ ID NO: 22:
8     SEQUENCE CHARACTERISTICS:
9         LENGTH: 361 amino acids
10        TYPE: amino acid
11        STRANDEDNESS: <Unknown>
12        TOPOLOGY: linear
13        MOLECULE TYPE: protein
14        FEATURE:
15

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; NAME/KEY: Protein
; LOCATION: 1..361
; OTHER INFORMATION: /note= "Rabbit leukocyte antigen (RLA)"
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-11-327-689-22

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Query Match 38.0%; Score 46; DB 7; Length 361;
Best Local Similarity 37.9%; Pred. No. 18;
Matches 11: Conservative 3; Mismatches 7; Indels 8; Gaps 1;

QY 1 LNTGVSFANYTAHGET-----AWAD 21
||| : | : ||| | |||
Db 102 LNTALRYNOSAGSHTEOTMEGCEVWAD 130

RESULT 5
US-10-449-902-48719
; Sequence 48719, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-Oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205V1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 48719

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; LENGTH: 373
; TYPE: prt
; ORGANISM: Oryza sativa
US-10-449-902-48719

Query Match      38.0%; Score 46; DB 6; Length 373;
Best Local Similarity 46.7%; Pred. No. 19;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      8 ANYTAHGETAWADP 22
Db      203 ANPSRYFTTFWSDP 217

RESULT 6
US-11-300-928-62
; Sequence 62, Application US/11300928
; Publication No. US20060166277A1
; GENERAL INFORMATION:
; APPLICANT: Karumanchi, S. Ananth
; APPLICANT: Sukhatme, Vikas P.
; TITLE OF INVENTION: Nucleic Acids and Polypeptides Useful For Diagnosing and Treating
; TITLE OF INVENTION: Complications of Pregnancy
; FILE REFERENCE: 01948/108002
; CURRENT APPLICATION NUMBER: US/11/300,928
; CURRENT FILING DATE: 2005-12-15
; PRIOR APPLICATION NUMBER: US 60/636,275
; PRIOR FILING DATE: 2004-12-15
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 62
; LENGTH: 614
; TYPE: prt
; ORGANISM: Homo sapiens
US-11-300-928-62

Query Match      38.0%; Score 46; DB 7; Length 614;
Best Local Similarity 53.3%; Pred. No. 33;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      5 VSFANYTAHGETAW 19
Db      94 VALGOYTSQGSVTAW 108

RESULT 7
US-11-056-355B-52484
; Sequence 52484, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 52484
; LENGTH: 317
; TYPE: prt
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(317)
; OTHER INFORMATION: Ceres Seq. ID no. 15177288
US-11-056-355B-52484

Query Match      37.2%; Score 45; DB 7; Length 317;
Best Local Similarity 64.3%; Pred. No. 23;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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```
QY      5 VSFANYTAHGETA 18
Db      149 VTFAGYWAYGSSTA 162

RESULT 8
US-11-056-355B-52483
; Sequence 52483, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 52483
; LENGTH: 383
; TYPE: prt
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(383)
; OTHER INFORMATION: Ceres Seq. ID no. 15177287
US-11-056-355B-52483

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Best Local Similarity 64.3%; Pred. No. 28;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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QY      5 VSFANYTAHGETA 18
Db      215 VTFAGYWAYGSSTA 228

RESULT 9
US-10-449-902-29639
; Sequence 29639, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 29639
; LENGTH: 392
; TYPE: prt
; ORGANISM: Oryza sativa
US-10-449-902-29639

Query Match      37.2%; Score 45; DB 6; Length 392;
Best Local Similarity 43.8%; Pred. No. 29;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
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QY      7 FANYTAHGETAWADP 22
Db      122 FSELTSAATTVMGDP 137
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RESULT 10
US-10-449-902-49669
; Sequence 49669, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49669
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-49669

Query Match 37.2%; Score 45; DB 6; Length 392;
Best Local Similarity 43.8%; Pred. No. 29;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 7 FANYTAHGETAWADP 22
| : | : | : | : |
Db 122 FSELTSGATTWGD 137

RESULT 11
US-11-056-355B-52482
; Sequence 52482, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590FUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 52482
; LENGTH: 435
; TYPE: prt
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(435)
; OTHER INFORMATION: Ceres Seq. ID no. 15177286
US-11-056-355B-52482

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Best Local Similarity 64.3%; Pred. No. 32;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 VSFANYTAHGETA 18
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Db 267 VTFAGYWAYGSSTA 280

RESULT 12
US-10-544-180-42
; Sequence 42, Application US/10544180
; Publication No. US20060150280A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
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; GENERAL INFORMATION:
; APPLICANT: Mohnen, Debra
; APPLICANT: Sterling, Jason D.
; APPLICANT: Doong, Ron L.
; APPLICANT: Kollu, Venkata S.K.
; APPLICANT: Hahn, Michael G.
; TITLE OF INVENTION: Galacturonosyltransferases, nucleic acids encoding same, and uses
; FILE REFERENCE: 14-03 US
; CURRENT APPLICATION NUMBER: US/10/544,180
; CURRENT FILING DATE: 2005-08-02
; PRIOR APPLICATION NUMBER: PCT/US2004/003545
; PRIOR FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US 60/445,539
; PRIOR FILING DATE: 2003-02-06
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-544-180-42

Query Match 36.4%; Score 44; DB 6; Length 351;
Best Local Similarity 46.7%; Pred. No. 36;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 8 ANYTAHGETAWADP 22
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Db 202 ANFTHYTRTFWSDP 216

RESULT 13
US-10-449-902-42939
; Sequence 42939, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42939
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-42939

Query Match 36.4%; Score 44; DB 6; Length 425;
Best Local Similarity 52.6%; Pred. No. 45;
Matches 10; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY 2 NTGVSFANYTAHGETAWA 20
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Db 274 NGMTFAEYRAHFS--IWA 290

RESULT 14
US-10-449-902-50133
; Sequence 50133, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
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; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50133
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-50133

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Query Match 36.4%; Score 44; DB 6; Length 425;
Best Local Similarity 52.6%;
Pred. No. 45;
Matches 10; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY 2 NTGVSEFANYTAHGSETAWA 20
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Db 274 NGGMTFAEYRAHFS--IWA 290

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RESULT 15
US-10-953-349-10213
; Sequence 10213, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
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; LENGTH: 506
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-10213

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Query Match	36.4%	Score 44;	DB 6;	Length 506;
Best Local Similarity	52.9%;	Pred. No. 54;		
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Db 123 GLSMENRANSGSEEAWA 139

Search completed: August 25, 2006, 18:26:51
Job time : 22.9767 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 25, 2006, 18:05:37 ; Search time 437.442 Seconds
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Title: US-10-387-977-2

Perfect score: 121

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Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	121	100.0	22	33	US-10-387-977-2
4	121	100.0	509	24	US-09-423-056B-101
5	121	100.0	509	24	US-09-423-056B-101
6	121	100.0	509	33	US-10-387-977-101
7	121	100.0	1731	39	US-10-915-002-176
8	121	100.0	1731	39	US-10-915-002-176
9	121	100.0	1731	39	US-10-915-002-211
10	121	100.0	1731	39	US-10-915-002-222
11	121	100.0	1731	49	US-60-495-589-176
12	121	100.0	1731	49	US-60-495-589-192
13	121	100.0	1731	49	US-60-495-589-211
14	121	100.0	1731	49	US-60-495-589-222
15	121	100.0	1732	27	US-09-174-517-10
16	121	100.0	1732	27	US-09-174-517-10
17	121	100.0	1732	27	US-09-791-537-18924
18	121	100.0	1732	32	US-10-229-066-11
19	114	94.2	1358	21	US-09-174-517-27
20	114	94.2	1723	27	US-09-791-537-86208
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23	110	90.9	509	25	US-09-543-696B-8
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26	82	67.8	21	33	US-10-387-977-1
27	82	67.8	491	24	US-09-423-056B-100
28	82	67.8	491	24	US-09-423-056B-100
29	82	67.8	491	33	US-10-387-977-100
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38	82	67.8	1706	27	US-09-791-537-113656
39	82	67.8	1706	32	US-10-229-066-10
40	82	67.8	1706	39	US-10-915-002-186
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43	82	67.8	1706	39	US-10-915-002-239
44	82	67.8	1706	40	US-11-052-554A-176
45	82	67.8	1706	49	US-60-495-589-186

ALIGNMENTS

RESULT 1
US-09-423-056-2
; Sequence 2, Application US/09423056
; GENERAL INFORMATION:

us-10-387-977-2.rapm

Mon Aug 28 11:30:42 2006

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; APPLICANT: Reynolds, Eric C.
; APPLICANT: O'Brien-Simpson, Neil M.
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: Synthetic peptide constructs for the diagnosis and
; TITLE OF INVENTION: treatment of periodontitis associated with
; TITLE OF INVENTION: Porphyromonas gingivalis
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/423,056
; CURRENT FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/AU98/00311
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: PO 6528
; PRIOR FILING DATE: 1997-04-30
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-09-423-056-2
Query Match 100.0%; Score 121; DB 24; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNTGVSFANYTAHGSETAWADP 22
Db 1 LNTGVSFANYTAHGSETAWADP 22

RESULT 2
US-09-423-056B-2
; Sequence 2, Application US/09423056B
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric Charles
; APPLICANT: O'Brien-Simpson, Neil Martin
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
; TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
; FILE REFERENCE: 529282000300
; CURRENT APPLICATION NUMBER: US/09/423,056B
; CURRENT FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/AU98/00311
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-09-423-056B-2
Query Match 100.0%; Score 121; DB 24; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNTGVSFANYTAHGSETAWADP 22
Db 1 LNTGVSFANYTAHGSETAWADP 22

RESULT 3
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; Sequence 2, Application US/10387977
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric Charles
; APPLICANT: O'Brien-Simpson, Neil Martin
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
; TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
; FILE REFERENCE: 529282000301

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; CURRENT APPLICATION NUMBER: US/10/387,977
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 09/423,056
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/AU98/00311
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: AU PO 6528
; PRIOR FILING DATE: 1997-04-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-387-977-2
Query Match 100.0%; Score 121; DB 33; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNTGVSFANYTAHGSETAWADP 22
Db 1 LNTGVSFANYTAHGSETAWADP 22

RESULT 4
US-09-423-056-101
; Sequence 101, Application US/09423056
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric C.
; APPLICANT: O'Brien-Simpson, Neil M.
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: Synthetic peptide constructs for the diagnosis and
; TITLE OF INVENTION: treatment of periodontitis associated with
; TITLE OF INVENTION: Porphyromonas gingivalis
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/423,056
; CURRENT FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/AU98/00311
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: PO 6528
; PRIOR FILING DATE: 1997-04-30
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-09-423-056-101
Query Match 100.0%; Score 121; DB 24; Length 509;
Best Local Similarity 100.0%; Pred. No. 4.8e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNTGVSFANYTAHGSETAWADP 22
Db 204 LNTGVSFANYTAHGSETAWADP 225

RESULT 5
US-09-423-056B-101
; Sequence 101, Application US/09423056B
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric Charles
; APPLICANT: O'Brien-Simpson, Neil Martin
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
; TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
; FILE REFERENCE: 529282000300
; CURRENT APPLICATION NUMBER: US/09/423,056B
; CURRENT FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/AU98/00311

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; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-09-423-056B-101

Query Match      100.0%; Score 121; DB 24; Length 509;
Best Local Similarity 100.0%; Pred. No. 4.8e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNTGVSPFANYTAHGETAWADP 22
Db 204 LNTGVSPFANYTAHGETAWADP 225

RESULT 6
US-10-387-977-101
; Sequence 101, Application US/10387977
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric Charles
; APPLICANT: O'Brien-Simpson, Neil Martin
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
; TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
; FILE REFERENCE: 52928200301
; CURRENT APPLICATION NUMBER: US/10/387,977
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 09/423,056
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/AU98/00311
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: AU PO 6528
; PRIOR FILING DATE: 1997-04-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-387-977-101

Query Match      100.0%; Score 121; DB 33; Length 509;
Best Local Similarity 100.0%; Pred. No. 4.8e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNTGVSPFANYTAHGETAWADP 22
Db 204 LNTGVSPFANYTAHGETAWADP 225

RESULT 7
US-10-915-002-176
; Sequence 176, Application US/10915002
; GENERAL INFORMATION:
; APPLICANT: Progulske-Fox, Ann
; APPLICANT: Hillman, Jeffrey D.
; APPLICANT: Handfield, Martin
; TITLE OF INVENTION: IDENTIFICATION OF PORPHYROMONAS GINGIVALIS VIRULENCE POLYNUCLEOTIDE
; TITLE OF INVENTION: USE IN DIAGNOSIS ANTIGENS FOR USE IN THE DIAGNOSIS, TREATMENT, A
; TITLE OF INVENTION: PERIODONTAL DISEASES
; FILE REFERENCE: 02-042
; CURRENT APPLICATION NUMBER: US/10/915,002
; CURRENT FILING DATE: 2004-08-10
; NUMBER OF SEQ ID NOS: 354
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 176
; LENGTH: 1731
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
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US-10-915-002-176

Query Match      100.0%; Score 121; DB 39; Length 1731;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNTGVSPFANYTAHGETAWADP 22
Db 432 LNTGVSPFANYTAHGETAWADP 453

RESULT 8
US-10-915-002-192
; Sequence 192, Application US/10915002
; GENERAL INFORMATION:
; APPLICANT: Progulske-Fox, Ann
; APPLICANT: Hillman, Jeffrey D.
; APPLICANT: Handfield, Martin
; TITLE OF INVENTION: IDENTIFICATION OF PORPHYROMONAS GINGIVALIS VIRULENCE POLYNUCLEOTIDE
; TITLE OF INVENTION: USE IN DIAGNOSIS ANTIGENS FOR USE IN THE DIAGNOSIS, TREATMENT, A
; TITLE OF INVENTION: PERIODONTAL DISEASES
; FILE REFERENCE: 02-042
; CURRENT APPLICATION NUMBER: US/10/915,002
; CURRENT FILING DATE: 2004-08-10
; NUMBER OF SEQ ID NOS: 354
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 192
; LENGTH: 1731
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-915-002-192

Query Match      100.0%; Score 121; DB 39; Length 1731;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNTGVSPFANYTAHGETAWADP 22
Db 432 LNTGVSPFANYTAHGETAWADP 453

RESULT 9
US-10-915-002-211
; Sequence 211, Application US/10915002
; GENERAL INFORMATION:
; APPLICANT: Progulske-Fox, Ann
; APPLICANT: Hillman, Jeffrey D.
; APPLICANT: Handfield, Martin
; TITLE OF INVENTION: IDENTIFICATION OF PORPHYROMONAS GINGIVALIS VIRULENCE POLYNUCLEOTIDE
; TITLE OF INVENTION: USE IN DIAGNOSIS ANTIGENS FOR USE IN THE DIAGNOSIS, TREATMENT, A
; TITLE OF INVENTION: PERIODONTAL DISEASES
; FILE REFERENCE: 02-042
; CURRENT APPLICATION NUMBER: US/10/915,002
; CURRENT FILING DATE: 2004-08-10
; NUMBER OF SEQ ID NOS: 354
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 211
; LENGTH: 1731
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-915-002-211

Query Match      100.0%; Score 121; DB 39; Length 1731;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNTGVSPFANYTAHGETAWADP 22
Db 432 LNTGVSPFANYTAHGETAWADP 453

RESULT 10
US-10-915-002-222
```

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; Sequence 222, Application US/10915002
; GENERAL INFORMATION:
; APPLICANT: Progulske-Fox, Ann
; APPLICANT: Hillman, Jeffrey D.
; APPLICANT: Handfield, Martin
; TITLE OF INVENTION: IDENTIFICATION OF PORPHYROMONAS GINGIVALIS VIRULENCE POLYNUCLEOTIDE
; TITLE OF INVENTION: USE IN DIAGNOSIS ANTIGENS FOR USE IN THE DIAGNOSIS, TREATMENT, AND MONITORING OF PERIODONTAL DISEASES
; FILE REFERENCE: 02-042
; CURRENT APPLICATION NUMBER: US/10/915,002
; CURRENT FILING DATE: 2004-08-10
; NUMBER OF SEQ ID NOS: 354
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 222
; LENGTH: 1731
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-915-002-222

Query Match      100.0%; Score 121; DB 39; Length 1731;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNTGVSFANYTAHGETAWADP 22
        |||||
Db      432 LNTGVSFANYTAHGETAWADP 453

RESULT 11
US-60-495-589-176
; Sequence 176, Application US/60495589
; GENERAL INFORMATION:
; APPLICANT: Progulske-Fox, Ann
; APPLICANT: Hillman, Jeffrey D.
; APPLICANT: Handfield, Martin
; TITLE OF INVENTION: IDENTIFICATION OF PORPHYROMONAS GINGIVALIS VIRULENCE POLYNUCLEOTIDE
; TITLE OF INVENTION: DIAGNOSIS, TREATMENT, AND MONITORING OF PERIODONTAL DISEASES
; FILE REFERENCE: 02-042
; CURRENT APPLICATION NUMBER: US/60/495,589
; CURRENT FILING DATE: 2003-08-15
; NUMBER OF SEQ ID NOS: 354
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 176
; LENGTH: 1731
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-60-495-589-176

Query Match      100.0%; Score 121; DB 49; Length 1731;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNTGVSFANYTAHGETAWADP 22
        |||||
Db      432 LNTGVSFANYTAHGETAWADP 453

RESULT 12
US-60-495-589-192
; Sequence 192, Application US/60495589
; GENERAL INFORMATION:
; APPLICANT: Progulske-Fox, Ann
; APPLICANT: Hillman, Jeffrey D.
; APPLICANT: Handfield, Martin
; TITLE OF INVENTION: IDENTIFICATION OF PORPHYROMONAS GINGIVALIS VIRULENCE POLYNUCLEOTIDE
; TITLE OF INVENTION: DIAGNOSIS, TREATMENT, AND MONITORING OF PERIODONTAL DISEASES
; FILE REFERENCE: 02-042
; CURRENT APPLICATION NUMBER: US/60/495,589
; CURRENT FILING DATE: 2003-08-15
; NUMBER OF SEQ ID NOS: 354
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 192
; LENGTH: 1731
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-387-977-2
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; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-60-495-589-192

Query Match      100.0%; Score 121; DB 49; Length 1731;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNTGVSFANYTAHGETAWADP 22
        |||||
Db      432 LNTGVSFANYTAHGETAWADP 453

RESULT 13
US-60-495-589-211
; Sequence 211, Application US/60495589
; GENERAL INFORMATION:
; APPLICANT: Progulske-Fox, Ann
; APPLICANT: Hillman, Jeffrey D.
; APPLICANT: Handfield, Martin
; TITLE OF INVENTION: IDENTIFICATION OF PORPHYROMONAS GINGIVALIS VIRULENCE POLYNUCLEOTIDE
; TITLE OF INVENTION: DIAGNOSIS, TREATMENT, AND MONITORING OF PERIODONTAL DISEASES
; FILE REFERENCE: 02-042
; CURRENT APPLICATION NUMBER: US/60/495,589
; CURRENT FILING DATE: 2003-08-15
; NUMBER OF SEQ ID NOS: 354
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 211
; LENGTH: 1731
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-60-495-589-211

Query Match      100.0%; Score 121; DB 49; Length 1731;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNTGVSFANYTAHGETAWADP 22
        |||||
Db      432 LNTGVSFANYTAHGETAWADP 453

RESULT 14
US-60-495-589-222
; Sequence 222, Application US/60495589
; GENERAL INFORMATION:
; APPLICANT: Progulske-Fox, Ann
; APPLICANT: Hillman, Jeffrey D.
; APPLICANT: Handfield, Martin
; TITLE OF INVENTION: IDENTIFICATION OF PORPHYROMONAS GINGIVALIS VIRULENCE POLYNUCLEOTIDE
; TITLE OF INVENTION: DIAGNOSIS, TREATMENT, AND MONITORING OF PERIODONTAL DISEASES
; FILE REFERENCE: 02-042
; CURRENT APPLICATION NUMBER: US/60/495,589
; CURRENT FILING DATE: 2003-08-15
; NUMBER OF SEQ ID NOS: 354
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 222
; LENGTH: 1731
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-60-495-589-222

Query Match      100.0%; Score 121; DB 49; Length 1731;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNTGVSFANYTAHGETAWADP 22
        |||||
Db      432 LNTGVSFANYTAHGETAWADP 453

RESULT 15
US-09-174-517-10
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; Sequence 10, Application US/09174517
; GENERAL INFORMATION:
; APPLICANT: Progulske-Fox, Ann
; APPLICANT: Tumwasorn, Somying
; APPLICANT: Lepine, Guylaine
; APPLICANT: Han, Naiming
; APPLICANT: Lantz, Marilyn
; APPLICANT: Patti, Joseph
; TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
; TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ted W. Whitlock
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/174,517
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/570,311
; FILING DATE:
; APPLICATION NUMBER: US 08/353,485
; FILING DATE: 09-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/647,119
; FILING DATE: 25-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/241,640
; FILING DATE: 08-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UFI5.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1732 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-174-517-10

Query Match 100.0%; Score 121; DB 21; Length 1732;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNTGVSPFANYTAHGSFADP 22
Db 432 LNTGVSPFANYTAHGSFADP 453
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Search completed: August 25, 2006, 18:20:50
Job time : 439.442 secs

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OM protein - protein search, using sw model

Run on: August 25, 2006, 18:06:46 ; Search time 27.6279 Seconds
(without alignments)
68.789 Million cell updates/sec

Title: US-10-387-977-2

Perfect score: 121

Sequence: 1 LNTGVSFANYTAHGETAWADP 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 363143 seqs, 86385820 residues

Total number of hits satisfying chosen parameters: 363143

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /EMC_Celerra_SID33/prodata/2/paa/US06_NEW_COMB.pep.*
3: /EMC_Celerra_SID33/prodata/2/paa/US07_NEW_COMB.pep.*
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5: /EMC_Celerra_SID33/prodata/2/paa/US09_NEW_COMB.pep.*
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8: /EMC_Celerra_SID33/prodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	121	100.0	1732	6	US-10-229-066A-24
2	82	67.8	1706	6	US-10-229-066A-21
3	57	47.1	468	1	PCT-US06-18535-26266
4	57	47.1	468	7	US-11-431-855-26266
5	56	46.3	471	1	PCT-US06-18535-26339
6	56	46.3	471	7	US-11-431-855-26339
7	52	43.0	433	1	PCT-US06-18535-26437
8	52	43.0	433	7	US-11-431-855-26437
9	47.5	39.3	445	6	US-10-385-305A-116
10	47.5	39.3	463	6	US-10-385-305A-318
11	47.5	39.3	463	6	US-10-385-305A-323
12	47.5	39.3	464	6	US-10-385-305A-126
13	47.5	39.3	471	6	US-10-385-305A-112
14	46.5	38.4	315	1	PCT-US06-18535-22801
15	46.5	38.4	315	7	US-11-431-855-22801
16	46	38.0	614	7	US-11-431-708-3588
17	46	38.0	614	7	US-11-431-708-3590
18	46	38.0	614	7	US-11-431-708-3601
19	46	38.0	614	7	US-11-431-708-3609
20	46	38.0	614	7	US-11-431-708-3614
21	46	38.0	614	7	US-11-475-062-6827
22	46	38.0	614	7	US-11-475-062-6829
23	46	38.0	614	7	US-11-475-062-6840
24	46	38.0	614	7	US-11-475-062-6848
25	46	38.0	614	7	US-11-475-062-6853

26	45	37.2	205	7	US-11-455-201-122	Sequence 122, App
27	45	37.2	205	7	US-11-478-144-778	Sequence 778, App
28	45	37.2	243	7	US-11-371-354-74171	Sequence 74171, A
29	44	36.4	2069	6	US-10-805-394A-4320	Sequence 4320, Ap
30	43.5	36.0	2544	1	PCT-US06-18535-23649	Sequence 23649, A
31	43.5	36.0	2544	7	US-11-431-855-23649	Sequence 23649, A
32	43	35.5	113	5	US-09-674-546B-976	Sequence 976, App
33	43	35.5	113	5	US-09-674-546B-980	Sequence 980, App
34	43	35.5	582	1	PCT-US06-30281-2649	Sequence 2649, Ap
35	43	35.5	582	1	PCT-US06-30281-20875	Sequence 20875, A
36	43	35.5	582	8	US-60-836-986-13044	Sequence 13044, A
37	43	35.5	1720	8	US-60-836-986-30809	Sequence 30809, A
38	43	35.5	14507	8	US-60-836-986-31920	Sequence 31920, A
39	42.5	35.1	3435	6	US-10-461-194A-132	Sequence 132, App
40	42	34.7	111	7	US-11-478-193-1051	Sequence 1051, Ap
41	42	34.7	116	1	PCT-US06-30281-6862	Sequence 6862, Ap
42	42	34.7	163	1	PCT-US06-18535-27585	Sequence 27585, A
43	42	34.7	163	7	US-11-431-855-27585	Sequence 27585, A
44	42	34.7	413	1	PCT-US06-18535-22856	Sequence 22856, A
45	42	34.7	413	7	US-11-431-855-22856	Sequence 22856, A

ALIGNMENTS

RESULT 1

US-10-229-066A-24
; Sequence 24, Application US/10229066A
; GENERAL INFORMATION:
; APPLICANT: REYNOLDS, ERIC CHARLES
; APPLICANT: BHOGAL, PETER SINGH
; APPLICANT: SLAKESKI, NADA
; TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE
; FILE REFERENCE: 4137-20
; CURRENT APPLICATION NUMBER: US/10/229,066A
; CURRENT FILING DATE: 2002-08-28
; PRIOR FILING DATE: 1998-09-15
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: PCT/AU96/00673
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: AU PN 6275
; PRIOR FILING DATE: 1995-10-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 24
; LENGTH: 1732
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-229-066A-24

Query Match 100.0%; Score 121; DB 6; Length 1732;

Best Local Similarity 100.0%; Pred. No. 4.6e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNTGVSFANYTAHGETAWADP 22

Db 432 LNTGVSFANYTAHGETAWADP 453

RESULT 2

US-10-229-066A-21
; Sequence 21, Application US/10229066A
; GENERAL INFORMATION:
; APPLICANT: REYNOLDS, ERIC CHARLES
; APPLICANT: BHOGAL, PETER SINGH
; APPLICANT: SLAKESKI, NADA
; TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE
; FILE REFERENCE: 4137-20
; CURRENT APPLICATION NUMBER: US/10/229,066A
; CURRENT FILING DATE: 2002-08-28
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: PCT/AU96/00673

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; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: AU PN 6275
; PRIOR FILING DATE: 1995-10-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 21
; LENGTH: 1706
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-229-066A-21

Query Match      67.8%; Score 82; DB 6; Length 1706;
Best Local Similarity 77.8%; Pred. No. 0.00042;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 NTGVSFANYTAHGETAW 19
Db      427 NNGISLANYTGHGETAW 444

RESULT 3
PCT-US06-18535-26266
; Sequence 26266, Application PC/TUS0618535
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark et. al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53708)A
; CURRENT APPLICATION NUMBER: PCT/US06/18535
; CURRENT FILING DATE: 2006-05-10
; NUMBER OF SEQ ID NOS: 33637
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26266
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Burkholderia cepacia R18194
PCT-US06-18535-26266

Query Match      47.1%; Score 57; DB 1; Length 468;
Best Local Similarity 83.3%; Pred. No. 0.86;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 TGVSFANYTAHG 14
Db      198 SGVGFANYTAHG 209

RESULT 4
US-11-431-855-26266
; Sequence 26266, Application US/11431855
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark et. al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53708)C
; CURRENT APPLICATION NUMBER: US/11/431.855
; CURRENT FILING DATE: 2006-05-10
; NUMBER OF SEQ ID NOS: 33637
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26266
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Burkholderia cepacia R18194
US-11-431-855-26266

Query Match      47.1%; Score 57; DB 7; Length 468;
Best Local Similarity 83.3%; Pred. No. 0.86;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 TGVSFANYTAHG 14
Db      198 SGVGFANYTAHG 209

RESULT 5
US-11-431-855-26266
; Sequence 26266, Application US/11431855
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark et. al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53708)C
; CURRENT APPLICATION NUMBER: US/11/431.855
; CURRENT FILING DATE: 2006-05-10
; NUMBER OF SEQ ID NOS: 33637
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26266
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Burkholderia cepacia R18194
US-11-431-855-26266

Query Match      47.1%; Score 57; DB 7; Length 468;
Best Local Similarity 83.3%; Pred. No. 0.86;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 TGVSFANYTAHG 14
Db      198 SGVGFANYTAHG 209

PCT-US06-18535-26339
; Sequence 26339, Application PC/TUS0618535
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark et. al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53708)A
; CURRENT APPLICATION NUMBER: PCT/US06/18535
; CURRENT FILING DATE: 2006-05-10
; NUMBER OF SEQ ID NOS: 33637
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26339
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Burkholderia cepacia R18194
PCT-US06-18535-26339

Query Match      46.3%; Score 56; DB 1; Length 471;
Best Local Similarity 75.0%; Pred. No. 1.2;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      3 TGVSFANYTAHG 14
Db      188 SGIGFANYTAHG 199

RESULT 6
US-11-431-855-26339
; Sequence 26339, Application US/11431855
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark et. al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53708)C
; CURRENT APPLICATION NUMBER: US/11/431.855
; CURRENT FILING DATE: 2006-05-10
; NUMBER OF SEQ ID NOS: 33637
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26339
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Burkholderia cepacia R18194
US-11-431-855-26339

Query Match      46.3%; Score 56; DB 7; Length 471;
Best Local Similarity 75.0%; Pred. No. 1.2;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      3 TGVSFANYTAHG 14
Db      188 SGIGFANYTAHG 199

RESULT 7
PCT-US06-18535-26437
; Sequence 26437, Application PC/TUS0618535
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark et. al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53708)A
; CURRENT APPLICATION NUMBER: PCT/US06/18535
; CURRENT FILING DATE: 2006-05-10
; NUMBER OF SEQ ID NOS: 33637
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26437
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Burkholderia cepacia R1808
PCT-US06-18535-26437

Query Match      43.0%; Score 52; DB 1; Length 433;
Best Local Similarity 66.7%; Pred. No. 4.7;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      3 TGVSFANYTAHG 14
```

```
Db      163 SGIGFANYTGHG 174
      :|: ||||| ||
      :|: ||||| ||

RESULT 8
US-11-431-855-26437
; Sequence 26437, Application US/11431855
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark et. al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53708)C
; CURRENT APPLICATION NUMBER: US/11/431.855
; CURRENT FILING DATE: 2006-05-10
; NUMBER OF SEQ ID NOS: 33637
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26437
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Burkholderia cepacia R1808
US-11-431-855-26437

Query Match      43.0%; Score 52; DB 7; Length 433;
Best Local Similarity 66.7%; Pred. No. 4.7;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      3 TGVSFANYTAHG 14
      :|: ||||| ||
      :|: ||||| ||

Db      163 SGIGFANYTGHG 174
      :|: ||||| ||
      :|: ||||| ||

RESULT 9
US-10-385-305A-116
; Sequence 116, Application US/10385305A
; GENERAL INFORMATION:
; APPLICANT: CALLEN, Walter
; APPLICANT: RICHARDSON, Toby
; APPLICANT: FREY, Gerhard
; APPLICANT: GRAY, Kevin A.
; APPLICANT: KEROVUO, Janne S.
; APPLICANT: SLUPSKA, Malgorzata
; APPLICANT: BARTON, Nelson R.
; APPLICANT: O'DONOGHUE, Eileen
; APPLICANT: MATHUR, Eric J.
; APPLICANT: SHORT, Jay M.
; TITLE OF INVENTION: AMYLASES, NUCLEIC ACIDS ENCODING THEM AND
; METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462006120
; CURRENT APPLICATION NUMBER: US/10/385,305A
; CURRENT FILING DATE: 2003-03-06
; PRIOR FILING DATE: 2002-02-21
; PRIOR FILING DATE: 2002-02-21
; PRIOR FILING DATE: 2001-05-14
; PRIOR FILING DATE: 2001-02-21
; PRIOR FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 435
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 116
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Eukaryote
US-10-385-305A-116

Query Match      39.3%; Score 47.5; DB 6; Length 445;
Best Local Similarity 41.7%; Pred. No. 23;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 LNTGVSFANYTAH---GSETAWAD 21
      :|: ||||| ||
      :|: ||||| ||

Db      380 VNVGSKFAGYTIHEYTGNLGGWVD 403
      :|: ||||| ||
      :|: ||||| ||

RESULT 10
US-10-385-305A-318
; Sequence 318, Application US/10385305A
; GENERAL INFORMATION:
; APPLICANT: CALLEN, Walter
; APPLICANT: RICHARDSON, Toby
; APPLICANT: FREY, Gerhard
; APPLICANT: GRAY, Kevin A.
; APPLICANT: KEROVUO, Janne S.
; APPLICANT: SLUPSKA, Malgorzata
; APPLICANT: BARTON, Nelson R.
; APPLICANT: O'DONOGHUE, Eileen
; APPLICANT: MATHUR, Eric J.
; APPLICANT: SHORT, Jay M.
; TITLE OF INVENTION: AMYLASES, NUCLEIC ACIDS ENCODING THEM AND
; METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462006120
; CURRENT APPLICATION NUMBER: US/10/385,305A
; CURRENT FILING DATE: 2003-03-06
; PRIOR FILING DATE: 2002-02-21
; PRIOR FILING DATE: 2002-02-21
; PRIOR FILING DATE: 2001-02-21
; PRIOR FILING DATE: 2001-05-14
; PRIOR FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 435
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 318
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone
US-10-385-305A-318

Query Match      39.3%; Score 47.5; DB 6; Length 463;
Best Local Similarity 41.7%; Pred. No. 24;
Matches 10; Conservative 2; Mismatches 9; Indels 3; Gaps 1;

QY      1 LNTGVSFANYTAH---GSETAWAD 21
      :|: ||||| ||
      :|: ||||| ||

Db      406 VNVGSKFAGYTIHEYTGNLGGWVD 429
      :|: ||||| ||
      :|: ||||| ||

RESULT 11
US-10-385-305A-323
; Sequence 323, Application US/10385305A
; GENERAL INFORMATION:
; APPLICANT: CALLEN, Walter
; APPLICANT: RICHARDSON, Toby
; APPLICANT: FREY, Gerhard
; APPLICANT: GRAY, Kevin A.
; APPLICANT: KEROVUO, Janne S.
; APPLICANT: SLUPSKA, Malgorzata
; APPLICANT: BARTON, Nelson R.
; APPLICANT: O'DONOGHUE, Eileen
; APPLICANT: MATHUR, Eric J.
; APPLICANT: SHORT, Jay M.
US-10-385-305A-323

Query Match      39.3%; Score 47.5; DB 6; Length 445;
Best Local Similarity 41.7%; Pred. No. 23;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53708)A
; CURRENT APPLICATION NUMBER: PCT/US06/18535
; CURRENT FILING DATE: 2006-05-10
; NUMBER OF SEQ ID NOS: 33637
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22801
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Magnaporthe grisea 70-15
PCT-US06-18535-22801

Query Match 38.4%; Score 46.5; DB 1; Length 315;
Best Local Similarity 40.9%; Pred. No. 24;
Matches 9; Conservative 3; Mismatches 7; Indels 3; Gaps 1;

QY 4 GVSFANYTAHG---SETAWADP 22
Db 157 GARIVNITSHGHQLSDVWWSDP 178

RESULT 15
US-11-431-855-22801
; Sequence 22801, Application US/11431855
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark et. al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53708)C
; CURRENT APPLICATION NUMBER: US/11/431,855
; CURRENT FILING DATE: 2006-05-10
; NUMBER OF SEQ ID NOS: 33637
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22801
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Magnaporthe grisea 70-15
US-11-431-855-22801

Query Match 38.4%; Score 46.5; DB 7; Length 315;
Best Local Similarity 40.9%; Pred. No. 24;
Matches 9; Conservative 3; Mismatches 7; Indels 3; Gaps 1;

QY 4 GVSFANYTAHG---SETAWADP 22
Db 157 GARIVNITSHGHQLSDVWWSDP 178

Search completed: August 25, 2006, 18:21:50
Job time : 29.6279 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 25, 2006, 17:58:43 ; Search time 24.5581 Seconds
(without alignments)
86.194 Million cell updates/sec

Title: US-10-387-977-2

Perfect score: 121
Sequence: 1 LNTGVSPANTAHGSETAWADP 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*

- 1: PIR1.*
- 2: PIR2.*
- 3: PIR3.*
- 4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	121	100.0	1732	2 T30836	lysine-specific cy
2	82	67.8	1526	2 S49763	gingipain R (EC 3
3	78	64.5	991	2 I40229	arginyln endopeptid
4	78	64.5	1704	2 A55426	gingipain R (EC 3
5	49.5	40.9	545	2 H86657	hypothetical prote
6	48	39.7	444	2 A70674	probable mbtC prot
7	47	38.8	307	2 E95939	probable inosine-u
8	47	38.8	311	2 G69731	PBSX prophage ORF
9	47	38.8	1672	2 C81675	polymorphic membra
10	46	38.0	197	2 F71248	probable proteasom
11	46	38.0	361	1 HLRB	MHC class I histoc
12	46	38.0	361	2 I46858	MHC class I RLA pr
13	46	38.0	503	2 B38745	cell adhesion mole
14	46	38.0	614	2 S68236	betaine/GABA trans
15	46	38.0	614	2 A41757	betaine transport
16	46	38.0	851	2 T31520	hypothetical prote
17	45.5	37.6	429	2 AH0630	4-hydroxyphenylace
18	45	37.2	214	2 C82950	glucose inhibited
19	45	37.2	219	2 H81107	uracil-DNA glycosy
20	45	37.2	219	2 B81908	probable uracil-DN
21	45	37.2	234	2 S37463	regulatory protein
22	45	37.2	348	2 D97490	hypothetical prote
23	45	37.2	379	2 E84274	membrane protein I
24	45	37.2	499	2 S46660	wetA protein - Pen
25	44	36.4	214	2 D89985	hypothetical prote
26	44	36.4	337	2 D87354	conserved hypothet
27	44	36.4	502	2 AH2289	4-alpha-glucanotra
28	44	36.4	506	2 AB2064	hypothetical prote
29	44	36.4	507	2 S52677	probable membrane

ALIGNMENTS

RESULT 1

T30836

lysine-specific cysteine proteinase porphypain (EC 3.4.22.-) - Porphyromonas gingivalis
N:Alternate names: lysine-specific cysteine proteinase 1, 60K
C:Species: Porphyromonas gingivalis
C:Date: 22-Oct-1999 #sequence revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30836; T30837; T30526; A53113
R:Barkocy-Gallagher, G.A.; Han, N.; Patti, J.M.; Whitlock, J.; Progulske-Fox, A.; Lantz
J. Bacteriol. 178, 2734-2741, 1996
A:Title: Analysis of the prtP gene encoding porphypain, a cysteine proteinase of Porphy
A:Reference number: Z20895; MUID:96213011; PMID:8631659
A:Accession: T30836
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1732 <BAR>
A:Cross-references: UNIPROT:Q51817; UNIPARC:UPI00000893C0; EMBL:U42210; NID:gl314325; P
R:Slakeski, N.; Cleal, S.M.; Reynolds, E.C.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z20896
A:Accession: T30837
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-795, 'I', '797-1389, 'N', '1391-1478, 'Y', '1480-1732 <SLA>
A:Cross-references: UNIPARC:UPI00000B61C4; EMBL:U75366; NID:g2182811; PID:g2182812; PID
R:Lewis, J.P.; Macrina, F.L.
Infect. Immun. 66, 3035-3042, 1998
A:Title: IS195, an insertion sequence-like element associated with protease genes in Por
A:Reference number: Z20844; MUID:98298016; PMID:9632563
A:Accession: T30526
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1350, 'N', '1352-1363, 'Y', '1365-1447, 'H', '1449-1732 <LEW>
A:Cross-references: UNIPARC:UPI00000BCA91; EMBL:AF017059; NID:g2738802; PID:g2738803; P
R:Pike, R.; McGraw, W.; Potempa, J.; Travis, J.
J. Biol. Chem. 269, 406-411, 1994
A:Title: Lysine- and arginine-specific proteinases from Porphyromonas gingivalis. Isolati
A:Reference number: A53113; MUID:94103245; PMID:8276827
A:Accession: A53113
A:Status: preliminary
A:Molecule type: protein
A:Residues: 229-249 <PIK>
A:Cross-references: UNIPARC:UPI00000BA1A1
A:Experimental source: H66
A:Note: sequence extracted from NCBI backbone (NCBIP:141690)
C:Genetics:
A:Gene: prtP; prtK
C:Keywords: cysteine proteinase; hydrolase

Query Match 100.0%; Score 121; DB 2; Length 1732;
Best Local Similarity 100.0%; Pred. No. 3.6e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1  LNTGVSFANYTAHGETAWADP 22
      |||||
Db      432 LNTGVSFANYTAHGETAWADP 453

RESULT 2
S49763
gingipain R (EC 3.4.22.37) precursor - Porphyromonas gingivalis (fragment)
C:Species: Porphyromonas gingivalis
C:Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C:Accession: S49763
R:Aduse-Opoku, J.; Muir, J.; Slaney, J.M.; Rangarajan, M.; Curtis, M.A.
submitted to the EMBL Data Library, November 1994
A:Description: Cloning, sequence analysis and expression in Escherichia coli of prpR1 of
A:Reference number: S49763
A:Accession: S49763
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1526 <ADU>
A:Cross-references: UNIPROT:Q51838; UNIPARC:UPI0000179912; EMBL:X82680
C:Genetics:
A:Gene: prpR1
C:Keywords: cysteine proteinase; hydrolase

      Query Match      67.8%; Score 82; DB 2; Length 1526;
      Best Local Similarity 77.8%; Pred. No. 0.00032;
      Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2  NTGVSFANYTAHGETAW 19
      |||||
Db      427 NGGISLVNYTGHGETAW 444

RESULT 3
I40229
arginyl endopeptidase - Porphyromonas gingivalis
C:Species: Porphyromonas gingivalis
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C:Accession: I40229
R:Okamoto, K.; Misumi, Y.; Kadowaki, T.; Yoneda, M.; Yamamoto, K.; Ikehara, Y.
Arch. Biochem. Biophys. 316, 917-925, 1995
A:Title: Structural characterization of argingipain, a novel arginine-specific cysteine
A:Reference number: I40229; MUID:95168884; PMID:7864651
A:Accession: I40229
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-991 <RES>
A:Cross-references: UNIPROT:P28784; UNIPARC:UPI000012829F; GB:D26470; NID:G927644; PIDN:

      Query Match      64.5%; Score 78; DB 2; Length 991;
      Best Local Similarity 72.2%; Pred. No. 0.00084;
      Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      2  NTGVSFANYTAHGETAW 19
      |||||
Db      427 NGGISLVNYTGHGETAW 444

RESULT 4
A55426
gingipain R (EC 3.4.22.37) precursor - Porphyromonas gingivalis
N:Alternate names: 50K high molecular mass arginine-specific cysteine proteinase; HGP; R
C:Species: Porphyromonas gingivalis
C:Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
C:Accession: A55426; D53113
R:Pavloff, N.; Potempa, J.; Pike, R.N.; Prochazka, V.; Kiefer, M.C.; Travis, J.; Barr, B.
J. Biol. Chem. 270, 1007-1010, 1995
A:Title: Molecular cloning and structural characterization of the Arg-gingipain proteina
A:Reference number: A55426; MUID:95138080; PMID:7836351
A:Accession: A55426
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1704 <PAV>

```

```

A:Cross-references: UNIPROT:Q51816; UNIPARC:UPI000000B7BC1; GB:U15282; NID:G557067; PIDN:
R:Pike, R.; McGraw, W.; Potempa, J.; Travis, J.
J. Biol. Chem. 269, 406-411, 1994
A:Title: Lysine- and arginine-specific proteinases from Porphyromonas gingivalis. Isolati
A:Reference number: A53113; MUID:94103245; PMID:8276827
A:Accession: D53113
A:Status: preliminary
A:Molecule type: protein
A:Residues: 228-249 <PIK>
A:Cross-references: UNIPARC:UPI000000B9226
A:Experimental source: H66
A:Note: sequence extracted from NCBI backbone (NCBIP:141694)
C:Keywords: cysteine proteinase; hydrolase

      Query Match      64.5%; Score 78; DB 2; Length 1704;
      Best Local Similarity 72.2%; Pred. No. 0.0015;
      Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      2  NTGVSFANYTAHGETAW 19
      |||||
Db      427 NGGISLVNYTGHGETAW 444

RESULT 5
H86667
hypochemical protein optA [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: H86667
R:Boilotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis es
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: H86667
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-545 <STO>
A:Cross-references: UNIPROT:Q9CIL2; UNIPARC:UPI000000C67F9; GB:AE005176; PID:G12723212; F
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: optA
C:Superfamily: dipeptide transport protein

      Query Match      40.9%; Score 49.5; DB 2; Length 545;
      Best Local Similarity 42.3%; Pred. No. 11;
      Matches 11; Conservative 2; Mismatches 6; Indels 7; Gaps 1;

QY      2  NTGVSFANYTAH-----GSETAWA 20
      |||||
Db      350 NTGVDFAKYAAQPKYDATAKAANA 375

RESULT 6
A70674
probable mbtC protein - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: A70674
R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: A70674
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-444 <COL>
A:Cross-references: UNIPROT:P1718; UNIPARC:UPI000001652E8; GB:Z81371; GB:AL123456; NID:
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: mbtC

```

C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prod
F;26-426/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS2>

Query Match 39.7%; Score 48; DB 2; Length 444;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 10 YTAHGETAWAD 21
|:|:|:|:|:|:
Db 230 YSAHASGTAWAE 241

RESULT 7

E95939
probable inosine-uridine preferring nucleoside hydrolase protein [imported] - Sinorhizob
C:Species: Sinorhizobium meliloti

C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

C:Accession: E95939

R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A:Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo
A:Reference number: A95942; MUID:21396508; PMID:11481431

A:Accession: E95939

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-307 <KUR>

A:Cross-references: UNIPROT:Q92VC7; UNIPARC:UPI00000CB661; GB:AL591985; PIDN:CAC49181.1;

A:Experimental source: strain 1021, megaplasmid pSymB

R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.

A:Title: The composite genome of the legume symbiont sinorhizobium meliloti.

A:Reference number: A96039; MUID:21368234; PMID:11474104

A:Contents: annotation

C:Genetics:

A:Gene: SMB21277

A:Genome: plasmid

C:Superfamily: yaaF protein

Query Match 38.8%; Score 47; DB 2; Length 307;
Best Local Similarity 52.6%; Pred. No. 14;
Matches 10; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 4 GVSFANYTAHGETAWADP 22
|:|:|:|:|:|:
Db 150 GVSNGNHTASAEFNAFADP 168

RESULT 8

G69731

PBSX prophage ORF xkdG - Bacillus subtilis

C:Species: Bacillus subtilis

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C:Accession: G69731

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruschini, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, M.; Sadaie, Y.; Sato, T.; Scanlon,

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K

A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: G69731

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-311 <KUN>

A:Cross-references: UNIPROT:P54327; UNIPARC:UPI000006027D; GB:Z99110; GB:AL009126; NID:9

A:Experimental source: strain 168

C:Genetics:

A:Gene: xkdG

Query Match 38.8%; Score 47; DB 2; Length 311;
Best Local Similarity 53.3%; Pred. No. 14;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 7 FANYTAHGETAWAD 21
|:|:|:|:|:|:
Db 193 PRFYTSHGLEVEWKD 207

RESULT 9

C81675

polymorphic membrane protein B/C family TC0694 [imported] - Chlamydia muridarum (strain
C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C:Accession: C81675

R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,

Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A:Reference number: A81500; MUID:20150255; PMID:10684935

A:Accession: C81675

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1672 <TET>

A:Cross-references: UNIPROT:Q9PUY2; UNIPARC:UPI0000057A0F; GB:AE002338; GB:AE002160; NID

A:Experimental source: strain Ni9g (MoPn)

C:Genetics:

A:Gene: TC0694

Query Match 38.8%; Score 47; DB 2; Length 1672;
Best Local Similarity 50.0%; Pred. No. 88;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 LNTGVSFANYTAHGETAWA 20
|:|:|:|:|:|:
Db 719 LKSLGSLFSNNTANSSSTGVA 738

RESULT 10

F71248

probable proteasome beta subunit - Pyrococcus horikoshii

C:Species: Pyrococcus horikoshii

C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004

C:Accession: F71248

R;Kawarayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi

DNA Res. 5, 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic

A:Reference number: A71000; MUID:98344137; PMID:9679194

A:Accession: F71248

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-197 <KAW>

A:Cross-references: UNIPROT:O57983; UNIPARC:UPI00000667C2; GB:AP000001; NID:g3236128; NID

A:Experimental source: strain OT3

A:Note: this accession replaces an interim accession for a sequence replaced by GenBank

C:Genetics:

A:Gene: PH0245

Query Match 38.0%; Score 46; DB 2; Length 197;
Best Local Similarity 58.8%; Pred. No. 13;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 4 GVSFANYTAHGETAWA 20

F;418/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 38.0%; Score 46; DB 2; Length 614;
Best Local Similarity 53.3%; Pred. No. 43;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5 VSFANYTAHGSETAW 19
|: ||: || ||
Db 94 VALGQYTSQGSVTAW 108

RESULT 15

A41757
betaine transport protein, renal - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: A41757
R;Yamauchi, A.; Uchida, S.; Kwon, H.M.; Preston, A.S.; Robey, R.B.; Garcia-Perez, A.; Bu
J. Biol. Chem. 267, 649-652, 1992
A>Title: Cloning of a Na(+)- and Cl(-)-dependent betaine transporter that is regulated b
A;Reference number: A41757; MUID:92112724; PMID:1370453
A;Accession: A41757
A:Molecule type: mRNA
A;Residues: 1-614 <YAM>
A;Cross-references: UNIPROT:P27799; UNIPARC:UPI00001354A6; GB:M80403; NID:g164031; PIDN:
C;Superfamily: gamma-aminobutyric acid transporter
C;Keywords: membrane protein

Query Match 38.0%; Score 46; DB 2; Length 614;
Best Local Similarity 53.3%; Pred. No. 43;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5 VSFANYTAHGSETAW 19
|: ||: || ||
Db 94 VALGQYTSQGSVTAW 108

Search completed: August 25, 2006, 18:05:14
Job time : 29.5581 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 25, 2006, 17:50:25 ; Search time 197.488 Seconds
(without alignments)
103.046 Million cell updates/sec

Title: US-10-387-977-2

Perfect score: 121

Sequence: 1 LNTGVSFANYTAHGETAWADP 22

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	121	100.0	1358	2	Q6Q4T4_PORGI
2	121	100.0	1732	2	O07442_PORGI
3	121	100.0	1732	2	O52050_PORGI
4	121	100.0	1732	2	O51817_PORGI
5	114	94.2	1358	2	P96967_PORGI
6	114	94.2	1723	2	P72194_PORGI
7	114	94.2	1723	2	P72197_PORGI
8	82	67.8	736	1	CPG2_PORGI
9	82	67.8	1706	2	O51838_PORGI
10	82	67.8	1706	2	O51839_PORGI
11	82	67.8	1706	2	Q7MRE2_PORGI
12	78	64.5	736	2	Q51844_PORGI
13	78	64.5	991	1	CPG1_PORGI
14	78	64.5	1687	2	Q9R9B7_PORGI
15	78	64.5	1704	2	O51816_PORGI
16	68.5	56.6	422	2	O51818_PORGI
17	57	47.1	468	2	Q39DM3_EURS3
18	56	46.3	468	2	Q44296_9BURK
19	56	46.3	468	2	Q4LK93_burkholderi
20	56	46.3	471	2	Q39L14_BURS3
21	55	45.5	1123	2	Q7MXX2_PORGI
22	54	44.6	458	2	Q3JV75_EURP1
23	54	44.6	458	2	Q63W19_EURS
24	53	43.8	459	2	Q2T0H9_BURTH
25	53	43.8	926	2	Q4AIR5_9CHLB
26	52	43.0	459	2	Q4BEX8_BURVI
27	51	42.1	527	2	Q12668_rhodotorula
28	51	42.1	847	2	Q90W12_ONCMY
29	51	42.1	893	2	Q6LFF5_PHOPR
30	50	41.3	297	2	Q3X551_rubrobacter
31	50	41.3	359	2	Q89N78_bradyrhizob

32	50	41.3	459	2	Q3FLJ2_9BURK	Q3FLJ2_burkholderi
33	50	41.3	475	2	Q3RT78_RALME	Q3RT78_ralstonia m
34	50	41.3	1175	2	Q5QJV8_9DIPT	Q5QJV8_culex trita
35	50	41.3	1473	2	Q7FA96_ORYSA	Q7FA96_oryza sativ
36	50	41.3	1528	2	Q7XKP3_ORYSA	Q7XKP3_oryza sativ
37	50	41.3	1535	2	Q53N07_ORYSA	Q53N07_oryza sativ
38	50	41.3	1735	2	Q6UU96_ORYSA	Q6UU96_oryza sativ
39	49.5	40.9	271	2	Q2JYD0_RHIET	Q2JYD0_rhizobium e
40	49.5	40.9	545	2	Q5CIL2_LACUD	Q5CIL2_lactococcus
41	49	40.5	527	2	Q52PM7_9CAUD	Q52PM7_xanthomonas
42	49	40.5	798	2	Q6LL21_PHOPR	Q6LL21_photobacter
43	49	40.5	951	2	Q2X684_9GAMM	Q2X684_shewanella
44	49	40.5	951	2	Q2ZNF2_SHEPU	Q2ZNF2_shewanella
45	49	40.5	1598	2	Q7XMF1_ORYSA	Q7XMF1_oryza sativ

ALIGNMENTS

RESULT 1
Q6Q4T4_PORGI
ID Q6Q4T4_PORGI PRELIMINARY; PRT; 1358 AA.
AC Q6Q4T4;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Lys-gingipain (Fragment).
GN Name=kpg;
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=M83variant;
RX PubMed=15297553; DOI=10.1128/JCM.42.8.3873-3876.2004;
RA Nadkarni M.A., Nguyen K.A., Chapple C.C., DeCarlo A.A., Jacques N.A., Hunter N.;
RT "Distribution of Porphyromonas gingivalis Biotypes Defined by Alleles of the kpg (Lys-Gingipain) Gene.";
RL J. Clin. Microbiol. 42:3873-3876(2004).
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EMBL: AY559244; AAS68176.1; -: Genomic DNA.
DR GO:0008234; F:cysteine-type peptidase activity; IEA.
DR GO:0009405; P:pathogenesis; IEA.
DR GO:0006508; P:proteolysis; IEA.
DR InterPro: IPR001769; Cleaved adhesin.
DR InterPro: IPR005536; Peptidase_C25.
DR InterPro: IPR005536; Peptidase_C25_C.
DR Pfam: PF07675; Cleaved_Adhesin; 3.
DR Pfam: PF01364; Peptidase_C25; 1.
DR Pfam: PF03785; Peptidase_C25_C; 1.
FT NON_TER 1
FT NON_TER 1358 1358
SQ SEQUENCE 1358 AA; 146666 MW; 4B6A5D52729BFECB CRC64;

Query Match 100.0%; Score 121; DB 2; Length 1358;
Best Local Similarity 100.0%; Pred. No. 8.5e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNTGVSFANYTAHGETAWADP 22
|||||
Db 79 LNTGVSFANYTAHGETAWADP 100

RESULT 2
O07442_PORGI
ID O07442_PORGI PRELIMINARY; PRT; 1732 AA.
AC O07442;
DT 01-JUL-1997, integrated into UniProtKB/TrEMBL.

```

DT 01-JUL-1997, sequence version 1.
DT 07-FEB-2006, entry version 27.
DE Lysine-specific cysteine proteinase.
GN Name=prtk;
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=W50;
RX MEDLINE=99235907; PubMed=10219167;
RX DOI=10.1034/j.1399-302X.1999.140203.x;
RA Slakeski N., Cleal S.M., Bhogal P.S., Reynolds E.C.;
RT "Characterization of a Porphyromonas gingivalis gene prtk that encodes
RT a lysine-specific cysteine proteinase and three sequence-related
RT adhesins.";
RL Oral Microbiol. Immunol. 14:92-97(1999).
CC -----
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CC -----
DR EMBL; U75366; AAB60809.1; -; Genomic_DNA.
DR MEROPS; C25.002; -.
DR GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR011628; Cleaved_adhesin.
DR InterPro; IPR000977; DNA_ligase.
DR InterPro; IPR001769; Peptidase_C25.
DR InterPro; IPR005536; Peptidase_C25_C.
DR Pfam; PF07675; Cleaved Adhesin; 3..
DR Pfam; PF01364; Peptidase_C25; 1..
DR Pfam; PF03785; Peptidase_C25_C; 1.
DR PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN 1.
SQ SEQUENCE 1732 AA; 187915 MW; 45DSB9137391703 CRC64;

Query Match 100.0%; Score 121; DB 2; Length 1732;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNTGVSFANYTAHGETAWADP 22
Db 432 LNTGVSFANYTAHGETAWADP 453

RESULT 3
O52050 PORGI PRELIMINARY; PRT; 1732 AA.
AC O52050;
DT 01-JUN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JUN-1998, sequence version 1.
DE Lysine specific cysteine protease.
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=W83;
RX MEDLINE=98298016; PubMed=9632563;
RA Lewis J.P., Macrina F.L.;
RT "IS195, an insertion sequence-like element associated with protease
RT genes in Porphyromonas gingivalis.";
RL Infect. Immun. 66:3035-3042(1998).
CC -----
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CC -----
DR EMBL; AF017059; AAC26523.1; -; Genomic_DNA.
DR MEROPS; C25.002; -.
DR GO; GO:0008234; F:cysteine-type peptidase activity; IEA.

```

```

DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR011628; Cleaved_adhesin.
DR InterPro; IPR000977; DNA_ligase.
DR InterPro; IPR001769; Peptidase_C25_C.
DR InterPro; IPR005536; Peptidase_C25_C.
DR Pfam; PF07675; Cleaved Adhesin; 3..
DR Pfam; PF01364; Peptidase_C25; 1.
DR Pfam; PF03785; Peptidase_C25_C; 1.
DR PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN 1.
KW Protease.
SQ SEQUENCE 1732 AA; 187932 MW; B2337463D5C85EA5 CRC64;

Query Match 100.0%; Score 121; DB 2; Length 1732;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNTGVSFANYTAHGETAWADP 22
Db 432 LNTGVSFANYTAHGETAWADP 453

RESULT 4
Q51817 PORGI PRELIMINARY; PRT; 1732 AA.
AC Q51817;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 28.
DE Porphyropain.
GN Name=prtp;
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=W12;
RX MEDLINE=96213011; PubMed=8631659;
RA Barkocy-Gallagher G.A., Han N., Patti J.M., Whitlock J.,
RA Progulski-Fox A., Lantz M.S.;
RT "Analysis of the prtp gene encoding porphyropain, a cysteine proteinase
RT of Porphyromonas gingivalis.";
RL J. Bacteriol. 178:2734-2741(1996).
CC -----
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CC -----
DR EMBL; U42210; AAB06565.1; -; Genomic_DNA.
DR PIR; T30836; T30836.
DR MEROPS; C25.002; -.
DR GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR011628; Cleaved_adhesin.
DR InterPro; IPR000977; DNA_ligase.
DR InterPro; IPR001769; Peptidase_C25.
DR InterPro; IPR005536; Peptidase_C25_C.
DR Pfam; PF07675; Cleaved Adhesin; 3..
DR Pfam; PF01364; Peptidase_C25; 1.
DR Pfam; PF03785; Peptidase_C25_C; 1.
DR PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN 1.
SQ SEQUENCE 1732 AA; 187875 MW; 654271DBEF7BCAE4 CRC64;

Query Match 100.0%; Score 121; DB 2; Length 1732;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNTGVSFANYTAHGETAWADP 22
Db 432 LNTGVSFANYTAHGETAWADP 453

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DR	EMBL; D83258; BAA11870.1; -; Genomic_DNA.
DR	MEROPS; C25_002; --
DR	GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR	GO; GO:0009405; P:pathogenesis; IEA.
DR	GO; GO:0006508; P:proteolysis; IEA.
DR	InterPro; IPR011628; Cleaved adhesin.
DR	InterPro; IPR000977; DNA_ligase.
DR	InterPro; IPR001769; Peptidase_C25.
DR	InterPro; IPR005536; Peptidase_C25_C.
DR	Pfam; PF07675; Cleaved Adhesin; 3.
DR	Pfam; PF01364; Peptidase_C25; 1.
DR	Pfam; PF03785; Peptidase_C25; 1.
DR	PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN 1.
SQ	SEQUENCE 1723 AA; 187262 MW; 5628963D251493EB CRC64;
Query Match 94.2%; Score 114; DB 2; Length 1723;	
Best Local Similarity 90.9%; Pred. No. 1.4e-08;	
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps	
Qy	1 LNTGVSPFANYTAHGETAWADP 22
Dd	432 LNTGCVGFANYTAHGETSWADP 453
RESULT 7	
ID	P72197_PORGI PRELIMINARY; PRT; 1723 AA.
AC	P72197;
DT	01-FEB-1997, integrated into UniProtKB/TrEMBL.
DT	01-FEB-1997, sequence version 1.
DT	07-FEB-2006, entry version 24.
DE	Lys-gingipain.
GN	Name=Kgp;
OS	Porphyromonas gingivalis (Bacteroides gingivalis).
OC	Bacteria; Bacteroidetes; Bacteroidetes (Class); Bacteroidales;
OC	Porphyromonadaceae; Porphyromonas.
OX	NCBI_TaxID=837;
RP	[1]
RN	NUCLEOTIDE SEQUENCE.
RA	Pavloff N., Pemberton P.A., Potempa J., Chen W.-C.A., Pike R.N.,
RA	Prochazka V., Kiefer M.C., Travis J., Barr P.J.;
RL	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
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CC	-----
EMBL; U54691; AAA99810.1; -; Genomic_DNA.	
DR	MEROPS; C25_002; --
DR	GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR	GO; GO:0009405; P:pathogenesis; IEA.
DR	GO; GO:0006508; P:proteolysis; IEA.
DR	InterPro; IPR011628; Cleaved adhesin.
DR	InterPro; IPR000977; DNA_ligase.
DR	InterPro; IPR001769; Peptidase_C25.
DR	InterPro; IPR005536; Peptidase_C25_C.
DR	Pfam; PF07675; Cleaved Adhesin; 2.
DR	Pfam; PF01364; Peptidase_C25; 1.
DR	Pfam; PF03785; Peptidase_C25; 1.
DR	PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN 1.
SQ	SEQUENCE 1723 AA; 186832 MW; 4508A7E50197CEBD CRC64;
Query Match 94.2%; Score 114; DB 2; Length 1723;	
Best Local Similarity 90.9%; Pred. No. 1.4e-08;	
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps	
Qy	1 LNTGVSPFANYTAHGETAWADP 22
Dd	432 LNTGCVGFANYTAHGETSWADP 453
RESULT 8	
CPG2_PORGI	STANDARD; PRT; 736 AA.

AC P95493; O33441;
DT 15-DEC-1998, integrated into UniProtKB/Swiss-Prot.
DT 03-OCT-2003, sequence version 2.
DT 07-MAR-2006, entry version 53.
DE Gingipain R2 precursor (EC 3.4.22.37) (Gingipain 2) (Arg-gingipain)
DE (RGP-2).
DE
DE Name:rgpB; Synonyms:ptrII, rgp2; OrderedLocusNames=PG0506;
GN Porphyromonas gingivalis (Bacteroides gingivalis).
OS Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND PROTEIN SEQUENCE OF 230-651.
RC STRAIN=HG66;
RX MEDLINE=98370998; PubMed=9705298; DOI=10.1074/jbc.273.34.21648;
RA Potempa J., Mikolajczyk-Pawlinska J., Brassell D., Nelson D.,
RA Thøgersen I.B., Enghild J.J., Travis J.;
RT "Comparative properties of two cysteine proteinases (gingipains R),
RT the products of two related but individual genes of Porphyromonas
RT gingivalis.";
RL J. Biol. Chem. 273:21648-21657(1998).
RN [2]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=W50;
RX MEDLINE=98304082; PubMed=9639929;
RA Slakeski N., Bhogal P.S., O'Brien-Simpson N.M., Reynolds E.C.;
RT "Characterization of a second cell-associated Arg-specific cysteine
RT proteinase of Porphyromonas gingivalis and identification of an
RT adhesin-binding motif involved in association of the prtr and prtK
RT proteinases and adhesins into large complexes.";
RL Microbiology 144:1583-1592(1998).
RN [3]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=W83;
RX MEDLINE=22829867; PubMed=12949112;
RX DOI=10.1128/JB.185.18.5591-5601.2003;
RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
RA Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
RA Dewhirst F.E., Fraser C.M.;
RT "Complete genome sequence of the oral pathogenic bacterium
RT Porphyromonas gingivalis strain W83.";
RL J. Bacteriol. 185:5591-5601(2003).
RN [4]
RN ENZYME REGULATION.
RX PubMed=11179305; DOI=10.1128/IAI.69.3.1402-1408.2001;
RA Gusman H., Travis J., Helmerhorst E.J., Potempa J., Troxler R.F.,
RA Oppenheim F.G.;
RT "Salivary histatin 5 is an inhibitor of both host and bacterial
RT enzymes implicated in periodontal disease.";
RL Infect. Immun. 69:1402-1408(2001).
RN [5]
RN X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RX MEDLINE=99452753; PubMed=10523290; DOI=10.1093/emboj/18.20.5453;
RA Eichinger A., Beisel H.-G., Jacob U., Huber R., Medrano F.-J.,
RA Bambula A., Potempa J., Travis J., Bode W.;
RT "Crystal structure of gingipain R: an Arg-specific bacterial cysteine
RT proteinase with a caspase-like fold.";
RL EMBO J. 18:5453-5462(1999).
CC -!- FUNCTION: Thiol protease which is believed to participate in
CC intracellular degradation and turnover of proteins. Its
CC proteolytic activity is a major factor in both periodontal tissue
CC destruction and in bacterial host defense mechanisms. Activates
CC complement C3 and C5 (By similarity).
CC -!- CATALYTIC ACTIVITY: Hydrolysis of proteins and small molecule
CC substrates, with a preference for Arg in P1.
CC -!- ENZYME REGULATION: Inhibited by human histatin-3 1/24 (histatin-
CC 5).
CC -!- SIMILARITY: Belongs to the peptidase C25 family.
CC
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CC
DR EMBL; U85038; AAB41892.1; -, Genomic DNA.
DR EMBL; AF007124; AAC26371.1; -, Genomic DNA.
DR EMBL; AE015924; AAO65700.1; -, Genomic DNA.
DR PDB; 1CVR; X-ray; A=230-664.
DR MEROPS; C25.003; -.
DR GenomeReviews; AE015924_GR; PG0506.
DR TIGR; PG0506; -.
DR BioCyc; PGIN242619; PG0506-MONOMER; -.
DR InterPro; IPR001769; Peptidase_C25.
DR InterPro; IPR005536; Peptidase_C25_C.
DR InterPro; IPR012600; Propeptide_C25.
DR Pfam; PF01364; Peptidase_C25; 1.
DR Pfam; PF03785; Peptidase_C25_C; 1.
DR Pfam; PF08126; Propeptide_C25; 1.
DR 3D-structure; Calcium; Complete proteome; Direct protein sequencing;
KW Hydrolase; Protease; Signal; Thiol protease; Virulence; Zymogen.
FT SIGNAL 1 24
FT PROPEP 25 229
FT FTId=PRO 0000026535.
FT Gingipain R2.
FT //FTId=PRO 0000026536.
FT Proton donor.
FT Nucleophile.
FT G -> D (in Ref. 1).
FT P -> A (in Ref. 1).
FT E -> G (in Ref. 1).
FT E -> K (in Ref. 1).
FT I -> V (in Ref. 1).
FT A -> V (in Ref. 1).
FT YNV -> FSM (in Ref. 1).
FT N -> D (in Ref. 1).
FT S -> Y (in Ref. 1).
FT S -> P (in Ref. 1).
FT K -> N (in Ref. 1).
FT K -> E (in Ref. 1).
FT CHAIN 230 736
FT ACT_SITE 440
FT ACT_SITE 473
FT CONFLICT 58
FT CONFLICT 246
FT CONFLICT 251
FT CONFLICT 254
FT CONFLICT 398
FT CONFLICT 435
FT CONFLICT 480
FT CONFLICT 510
FT CONFLICT 512
FT CONFLICT 515
FT CONFLICT 560
FT CONFLICT 582
FT TURN 237
FT STRAND 240
FT HELIX 247
FT HELIX 252
FT TURN 263
FT STRAND 266
FT HELIX 271
FT STRAND 272
FT STRAND 277
FT HELIX 281
FT STRAND 284
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FT STRAND 299
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FT STRAND 409
FT HELIX 421
FT STRAND 433

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FT STRAND 441 441
FT STRAND 443 446
FT TURN 447 449
FT STRAND 452 452
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FT TURN 478 479
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FT HELIX 539 564
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FT STRAND 578 578
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FT STRAND 585 586
FT STRAND 589 592
FT TURN 593 594
FT STRAND 596 604
FT TURN 605 606
FT STRAND 608 613
FT TURN 614 615
FT STRAND 616 622
FT STRAND 624 624
FT TURN 625 626
FT STRAND 627 631
FT STRAND 633 634
FT TURN 637 638
FT STRAND 640 647
FT TURN 649 650
FT STRAND 651 651
FT STRAND 654 661
SQ SEQUENCE 736 AA; 80967 MW; C848DD3FAB420833 CRC64;

Query Match 67.8%; Score 82; DB 1; Length 736;
Best Local Similarity 77.8%; Pred. No. 0.00069;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 NTGVSFANYTAHGSETAW 19
Db 429 NGGISLANYTGHGSETAW 446
| | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | |

RESULT 9
Q51838_PORGI PRELIMINARY; PRT; 1706 AA.
AC Q51838;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1997, sequence version 2.
DT 07-FEB-2006, entry version 26.
DE Protease precursor.
GN Name=prpR1;
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=W50;

Query Match 67.8%; Score 82; DB 2; Length 1706;
Best Local Similarity 77.8%; Pred. No. 0.0017;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 NTGVSFANYTAHGSETAW 19
Db 427 NGGISLANYTGHGSETAW 444
| | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | |

RESULT 10
Q51839_PORGI PRELIMINARY; PRT; 1706 AA.
AC Q51839; Q51840;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 27.
DE Arginine-specific thiol protease precursor.
GN Name=prtr;
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=W50;
RX MEDLINE=95160709; PubMed=7857299;
RA Kirsbaum L., Sotiropoulos C., Jackson C., Cleal S., Slakeski N.,
RA Reynolds E.C.;
RT "Complete nucleotide sequence of a gene prtr of Porphyromonas
gingivalis W50 encoding a 132 kDa protein that contains an arginine-
specific thiol endopeptidase domain and a haemagglutinin domain.";
RL Biochem. Biophys. Res. Commun. 207:424-431(1995).
RN [2]
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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=W50;
RC MEDLINE=96311339; PubMed=8713096; DOI=10.1006/bbrc.1996.1073;
RX Slakeski N., Cleal S.M., Reynolds E.C.;
RT "Characterization of a Porphyromonas gingivalis gene prTR that encodes
RT an arginine-specific thiol proteinase and multiple adhesins.";
RT Biochem. Biophys. Res. Commun. 224:605-610(1996).
RN [3]
RN NUCLEOTIDE SEQUENCE OF 212-455.
RP STRAIN=W50;
RC STRAIN=W50;
RC Reynolds E.;
RA Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
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CC -----
EMBL; L26341; AAC18876.1; -; Genomic_DNA.
DR HSSP; P95493; 1CVR.
DR SMR; Q51839; 228-655.
DR GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR011628; Cleaved adhesin.
DR InterPro; IPR000977; DNA_ligase.
DR InterPro; IPR001769; Peptidase_C25.
DR InterPro; IPR005536; Peptidase_C25_C.
DR InterPro; IPR012600; Propeptide_C25.
DR Pfam; PF07675; Cleaved Adhesin_2.
DR Pfam; PF01364; Peptidase_C25_1.
DR Pfam; PF03785; Peptidase_C25_1.
DR Pfam; PF08126; Propeptide_C25_1.
DR PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN_1.
FT SIGNAL
FT CHAIN
FT CHAIN 228 1706 arginine-specific thiol protease.
SQ SEQUENCE 1706 AA; 185627 MW; E8BDF07C9813B844 CRC64;

Query Match 67.8%; Score 82; DB 2; Length 1706;
Best Local Similarity 77.8%; Pred. No. 0.0017;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps

Qy 2 NTGVSFANYTAHGSETAW 19
Db 427 NGGISLANYTGHGSETAW 444

RESULT 11
ID Q7MTE2 PORGI PRELIMINARY; PRT; 1706 AA.
AC Q7MTE2;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DE 07-FEB-2006, entry version 12.
DE Hemagglutinin protein Hage.
GN Name=hAgE; OrderedLocNames=PG2024; ORFNames=PG_2024;
OS Porphyromonas gingivalis [Bacteroides gingivalis].
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OC NCBI_TaxID=837;
OC [1]
RN RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=W83;
RX MEDLINE=22829867; PubMed=12949112;
RX DOI=10.1128/JB.185.18.5591-5601.2003;
RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
RA Granger D., Tetzelin H., Dong H., Galvin J.L., Duncan M.J.,
RA Dewhirst F.E., Fraser C.M.;
RT "Complete genome sequence of the oral pathogenic bacterium
RT Porphyromonas gingivalis strain W83.";
RL J. Bacteriol. 185:5591-5601(2003).
CC -----

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EMBL; AE015924; AAO66991.1; -; Genomic_DNA.
HSSP; P95493; 1CVR.
SNR; Q7MTE2; 228-655.
TIGR; PG2024; -.
DR BLOCYC; PGIN242619.PG2024-MONOMER; -;
DR GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR011628; Cleaved_adhesin.
DR InterPro; IPR000977; DNA_ligase.
DR InterPro; IPR001769; Peptidase_C25.
DR InterPro; IPR055536; Peptidase_C25_C.
DR InterPro; IPR012600; Propeptide_C25.
DR Pfam; PF07675; Cleaved_Adhesin_2.
DR Pfam; PF01364; Peptidase_C25_1.
DR Pfam; PF03785; Peptidase_C25_C; 1.
DR Pfam; PF08126; Propeptide_C25; 1.
DR PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWNW_1.
KW Complete proteome.
SQ SEQUENCE 1706 AA; 185673 MW; 6FE9B83AA98A2815 CRC64;

Query Match 67.8%; Score 82; DB 2; Length 1706;
Best Local Similarity 77.8%; Pred.No. 0.0017;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NTGVSFANYTAHGSETAW 19
| | : | |||||
Db 427 NGGISLANYTGHSGETAW 444

RESULT 12

Q51844_PORGI PRELIMINARY; PRT; 736 AA.
ID Q51844;
AC Q51844;
DT 01-NOV-1996, integrated into UniprotKB/TREMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE Arginine-specific cysteine proteinase (Arg-gingipain).
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC33277;
RX MEDLINE=96007508; PubMed=7559528; DOI=10.1074/jbc.270.40.23619;
RA Nakayama K., Kadowaki T., Okamoto K., Yamamoto K.;
RT "Construction and characterization of arginine-specific cysteine
RT proteinase (Arg-gingipain)-deficient mutants of Porphyromonas
RT gingivalis. Evidence for significant contribution of Arg-gingipain to
RT virulence.";
RT J. Biol. Chem. 270:23619-23626(1995).
RN [2]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC33277;
RX MEDLINE=97276476; PubMed=9130229;
RA Nakayama K.;
RT "Domain-specific rearrangement between the two Arg-gingipain-encoding
RT genes in Porphyromonas gingivalis: possible involvement of
RL nonreciprocal recombination.";
RL Microbiol. Immunol. 41:185-196(1997).

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EMBL; D64081; BRA10963.1; -; Genomic_DNA.
HSSP; P95493; 1CVR.
DR SMR; Q51844; 230-661.
DR GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.

DR	InterPro; IPRO12600; Propeptide_C25.
DR	Pfam; PF01364; Peptidase_C25; 1.
DR	Pfam; PF03785; Peptidase_C25_C; 1.
DR	Pfam; PF08126; Propeptide_C25; 1.
DR	Calcium; Direct protein sequencing; Hydrolase; Protease; Signal;
KW	Thiol protease; Virulence; Zymogen.
FT	SIGNAL 1 24
FT	PROPEP 25 227
FT	
FT	CHAIN 228 991 /FTId=PRO_0000026533. Gingipain R1.
FT	
FT	ACT_SITE 438 438 /FTId=PRO_0000026534. Proton donor (By similarity).
FT	ACT_SITE 471 471 Nucleophile (By similarity).
FT	CONFLICT 264 265 RT -> TK (in Ref. 2).
SQ	SEQUENCE 991 AA; 108782 MW; 03EE3F43CEBE2544 CRC64;
Query Match	64.5%; Score 78; DB 1; Length 991;
Best Local Similarity	72.2%; Pred. No. 0.0041;
Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0	
QY	2 NTGVSFANYTAHGSETAW 19 :
Db	427 NGGISLVNYTGHGSETAW 444
RESULT 14	
Q9R9B7_PORGI	
ID Q9R9B7_PORGI PRELIMINARY; PRT; 1687 AA.	
AC Q9R9B7;	
DC 01-MAY-2000, integrated into UniProtKB/TREMBL.	
DT 01-MAY-2000, sequence version 1.	
DT 07-FEB-2006, entry version 19.	
DE Hemagglutinin/protease.	
GN Name;haige;	
OS Porphyromonas gingivalis (Bacteroides gingivalis).	
OC Bacteria; Bacteroidetes; Bacteroidales;	
OC Porphyromonadaceae; Porphyromonas.	
OX NCBI_TaxID=837;	
RN [1]	
RP NUCLEOTIDE SEQUENCE.	
RC STRAIN=381;	
RA Han N., Dong H., Progulske-Fox A.;	
RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.	
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CC -----	
DR EMBL; AF026946; AACD01810.1; -; Genomic_DNA.	
DR HSSP; P95493; 1CVR.	
DR SMR; Q9R9B7; 209-636.	
DR GO; GO:0008234; F:cysteine-type peptidase activity; IEA.	
DR GO; GO:0009405; P:pathogenesis; IEA.	
DR GO; GO:0006508; P:proteolysis; IEA.	
DR InterPro; IPR011628; Cleaved_adhesin.	
DR InterPro; IPR000977; DNA_ligase.	
DR InterPro; IPR001769; Peptidase_C25.	
DR InterPro; IPR005536; Peptidase_C25_C.	
DR InterPro; IPR012600; Propeptide_C25.	
DR Pfam; PF07675; Cleaved Adhesin; 2.	
DR Pfam; PF01364; Peptidase_C25; 1.	
DR Pfam; PF03785; Peptidase_C25_C; 1.	
DR Pfam; PF08126; Propeptide_C25; 1.	
DR PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN_1.	
KW Protease.	
SQ SEQUENCE 1687 AA; 183703 MW; D085B516A399FE70 CRC64;	
Query Match	64.5%; Score 78; DB 2; Length 1687;
Best Local Similarity	72.2%; Pred. No. 0.0074;
Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0	
QY	2 NTGVSFANYTAHGSETAW 19 :
Db	408 NGGISLVNYTGHGSETAW 425

Mon Aug 28 11:30:42 2006

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RESULT 15
Q51816 PORGI
ID Q51816 PORGI PRELIMINARY; PRT; 1704 AA.
AC Q51816
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE Arg-gingipain-1 proteinase.
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_taxid=837;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95138080; PubMed=7836351; DOI=10.1074/jbc.270.3.1007;
RA Pavloff N., Potempa J., Pike R.N., Prochazka V., Kiefer M.C.,
RA Travis J., Barr P.J.;
RT "Molecular cloning and structural characterization of the Arg-
RT gingipain proteinase of Porphyromonas gingivalis. Biosynthesis as a
RT proteinase-adhesin polypeptide."
RL J. Biol. Chem. 270:1007-1010(1995).
CC -----
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CC -----
DR EMBL; U15282; AAA69539.1; -; Genomic_DNA.
DR PIR; A55426; A55426.
DR HSP; P95493; LCVR.
DR SMR; Q51816; 228-655.
DR GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR011628; Cleaved adhesin.
DR InterPro; IPR000977; DNA ligase.
DR InterPro; IPR001769; Peptidase_C25.
DR InterPro; IPR005536; Peptidase_C25_C.
DR InterPro; IPR012600; Propeptide_C25.
DR Pfam; PF07675; Cleaved Adhesin; 2.
DR Pfam; PF01364; Peptidase_C25; 1.
DR Pfam; PF03785; Peptidase_C25_C; 1.
DR Pfam; PF08126; Propeptide_C25; 1.
DR PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN 1.
FT CHAIN 228 719 mature 50-kDa cysteine proteinase
FT CHAIN 228 719 gingipain.
SQ SEQUENCE 1704 AA; 185437 MW; 6A34B40131C2A676 CRC64;
Query Match 64.5%; Score 78; DB 2; Length 1704;
Best Local Similarity 72.2%; Pred. No. 0.0075;
Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 2 NTGVSFANYTAHGSSETAW 19
Db 427 NGGISLVNYTGHGSETAW 444

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Search completed: August 25, 2006, 18:04:21
Job time : 203.488 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 26, 2006, 17:03:02 ; Search time 137 Seconds
(without alignments)
410.514 Million cell updates/sec

Title: US-10-018-892-3
Perfect score: 662
Sequence: 1 AAQNTTSANWSQDPFGTGA.....KSTLPAGTFTATFYVQYQN 128

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 21:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*
9: Geneseqp2005s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query		Length	DB	ID	Description
			Match	%				
1	662	100.0	128	4	AAB31431		Aab31431 Amino aci	
2	662	100.0	144	2	AAB47082		Aaw47082 Salmonell	
3	662	100.0	165	2	AAW23571		Aaw23571 Salmonell	
4	662	100.0	165	4	AAB31430		Aab31430 Amino aci	
5	662	100.0	176	2	AAR23731		Aar23731 Fimbrial	
6	662	100.0	176	2	AAR42173		Aar42173 SE fimbri	
7	662	100.0	180	2	AAR47081		Aaw47081 Salmonell	
8	653	98.6	165	2	AAR62752		Aar62752 Sefa sequ	
9	93.5	14.1	431	3	AAG32324		Aag32324 Arabidops	
10	93.5	14.1	431	3	AAG09613		Aag09613 Arabidops	
11	93.5	14.1	431	8	ADI43535		Adi43535 Plant tra	
12	93.5	14.1	431	9	AEA26765		Aea26765 Stress to	
13	93.5	14.1	435	3	AAG09612		Ang09612 Arabidops	
14	93.5	14.1	440	3	AAG49463		Aag49463 Arabidops	
15	93.5	14.1	443	3	AAG49462		Aag49462 Arabidops	
16	91.5	13.8	2468	6	ABU38411		Abu38411 Protein e	
17	91.5	13.8	2468	6	ABP59933		Abp59933 Microbial	
18	88.5	13.4	439	8	ADY25088		Ady25088 Plant ful	
19	87.5	13.2	328	2	AAR39298		Aar39298 Maize dwa	
20	86.5	13.1	2736	7	ABO81481		AbO81481 Pseudomon	
21	83.5	12.6	219	8	ADJ22824		Adj22824 Plant ful	
22	83.5	12.6	346	8	ADJ34954		Adj34954 Xylanase	
23	83	12.5	524	6	ABU34449		Abu34449 protein e	
24	83	12.5	549	4	AAG81139		Aag81139 Mycobacte	

Cellcore

ABJ04694 Mycobacte
ABU36587 Protein e
Aav01303 Human tro
Abo77692 Pseudomon
Aaw10344 Maize dwa
Adj35006 Xylanase
Abo70421 Pseudomon
Abb57364 Mouse isc
Adw44460 Murine pr
Abu34624 Protein e
Abu36440 Protein e
Aeb91424 Microbial
Abo58582 Human gen
ABU20015 Protein e
Ada55641 Human pro
Abu19388 Protein e
Adu07619 Amino aci
Abu19799 Protein e
Adj70227 Human hea
Abu21833 Protein e
Adq65871 Novel hum

25 83 12.5 549 5 ABJ04694
26 83 12.5 549 6 ABU36587
27 83 12.5 660 2 AAV01303
28 82.5 12.5 1415 7 ABO77692
29 82.5 12.5 2763 2 AAW10344
30 82 12.4 347 8 ADJ35006
31 81.5 12.3 693 7 ABO70421
32 81.5 12.3 1373 5 ABB57364
33 81.5 12.3 1373 9 ADM44460
34 81.5 12.3 1721 6 ABU34624
35 81.5 12.3 2204 6 ABU36440
36 81.5 12.3 2204 9 AEB91424
37 81 12.2 329 8 ABO58582
38 81 12.2 334 6 ABU20015
39 81 12.2 605 6 ADA55641
40 81 12.2 827 6 ABU19388
41 80.5 12.2 558 8 ADU07619
42 80.5 12.2 595 6 ABU19799
43 80.5 12.2 999 7 ADJ70227
44 80.5 12.2 1862 6 ABU21833
45 79.5 12.0 570 8 ADQ65871

ALIGNMENTS

RESULT 1
AAB31431
ID AAB31431 standard; peptide; 128 AA.
AC AAB31431;
XX
DT 20-APR-2001 (first entry)
XX
DE Amino acid sequence of the C128 fragment of the Sef14 antigen.
KW C128 fragment; fimbrial Sef14 antigen; fimbrial protein;
KW flagellin protein; poultry.
XX Salmonella enteritidis.
OS
PN WO200078995-A1.
XX
PD 28-DEC-2000.
XX
PF 22-JUN-1999; 99WO-SG000061.
XX
PR 22-JUN-1999; 99WO-SG000061.
XX (MOLE-) INST MOLECULAR AGROBIOLOGY.
XX Kwang H, Liu W, Low SS, Loh KYH;
XX WPI; 2001-071400/08.
XX
PT New method for the specific detection of Salmonella enteritidis
PT infections of poultry comprises contacting a biological sample with
PT antigenic fragments of S. enteritidis fimbrial and/or flagellin proteins.
XX Claim 18; Page 42; 49pp; English.

XX The present sequence represents the C128 fragment of the fimbrial Sef14
XX antigen of Salmonella enteritidis. The specification describes a method
XX for detecting S. enteritidis in a biological sample obtained from
XX poultry. The method comprises contacting the sample with an antigenic
XX fragment of S. enteritidis fimbrial or flagellin protein and detecting
XX the formation of a complex, where the fragment is specifically recognized
XX by S. enteritidis antibodies. The antigenic fragments are specific to
XX Salmonella enteritidis and enable specific detection of S. enteritidis
XX even in the presence of other Salmonella spp. The methods are useful for
XX the specific detection of S. enteritidis infections in biological samples
XX derived from poultry

SQ Sequence 128 AA;

Query Match 100.0%; Score 662; DB 4; Length 128;

Best Local Similarity 100.0%; Pred. No. 3e-59; Mismatches 0; Indels 0; Gaps 0;

Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAQNTTSANWSQDPGFTGPAVAAGQKVGTLSITATGPHNSVSIAGKASVSGGVATVPFV 60
 DB 1 AAQNTTSANWSQDPGFTGPAVAAGQKVGTLSITATGPHNSVSIAGKASVSGGVATVPFV 60
 QY 61 DGQGPVFRGRIQGANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTTTAT 120
 DB 61 DGQGPVFRGRIQGANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTTTAT 120
 QY 121 FYVQOYQN 128
 DB 121 FYVQOYQN 128

RESULT 2

AAW47082
ID AAW47082 standard; protein; 144 AA.

XX AC AAW47082;

DT 25-JUN-1998 (first entry)

XX Salmonella Sef14 protein fragment.

XX Sefa gene; Sef14 protein; infection; bird; chicken; turkey;
 KW anti-Salmonella enteritidis antibody; vaccine; poultry.

XX Salmonella enteritidis.

XX WO9803656-A1.

XX 29-JAN-1998.

XX 18-JUL-1997; 97MO-US012639.

XX 19-JUL-1996; 96US-0022191P.

XX (MINU) UNIV MINNESOTA.

XX Rajashekara G, Nagaraja KV, Kapur V;

XX WPI; 1998-120780/11.

XX N-PSDB; AAV13948.

XX Detecting antibodies against Salmonella enteritidis using truncated
 PT fibrillar antigen Sef14 - in immunoassays, particularly for diagnosing
 PT infection in poultry, also new antigens.

XX Claim 4; Page 23-24; 38pp; English.

XX This sequence is a fragment of the Salmonella enteritidis (Se) Sef14
 CC protein, encoded by the sefA gene. The method of the invention is for
 CC detecting antibodies (Ab) against Se in an animal by treating a sample
 CC with a truncated Sef14 antigen (Ag), lacking at least the native Sef14
 CC signal peptide, and detecting any Ab-Ag complex formed. Detection (by
 CC enzyme-linked immunosorbent assay or agglutination tests) of the Ab is
 CC used to diagnose Se infection in birds, especially chickens and turkeys.
 CC The Ag can also be used in vaccines to protect poultry against Se
 CC infection. Detection of the Ab is a sensitive, specific method for
 CC reliable and routine screening of animals. The Ag are easily produced in
 CC large quantities, in pure form, without requiring special growing
 CC conditions, so are suitable for large scale screening of flocks

XX Sequence 144 AA;

Query Match

Best Local Similarity 100.0%; Score 662; DB 2; Length 144;

Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAQNTTSANWSQDPGFTGPAVAAGQKVGTLSITATGPHNSVSIAGKASVSGGVATVPFV 60
 DB 17 AAQNTTSANWSQDPGFTGPAVAAGQKVGTLSITATGPHNSVSIAGKASVSGGVATVPFV 76
 QY 61 DGQGPVFRGRIQGANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTTTAT 120
 DB 77 DGQGPVFRGRIQGANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTTTAT 136
 QY 121 FYVQOYQN 128
 DB 137 FYVQOYQN 144

RESULT 3

AAW23571
ID AAW23571 standard; protein; 165 AA.

XX AC AAW23571;

XX 25-MAR-2003 (revised)

DT 29-SEP-1997 (first entry)

XX Salmonella enteritidis sefa.

XX Enteropathogenic bacteria; enterobacteria; S. enteritidis; antibody.

XX Salmonella enteritidis.

XX US5635617-A.

XX 03-JUN-1997.

XX 26-APR-1994; 94US-00233788.

XX 26-APR-1993; 93US-00054452.

XX (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.

XX Collinson SK, Kay WM, Doran JL;

XX WPI; 1997-309886/28.

XX N-PSDB; AAT74143.

XX Isolated Salmonella gene agfa - used for diagnosis of Salmonella or
 PT enteropathogenic bacteria of the Enterobacteria family.

XX Example 9; Fig 2; 85pp; English.

XX The present sequence represents sefa found in the sef gene cluster from
 CC Salmonella enteritidis. The nucleic acid can be used to provide
 CC diagnostic assays for Salmonella and/or enteropathogenic bacteria of the
 CC family Enterobacteria. It can also be used to provide proteins and
 CC antibodies which can be used for assays. The nucleic acid sequence can be
 CC used to provide probes or primers which can specifically hybridize to
 CC nucleic acid molecules from greater than 99% of Salmonella strains that
 CC are pathogenic to warm-blooded animals relative to nucleic acid molecules
 CC from virtually all other microbial organisms. (Updated on 25-MAR-2003 to
 CC correct PF field.)

XX Sequence 165 AA;

Query Match

Best Local Similarity 100.0%; Score 662; DB 2; Length 165;

Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAQNTTSANWSQDPGFTGPAVAAGQKVGTLSITATGPHNSVSIAGKASVSGGVATVPFV 60
 DB 38 AAQNTTSANWSQDPGFTGPAVAAGQKVGTLSITATGPHNSVSIAGKASVSGGVATVPFV 97

QY 61 DGQGPVFRGRIQGANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTTTAT 120
 DB 98 DGQGPVFRGRIQGANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTTTAT 157

Qy 121 FYVQYQN 128
 |||||
 Db 158 FYVQYQN 165

RESULT 4
 AAB31430
 ID AAB31430 standard; protein; 165 AA.

XX AAB31430;

XX 20-APR-2001 (first entry)

XX Amino acid sequence of the Sef14 antigen.

XX C128 fragment; fimbrial Sef14 antigen; fimbrial protein;
 KW flagellin protein; poultry.

XX Salmonella enteritidis.

OS WO200078995-A1.

PN 28-DEC-2000.

XX 22-JUN-1999; 99WO-SG000061.

XX 22-JUN-1999; 99WO-SG000061.

XX (MOLE-) INST MOLECULAR AGROBIOLOGY.

PA Kwang H, Liu W, Low SS, Loh KYH;

PI WPI; 2001-071400/08.

XX N-PSDB; AAF24784.

XX New method for the specific detection of Salmonella enteritidis
 PT infections of poultry comprises contacting a biological sample with
 PT antigenic fragments of S. enteritidis fimbrial and/or flagellin proteins.

XX Disclosure; Page 42; 49pp; English.

XX The present sequence represents the fimbrial Sef14 antigen of Salmonella
 CC enteritidis. The specification describes a method for detecting S.
 CC enteritidis in a biological sample obtained from poultry. The method
 CC comprises contacting the sample with an antigenic fragment of S.
 CC enteritidis fimbrial or flagellin protein and detecting the formation of
 CC a complex, where the fragment is specifically recognized by S.
 CC enteritidis antibodies. The antigenic fragments are specific to
 CC Salmonella enteritidis and enable specific detection of S. enteritidis
 CC even in the presence of other Salmonella spp. The methods are useful for
 CC the specific detection of S. enteritidis infections in biological samples
 CC derived from poultry

SQ Sequence 165 AA;

Query Match 100.0%; Score 662; DB 4; Length 165;
 Best Local Similarity 100.0%; Pred. No. 4.1e-59;
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAOQNTTSANWSQDPGFTGPAVAAGQKVGTLSTATGPHNSVSIAGKASVSGGVATVPFV 60
 |||||
 Db 38 AAOQNTTSANWSQDPGFTGPAVAAGQKVGTLSTATGPHNSVSIAGKASVSGGVATVPFV 97
 |||||

Qy 61 DGCGQPVFRGRIQGANINDQANTGIDGLAGWRVASSQETLNPVTTFGKSTLPAGTFTAT 120

Db 98 DGCGQPVFRGRIQGANINDQANTGIDGLAGWRVASSQETLNPVTTFGKSTLPAGTFTAT 157

Qy 121 FYVQYQN 128
 |||||
 Db 158 FYVQYQN 165

RESULT 5

AAR23731

ID AAR23731 standard; protein; 176 AA.

XX AAR23731;

XX 25-MAR-2003 (revised)

DT 02-NOV-1992 (first entry)

XX Fimbrial antigen.

XX S. dublin; S. moscow; fimbria-like structure; epitope.

OS Salmonella enteritidis.

PN WO9206198-A.

XX 16-APR-1992.

XX 01-OCT-1991; 91WO-GB001691.

PR 01-OCT-1990; 90GB-00021338.

PR 17-OCT-1990; 90GB-00022570.

XX (UKAG-) UK MIN AGRIC FISH.

XX Woodward MJ;

XX WPI; 1992-150883/18.

XX Detection and identification of salmonella - by using monoclonal
 PT antibodies to detect epitope(s) of these serotypes in culture.

XX Disclosure; Page 3; 48pp; English.

XX The sequence given is Salmonella enteritidis fimbrial antigen (SEFA).
 CC Salmonella organisms have fimbria-like structures on their surfaces and
 CC it has been suggested that there are antigenically distinct types of
 CC fimbria, ie. possessing specific epitopes on the fimbrial antigens. This
 CC sequence has an amino acid sequence which forms an epitope on the fimbria
 CC "in vivo" which is specifically encoded by DNA of the species S.
 CC enteritidis, and some strains of the species S. dublin and S. moscow but
 CC which is apparently absent in virtually all other serotypes. This
 CC antigen can be used for testing for the presence of Salmonella
 CC microorganisms in clinical samples such as animal remains or prods., food
 CC samples and infected environmental samples. (Updated on 25-MAR-2003 to
 CC correct PF field.)

SQ Sequence 176 AA;

Query Match 100.0%; Score 662; DB 2; Length 176;
 Best Local Similarity 100.0%; Pred. No. 4.4e-59;
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAOQNTTSANWSQDPGFTGPAVAAGQKVGTLSTATGPHNSVSIAGKASVSGGVATVPFV 60
 |||||
 Db 49 AAOQNTTSANWSQDPGFTGPAVAAGQKVGTLSTATGPHNSVSIAGKASVSGGVATVPFV 108
 |||||

Qy 61 DGCGQPVFRGRIQGANINDQANTGIDGLAGWRVASSQETLNPVTTFGKSTLPAGTFTAT 120

Db 109 DGCGQPVFRGRIQGANINDQANTGIDGLAGWRVASSQETLNPVTTFGKSTLPAGTFTAT 168

Qy 121 FYVQYQN 128

Db 169 FYVQYQN 176

RESULT 6

AAR42173

ID AAR42173 standard; protein; 176 AA.

XX AAR42173;

DT 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 03-MAY-1994 (first entry)
 XX SE fimbrial antigen (SEFA).
 DE Salmonella enteritidis fimbrial antigen; SEFA; Salmonella typhi;
 KW Salmonella dublin; serotype.
 XX Salmonella enteritidis.
 OS Salmonella typhi.
 XX WO9320231-A1.
 XX 14-OCT-1993.
 XX 29-MAR-1993; 93WO-GB000647.
 XX 31-MAR-1992; 92GB-00007069.
 XX (UKAG-) UK MIN FISHERIES & FOOD.
 XX Woodward MJ, Thorns CJ;
 XX WPI; 1993-336937/42.
 DR N-PSDB; AAQ49882.
 XX Testing for Salmonella serotypes, esp. S. Typhi - using test kit for
 PT detecting nucleic acid sequences specific to certain sero-types.
 XX Claim 2; Page 19-21; 37pp; English.
 CC DNA encoding SEFA is common to members of the enteritidis, dublin and
 CC typhi serogroups and can therefore be used in the detection of such
 CC organisms. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-
 CC AUG-2003 to correct OS field.)
 XX Sequence 176 AA;
 SQ
 Query Match 100.0%; Score 662; DB 2; Length 176;
 Best Local Similarity 100.0%; Pred. No. 4.4e-59;
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAQNTTSANWSQDPGFTGPAVAAGKVGTLTITATGPHNSVSIAGKGSVSGGVATVPFV 60
 DB 49 AAQNTTSANWSQDPGFTGPAVAAGKVGTLTITATGPHNSVSIAGKGSVSGGVATVPFV 108
 QY 61 DGQGPVFRGRIQGANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTFTAT 120
 DB 109 DGQGPVFRGRIQGANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTFTAT 168
 QY 121 FYVQOYQN 128
 DB 169 FYVQOYQN 176
 RESULT 7
 AAW47081
 ID AAW47081 standard; protein; 180 AA.
 XX
 AC AAW47081;
 XX 25-JUN-1998 (first entry)
 DE Salmonella Sef14 protein fragment.
 KW Sefa gene; Sef14 protein; infection; bird; chicken; turkey;
 KW anti-Salmonella enteritidis antibody; vaccine; poultry.
 XX Salmonella enteritidis.
 OS WO9803656-A1.
 XX

PD 29-JAN-1998.
 XX 18-JUL-1997; 97WO-US012639.
 XX 19-JUL-1996; 96US-0022191P.
 XX (MINU) UNIV MINNESOTA.
 XX Rajashekara G, Nagaraja KV, Kapur V;
 XX WPI; 1998-120780/11.
 DR N-PSDB; AAV13974.
 XX Detecting antibodies against Salmonella enteritidis using truncated
 PT fimbrial antigen Sef14 - in immunoassays, particularly for diagnosing
 PT infection in poultry, also new antigens.
 XX Claim 3; Page 21-22; 38pp; English.
 XX This sequence is a fragment of the Salmonella enteritidis (Se) Sef14
 CC protein, encoded by the sefa gene. The method of the invention is for
 CC detecting antibodies (Ab) against Se in an animal by treating a sample
 CC with a truncated Sef14 antigen (Ag), lacking at least the native Sef14
 CC signal peptide, and detecting any Ab-Ag complex formed. Detection (by
 CC enzyme-linked immunosorbent assay or agglutination tests) of the Ab is
 CC used to diagnose Se infection in birds, especially chickens and turkeys.
 CC The Ag can also be used in vaccines to protect poultry against Se
 CC infection. Detection of the Ab is a sensitive, specific method for
 CC reliable and routine screening of animals. The Ag are easily produced in
 CC large quantities, in pure form, without requiring special growing
 CC conditions, so are suitable for large scale screening of flocks
 XX Sequence 180 AA;
 SQ
 Query Match 100.0%; Score 662; DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. No. 4.6e-59;
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAQNTTSANWSQDPGFTGPAVAAGKVGTLTITATGPHNSVSIAGKGSVSGGVATVPFV 60
 DB 53 AAQNTTSANWSQDPGFTGPAVAAGKVGTLTITATGPHNSVSIAGKGSVSGGVATVPFV 112
 QY 61 DGQGPVFRGRIQGANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTFTAT 120
 DB 113 DGQGPVFRGRIQGANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTFTAT 172
 QY 121 FYVQOYQN 128
 DB 173 FYVQOYQN 180
 RESULT 8
 AAR62752
 ID AAR62752 standard; protein; 165 AA.
 XX
 AC AAR62752;
 XX 21-OCT-2004 (revised)
 DT 25-MAR-2003 (revised)
 DT 26-JUN-1995 (first entry)
 XX Sefa sequence.
 DE Salmonella; Sefa; vaccine.
 KW Salmonella sp.
 OS Unidentified.
 XX WO9425598-A2.
 XX 10-NOV-1994.
 PD 26-APR-1994; 94WO-IB000207.
 XX

PR 19-JUL-1999; 99US-0144335P.
 PR 20-JUL-1999; 99US-0144352P.
 PR 20-JUL-1999; 99US-0144632P.
 PR 20-JUL-1999; 99US-0144884P.
 PR 21-JUL-1999; 99US-0144814P.
 PR 21-JUL-1999; 99US-0145086P.
 PR 21-JUL-1999; 99US-0145088P.
 PR 22-JUL-1999; 99US-0145085P.
 PR 22-JUL-1999; 99US-0145087P.
 PR 22-JUL-1999; 99US-0145089P.
 PR 22-JUL-1999; 99US-0145192P.
 PR 23-JUL-1999; 99US-0145145P.
 PR 23-JUL-1999; 99US-0145218P.
 PR 23-JUL-1999; 99US-0145224P.
 PR 26-JUL-1999; 99US-0145276P.
 PR 27-JUL-1999; 99US-0145913P.
 PR 27-JUL-1999; 99US-0145918P.
 PR 27-JUL-1999; 99US-0145919P.
 PR 28-JUL-1999; 99US-0145951P.
 PR 02-AUG-1999; 99US-0146386P.
 PR 02-AUG-1999; 99US-0146388P.
 PR 02-AUG-1999; 99US-0146389P.
 PR 03-AUG-1999; 99US-0147038P.
 PR 04-AUG-1999; 99US-0147204P.
 PR 04-AUG-1999; 99US-0147302P.
 PR 05-AUG-1999; 99US-0147192P.
 PR 06-AUG-1999; 99US-0147260P.
 PR 06-AUG-1999; 99US-0147303P.
 PR 06-AUG-1999; 99US-0147416P.
 PR 09-AUG-1999; 99US-0147431P.
 PR 09-AUG-1999; 99US-0147935P.
 PR 10-AUG-1999; 99US-0148171P.
 PR 11-AUG-1999; 99US-0148319P.
 PR 13-AUG-1999; 99US-0148341P.
 PR 13-AUG-1999; 99US-0148565P.
 PR 13-AUG-1999; 99US-0148684P.
 PR 16-AUG-1999; 99US-0149368P.
 PR 17-AUG-1999; 99US-0149175P.
 PR 18-AUG-1999; 99US-0149426P.
 PR 20-AUG-1999; 99US-0149723P.
 PR 20-AUG-1999; 99US-0149923P.
 PR 20-AUG-1999; 99US-0149902P.
 PR 23-AUG-1999; 99US-0149930P.
 PR 25-AUG-1999; 99US-0150566P.
 PR 26-AUG-1999; 99US-0150884P.
 PR 27-AUG-1999; 99US-0151065P.
 PR 27-AUG-1999; 99US-0151066P.
 PR 27-AUG-1999; 99US-0151080P.
 PR 30-AUG-1999; 99US-0151303P.
 PR 31-AUG-1999; 99US-0151438P.
 PR 01-SEP-1999; 99US-0151930P.
 PR 07-SEP-1999; 99US-0152363P.
 PR 10-SEP-1999; 99US-0153070P.
 PR 13-SEP-1999; 99US-0153758P.
 PR 15-SEP-1999; 99US-0154018P.
 PR 16-SEP-1999; 99US-0154039P.
 PR 20-SEP-1999; 99US-0154779P.
 PR 22-SEP-1999; 99US-0155139P.
 PR 23-SEP-1999; 99US-0155486P.
 PR 24-SEP-1999; 99US-0155659P.
 PR 28-SEP-1999; 99US-0156458P.
 PR 29-SEP-1999; 99US-0156596P.
 PR 04-OCT-1999; 99US-0157117P.
 PR 05-OCT-1999; 99US-0157753P.
 PR 06-OCT-1999; 99US-0157863P.
 PR 07-OCT-1999; 99US-0158023P.
 PR 08-OCT-1999; 99US-0158332P.
 PR 12-OCT-1999; 99US-0158316P.
 PR 13-OCT-1999; 99US-0159239P.
 PR 13-OCT-1999; 99US-0159294P.
 PR 13-OCT-1999; 99US-0159295P.
 PR 14-OCT-1999; 99US-0159329P.

PR 14-OCT-1999; 99US-0159330P.
 PR 14-OCT-1999; 99US-0159331P.
 PR 14-OCT-1999; 99US-0159637P.
 PR 14-OCT-1999; 99US-0159638P.
 PR 18-OCT-1999; 99US-0159584P.
 PR 21-OCT-1999; 99US-0160741P.
 PR 21-OCT-1999; 99US-0160767P.
 PR 21-OCT-1999; 99US-0160768P.
 PR 21-OCT-1999; 99US-0160770P.
 PR 21-OCT-1999; 99US-0160814P.
 PR 21-OCT-1999; 99US-0160815P.
 PR 22-OCT-1999; 99US-0160980P.
 PR 22-OCT-1999; 99US-0160981P.
 PR 22-OCT-1999; 99US-0160989P.
 PR 25-OCT-1999; 99US-0161404P.
 PR 25-OCT-1999; 99US-0161405P.
 PR 25-OCT-1999; 99US-0161406P.
 PR 25-OCT-1999; 99US-0161359P.
 PR 26-OCT-1999; 99US-0161360P.
 PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161992P.
 PR 28-OCT-1999; 99US-0161993P.
 PR 29-OCT-1999; 99US-0162142P.

Query Match 14.1%; Score 93.5; DB 3; Length 431;
 Best Local Similarity 33.3%; Pred.No.0.94; Indels 11; Gaps 6;
 Matches 36; Conservative 14; Mismatches 47; Indels 11; Gaps 6;

QY 1 AAQNTTSANWSQDPGFTGPAVAAAGQKVG-TLSITATGPHNSVSIAGKGA-SVSGGVATVP 58
 DB 68 ATANTTTASSSDSPSSAAAAAANQWLSSSSFLQNNNNNASIVGDGDDVTGGADTMI 127
 QY 59 FVDGQGPVFRIGRIQGANINDQAN-TGIDGLAGRWASSQ-ETLVNVPV 104
 DB 128 ----QEMKTTGG---GENKNDGGGATAADGVVSWQNAHKAEITLSHPL 168

RESULT 10
 AAG09613
 ID AAG09613 standard; protein; 431 AA.
 XX AAG09613;
 AC AAG09613;
 XX 17-OCT-2000 (first entry)
 DT Arabidopsis thaliana protein fragment SEQ ID NO: 7614.
 DE Arabidopsis thaliana protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX Arabidopsis thaliana.
 OS Arabidopsis thaliana.
 XX EP1033405-A2.
 PN 06-SEP-2000.
 PD 25-FEB-2000; 2000EP-00301439.
 PF 25-FEB-1999; 99US-0121825P.
 XX 05-MAR-1999; 99US-0123180P.
 PR 03-MAR-1999; 99US-0123548P.
 PR 23-MAR-1999; 99US-0125788P.
 PR 25-MAR-1999; 99US-0126264P.
 PR 29-MAR-1999; 99US-0126785P.
 PR 01-APR-1999; 99US-0127462P.
 PR 06-APR-1999; 99US-0128234P.
 PR 08-APR-1999; 99US-0128714P.
 PR 16-APR-1999; 99US-0129845P.
 PR 19-APR-1999; 99US-0130077P.
 PR 21-APR-1999; 99US-0130449P.
 PR 23-APR-1999; 99US-0130510P.

PR 23-APR-1999;	99US-0130891P.	PR 20-JUL-1999;	99US-0144884P.
PR 28-APR-1999;	99US-0131449P.	PR 21-JUL-1999;	99US-0144814P.
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 Db 68 ATANTTTASSSSDPSSAAAAAANQWLSSFLQRNNNNASIVGDIDDVTGGADTMI 127
 QY 59 FVDSGQGVFRGRIQGANINDQAN-TGIDGLAGHRVASSQ-ETLNVVPV 104
 Db 128 ----QGEKMTGG---GENKNDGGGATAADGVWSQNAHKAELSHPL 168

RESULT 11
 ADI43535
 ID ADI43535 standard; protein; 431 AA.
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 AC ADI43535;
 XX

DT 22-APR-2004 (first entry)
 XX

XX Plant transcription factor #640.
 DE transgenic; plant; enhanced tolerance to abiotic stress;
 XX glyphosate tolerance; hormone sensitivity; disease resistance;
 KW sugar sensing; flowering; flower structure; stem bifurcation;
 KW branching pattern; apical dominance; trichome; stem morphology;
 KW root growth; root hair; seed development; cell proliferation;
 KW cell differentiation; premature senescence; necrosis; plant size;
 KW leaf morphology; seed morphology; seed biochemistry; root anthocyanin;
 KW plant anthocyanin; light response; shade avoidance; bioinformatic;
 KW transcription factor; gene; ds.

XX Arabidopsis thaliana.

XX US2004019927-A1.

XX 29-JAN-2004.

XX 25-FEB-2003; 2003US-00374780.

XX 18-APR-2001; 2001US-00837944.

XX (SHER/) SHERMAN B K.

PA (RIEC/) RIECHMANN J L.

PA (JIAN/) JIANG C.

PA (HEAR/) HEARD J E.

PA (HAAR/) HAAKE V.

PA (CREE/) CREELMAN R A.

PA (RATC/) RATCLIFFE O.

PA (ADAM/) ADAM L J.

PA (REUB/) REUBER T L.
 PA (KEDD/) KEDDIE J.
 PA (BROU/) BROUN P R.
 PA (FILG/) FILGRIM M L.
 PA (DUBE/) DUBELL A N.
 PA (PINE/) PINEDA O.
 PA (YUGG/) YU G.

PI Sherman BK, Riechmann JL, Jiang C, Heard JE, Haake V;
 PI Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Broun PE;
 PI Pilgrim ML, Dubell AN, Pineda O, Yu G;
 XX WPI; 2004-132245/13.

PT New transgenic plant comprising a recombinant polynucleotide of any one
 FT of more than 500 nucleotide sequences, useful in bioinformatic search
 FT methods.

PS Claim 1; SEQ ID NO 1998; 435pp; English.

XX The invention describes a transgenic plant comprising a recombinant
 CC polynucleotide of any one of more than 500 nucleotide sequences fully
 CC defined in the specification or its complement. The method of the
 CC invention can be used to produce a plant having altered traits such as:
 CC enhanced tolerance to abiotic stress; glyphosate tolerance; hormone
 CC sensitivity; disease resistance; sugar sensing; early or late flowering;
 CC altered flower structure; change in stem bifurcations; altered branching
 CC pattern; reduced apical dominance; reduced trichome density; lack of
 CC trichomes; reduced ectopic trichome development; altered trichome
 CC development; increase in trichome number; altered stem morphology;
 CC increased root growth; increased root hairs; altered seed development;
 CC altered cell proliferation or cell differentiation; rapid development;
 CC premature senescence; increased necrosis; increase in seedling or plant
 CC size; decreased plant size; leaf morphology; seed morphology; seed
 CC biochemistry; increase in root anthocyanins; increase in plant
 CC anthocyanins; or alteration in light response or shade avoidance. The
 CC transgenic plant, polynucleotides and polypeptides are useful in
 CC bioinformatic search methods. This is the amino acid sequence of a plant
 CC transcription factor, and an orthologue of Arabidopsis thaliana
 CC transcription factor, isolated in the invention, that can be used in the
 CC creation of a transgenic plant with altered traits.

XX Sequence 431 AA;

Query Match 14.1%; Score 93.5; DB 8; Length 431;
 Best Local Similarity 33.3%; Pred. No. 0.94;
 Matches 36; Conservative 14; Mismatches 47; Indels 11; Gaps 6;

QY 1 AAQNTTSANWSQDPGFTGPAVAGQKVG-TLSITATGPHNSVSIAGKGA-SVSGGVATVP 58

Db 68 ATANTTTASSSSDPSSAAAAAANQWLSSFLQRNNNNASIVGDIDDVTGGADTMI 127

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Db 128 ----QGEKMTGG---GENKNDGGGATAADGVWSQNAHKAELSHPL 168

RESULT 12

AEA26765

ID AEA26765 standard; protein; 431 AA.

XX AEA26765;

XX 28-JUL-2005 (first entry)

DE Stress tolerant plant-related transcription factor protein SeqID606.

XX transcription factor; transgenic plant; agriculture; drought resistance;
 KW stress tolerance.

XX Arabidopsis thaliana.

XX WO2005047516-A2.

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XX PD 26-MAY-2005.
XX PD 12-NOV-2004; 2004WO-US037584.
XX PF 13-NOV-2003; 2003US-00714887.
XX PR 05-DEC-2003; 2003US-0527658P.
XX PR 05-FEB-2004; 2004US-0542928P.
XX PA (MEND-) MENDEL BIOTECHNOLOGY INC.
XX PI Heard JE, Riechmann JL, Creelman RA, Ratcliffe OJ, Canales RD;
PI Repetti P, Kumimoto RW, Guterson NI, Reuber TL, Pinada O;
PI Sherman BK, Morrison TA, Keddle JS, Jiang C, Century KS, Adam L;
PI Zhang JZ, Hempel FD, Libby JM;
XX DR WPI; 2005-372386/38.
XX DR N-FSDB; AEA26764.
XX XX
XX PT New transgenic plants for producing commercially or agriculturally useful
XX PT plants having improved tolerance to drought, shade and low nitrogen
XX PT conditions.
XX PS Disclosure; SEQ ID NO 606; 407pp; English.
XX XX
XX CC This invention relates to a novel plant transcription factor
XX CC polypeptides, the DNA sequences which encode them and their use in
XX CC creating transgenic plants. The transgenic plant and methods are useful
XX CC for producing commercially or agriculturally useful plants having
XX CC improved tolerance to drought, shade and low nitrogen conditions when
XX CC compared to wild-type reference plants. The present sequence is that of a
XX CC plant transcription factor protein which was used during the development
XX CC of the transgenic plants of the invention.
XX XX
XX SQ Sequence 431 AA;
Query Match 14.1%; Score 93.5; DB 9; Length 431;
Best Local Similarity 33.3%; Pred. No. 0.94;
Matches 36; Conservative 14; Mismatches 47; Indels 11; Gaps 6;
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Db 68 ATANTTTASSSDSPSSAAAAAANQWLSSRSFLQRNNNNNASIVGDGIDVDTGGADTMI 127
Qy 59 FVDCGQGPVFGRIQGANINDQAN-TGIDGLAGHRVASSQ-ETLNVPV 104
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XX AC AAG09612;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 7613.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX XX
XX XX 25-FEB-2000; 2000EP-00301439.
XX PF 25-FEB-1999; 99US-0121825P.
XX PR 05-MAR-1999; 99US-0123180P.
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PR 29-OCT-1999; 99US-0162142P.

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Best Local Similarity 33.3%; Pred. No. 0.95;
Matches 36; Conservative 14; Mismatches 47; Indels 11; Gaps 6;

QY 1 AAQNTTSANWSQDPCFTGPAVAAGOKVG-TLSITATGPHNSVSIAGKA-SVSGGVATVP 58
Db 72 ATANTTTASSDSSPSSAAAAAANQWLSLSSFLORNNNNASIVGDDGDDVTGGADTMI 131
QY 59 FVDGQGPVFRIGRIQGANINDQAN-TGIDGLAGWRVASSQ-ETLNVPV 104
Db 132 ----QGEKMTGG--GENKNDGGGATAADGVVSWQNAHKAELSHPL 172

RESULT 14
AAG49463
ID AAG49463 standard; protein; 440 AA.
XX
AC AAG49463;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 62578.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PP 25-FEB-2000; 2000EP-00301439.
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PR	29-OCT-1999;	99US-0162142P.	PR	04-JUN-1999;	99US-0137502P.
Query Match 14.1%; Score 93.5; DB 3; Length 440;					
Best Local Similarity 33.3%; Pred. No. 0.97; Matches 36; Conservative 14; Mismatches 47; Indels 11; Gaps 6;					
QY	1	AAQNTTSANWSQDPGFTGPAVAGQKVG-TLSITATGPHNSVSIAGKGA-SVSGGVATVP 58	PR	08-APR-1999;	99US-0128714P.
Db	68	ATANTTTASSDSFSSAAAAANQWLRSRSSFLORNNNNNASIVGDIIDVTGADTMI 127	PR	16-APR-1999;	99US-0129845P.
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AC	AAG49462;				
XX	18-OCT-2000 (first entry)				
DT	Arabidopsis thaliana protein fragment SEQ ID NO: 62577.				
DE	Arabidopsis thaliana.				
XX	Protein identification; signal transduction pathway; metabolic pathway;				
KW	hybridisation assay; genetic mapping; gene expression control; promoter;				
KW	termination sequence.				
XX	Arabidopsis thaliana.				
OS	EP1033405-A2.				
PN	06-SEP-2000.				
PD	25-FEB-2000; 2000EP-00301439.				
PF	25-FEB-1999; 99US-0121825P.				
XX	05-MAR-1999; 99US-0123160P.				
PR	09-MAR-1999; 99US-0123548P.				
PR	23-MAR-1999; 99US-0125788P.				
PR	25-MAR-1999; 99US-0126264P.				
PR	29-MAR-1999; 99US-0126785P.				
PR	01-APR-1999; 99US-0127462P.				
PR	06-APR-1999; 99US-0128234P.				

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 26, 2006, 17:02:58 ; Search time 74 Seconds
(without alignments)
1220.373 Million cell updates/sec

Title: US-10-018-892-3

Perfect score: 682

Sequence: 1 AAQNTSANWSQDGFPGA.....KSTLPAGTFTATFYQQVQN 128

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	662	100.0	165	1 FM_SALEN	P12061 salmonella
2	637	96.2	165	2 Q5PM43 SALPA	Q5pm43 salmonella
3	295	44.6	166	2 Q9X6U1 ECOLI	Q9x6u1 escherichia
4	270	40.8	166	2 Q47405 ECOLI	Q47405 escherichia
5	98	14.8	656	2 Q50Q12 ENTHI	Q50q12 entamoeba h
6	94.5	14.3	1929	2 Q54J74 DICDI	Q54j74 dictyosteli
7	93.5	14.1	431	1 KNAT3 ARATH	P48000 arabidopsis
8	93.5	14.1	431	2 Q8LDC1 ARATH	Q8ldc1 arabidopsis
9	93	14.0	398	2 Q6VA08 TREPA	Q6va08 treponema p
10	93	14.0	400	2 Q6VAL3 TREPA	Q6val3 treponema p
11	93	14.0	401	2 Q6VA23 TREPA	Q6va23 treponema p
12	93	14.0	405	2 Q6VA22 TREPA	Q6va22 treponema p
13	91.5	13.8	2468	2 Q9I2M3 PSEAB	Q9i2m3 pseudomonas
14	90.5	13.7	1973	2 Q7NP45 GLOVI	C7np45 gloeobacter
15	90	13.6	476	2 Q4J4Q1 AZOVI	Q4j4q1 azotobacter
16	88	13.3	405	2 Q6VAL9 TREPA	Q6val9 treponema p
17	88	13.3	499	2 Q9EUA1 TREPA	Q9eua1 treponema p
18	87.5	13.2	380	1 POLG MDWV	P32652 maize dwarf
19	87	13.1	394	2 Q6VA59 TREPA	Q6va59 treponema p
20	87	13.1	609	2 Q82K19 STRAW	Q82k19 streptomyc
21	87	13.1	1778	2 Q7SZY1 BRARE	Q7szy1 brachydanio
22	86.5	13.1	399	2 Q6V920 TREPA	Q6v920 treponema p
23	86.5	13.1	1356	1 CO1A2 ONCMY	O93484 oncorhynch
24	86	13.0	1472	2 Q90ZAO CHICK	Q90za0 gallus gall
25	86	13.0	2751	2 Q8UK00 RALSO	Q8uk00 ralstonia s
26	85.5	12.9	1346	2 Q8UJ73 ONCKE	Q8uj73 oncorhynch
27	85	12.8	173	2 Q6PFR1 ACTAD	Q6pfr1 acinetobact
28	85	12.8	400	2 Q6VA53 TREPA	Q6va53 treponema p
29	85	12.8	496	2 Q84AM4 TREPA	Q84am4 treponema p
30	85	12.8	496	2 Q84AM5 TREPA	Q84am5 treponema p
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32 85 12.8 786 2 Q21027 CAEEL Q21027 caenorhabdi
33 85 12.8 1613 2 Q840U5 GRICK Q840u5 rickettsia
34 84.5 12.8 943 1 YL61 SCHPO Q840u5 schizosacch
35 84.5 12.8 1011 2 Q4KGN9 PSEPS Q4kgn9 pseudomonas
36 84.5 12.8 2734 2 Q89C73 BRAJA Q89c73 bradyrhizob
37 84 12.7 435 2 Q4NAK9 SMICC Q4nak9 arthrobacte
38 84 12.7 591 2 Q8YDM6 BRUMB Q8ydm6 bruceella m
39 84 12.7 2724 2 Q4RZK3 TETNG Q4rzk3 tetraodon n
40 84 12.7 3420 2 Q8FUS1 BRUSU Q8fusi bruceella su
41 84 12.7 3422 2 Q576H6 BRUAB Q576h6 bruceella ab
42 83.5 12.6 115 2 Q9PXU5 POTV Q9pxu5 sugarcane m
43 83.5 12.6 401 2 Q6VA20 TREPA Q6va20 treponema p
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45 83.5 12.6 2199 2 Q4UJZ8 RICFE Q4ujz8 rickettsia

ALIGNMENTS

RESULT 1

FM_SALEN STANDARD; PRT; 165 AA.
AC P12061;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Fimbrial protein precursor.
GN Name=sefa; Synonyms=sef14;
OS Salmonella enteritidis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=592;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=27655-3B;
RX MEDLINE=93239677; PubMed=8097515;
RA Clouthier S.C., Mueller K.-H., Doran J.L., Collinson S.K., Kay W.W.;
RT "Characterization of three fimbrial genes, sefABC, of Salmonella enteritidis".
RL J. Bacteriol. 175:2523-2533 (1993).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91072589; PubMed=1701443;
RA Thorns C.J., Sojka M.G., Chasey D.C.;
RT "Detection of a novel fimbrial structure on the surface of Salmonella enteritidis by using a monoclonal antibody".
RL J. Clin. Microbiol. 28:2409-2414 (1990).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Ogunniyi A.D., Kotlarski I., Morona R., Manning P.A.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP PROTEIN SEQUENCE OF 22-85.
RX MEDLINE=87008384; PubMed=2875990;
RA Feutrier J., Kay W.W., Trust T.J.;
RT "Purification and characterization of fimbriae from Salmonella enteritidis".
RL J. Bacteriol. 168:221-227 (1986).
CC -!- FUNCTION: Structural subunit of the sef14 fimbriae (S. enteritidis filamentous fimbriae).
CC -!- SUBCELLULAR LOCATION: Fimbria.

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CC EMBL; L11008; AAA27219.1; -; Genomic DNA.
CC EMBL; L03833; AAA71892.1; -; Unassigned DNA.
CC EMBL; X98516; CAA67141.1; -; Genomic DNA.
CC PIR; A40618; A40618.
CC PDB; 1LU0; Model; A-1-165.

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DR InterPro; IPR010498; SEF14 adhesin.
DR Pfam; PF06443; SEF14 adhesin; 1.
KW 3D-structure; Direct protein sequencing; Fimbria; Signal.
FT SIGNAL 1 21
FT CHAIN 22 165 Fimbrial protein.
FT CONFLICT 30 30 V -> E (in Ref. 2 and 3).
FT CONFLICT 84 85 GA -> QW (in Ref. 4).
SQ SEQUENCE 165 AA; 16477 MW; 5B33798A3F0F9091 CRC64;

Query Match 100.0%; Score 662; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 5.4e-50;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 98 DGQGPVFRGRIQGANINDQANTGIDGLAGRWVASSQETLNVPVTTFGKSTLPAGTTAT 157
QY 121 FYVQOYQN 128
Db 158 FYVQOYQN 165

RESULT 2
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ID QSPM43 SALPA PRELIMINARY; PRT; 165 AA.
AC QSPM43; 2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Fimbrial structural protein.
GN Name=sefa; OrderedLocusNames=SPAA304;
OS Salmonella paratyphi-a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=54388;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 9150;
RX PubMed=15531882; DOI=10.1038/ng1470;
RA McClelland M., Sanderson K.E., Clifton S.W., Latreille P.,
RA Porwollik S., Sabo A., Meyer R., Bieri T., Ozersky P., McLellan M.,
RA Harkins C.R., Wang C., Nguyen C., Berghoff A., Elliott G.,
RA Kohlberg S., Strong C., Du F., Carter J., Kremizki C., Layman D.,
RA Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P., Florea L.,
RA Delehaanty K., Fronick C., Magrini V., Nhan M., Warren W., Florea L.,
RA Spieth J., Wilson R.K.;
RT "Comparison of genome degradation in Paratyphi A and Typhi, human-
RT restricted serovars of Salmonella enterica that cause typhoid.";
RL Nat. Genet. 36:1268-1274(2004).
DR EMBL; CP000026; AAV80033.1; -; Genomic_DNA.
DR InterPro; IPR010498; SEF14 adhesin.
DR Pfam; PF06443; SEF14 adhesin; 1.
KW Complete proteome.
SQ SEQUENCE 165 AA; 16665 MW; 8A32BE3F43C91520 CRC64;

Query Match 96.2%; Score 637; DB 2; Length 165;
Best Local Similarity 96.1%; Pred. No. 8.3e-48;
Matches 123; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAQNTTSANWSQDPGFTGPAVAAGQKVGTLSTATGPHNSVSIAGKASVSGGVATVPFV 60
Db 38 AAQNTTSANWSQDPGFTGPAVAAGQKVGTLSTATGPHNSVSIAGKASVSGGVATVPFV 97
QY 61 DGQGPVFRGRIQGANINDQANTGIDGLAGRWVASSQETLNVPVTTFGKSTLPAGTTAT 120
Db 98 DGQGPVFRGRIQGANINDQANTGIDGLAGRWVASSQETLNVPVTTFGKSTLPAGTTAT 157
QY 121 FYVQOYQN 128
Db 158 FYVQOYQN 165

Query Match 44.6%; Score 295; DB 2; Length 166;
Best Local Similarity 45.8%; Pred. No. 6.2e-18;
Matches 60; Conservative 26; Mismatches 41; Indels 4; Gaps 3;

QY 1 AAQNTTSANWSQDPGFTGPAVAAGQKVGTLSTATGPHNSVSIAGKASVSGGVATVPFV 60
Db 37 SAQNTINATWTQDPSVSGSSVQAMQKLGTLNQLTGHAGVYVSGDGTGSGGLVTIPFK 96
QY 61 DGQGPVFRGRIQGANINDQANTGIDGLA--GWRVASSQETLNVPVTTFGKSTLPAGTF 117
Db 97 NAAQGIPIFRGR-TNADIGQASNTLIAGHSGPGWNLDPDAGNNISLDIKAFQKNDIPAGTY 155
QY 118 TATFYVQOYQN 128
Db 156 TATFYIQYQS 166

RESULT 4
Q47405_ECOLI
ID Q47405_ECOLI PRELIMINARY; PRT; 166 AA.
AC Q47405;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Antigen 8786.
GN Name=nfaA;
OS Escherichia coli.
OG Plasmid.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=8786;
RA Aubel D., Darfeuille-Michaud A., Martin C., Joly B.;
RT "Nucleotide sequence of the nfaA gene encoding the antigen 8786
RT adhesive factor of enterotoxigenic escherichia coli.";
RL FEMS Microbiol. Lett. 98:277-284(1992).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=8786;
RX MEDLINE=93093418; PubMed=1281130; DOI=10.1016/0378-1097(92)90169-O;
RA Aubel D., Darfeuille-Michaud A., Martin C., Joly B.;

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RT "Nucleotide sequence of the nfaA gene encoding the antigen 87B86
RT adhesive factor of enterotoxigenic Escherichia coli.¹⁷
RL FEMS Microbiol. Lett. 77:277-284 (1992).
DR EMBL; X64623; CAA45906.1; -; Genomic_DNA.
DR InterPro: IPR010498; SEF14 adhesin.
DR Pfam; PP06443; SEF14_adhesin; 1.
KW Plasmid.
SQ Sequence 166 AA; 17441 MW 28D37F831EE9DAD8 CRC64;

	Query Match	40.8%;	Score 270;	DB 2;	Length 166;
	Best Local Similarity	42.7%;	Pred.No. 9.5e-16;		
	Matches 56; Conservative	24;	Mismatches 47;	Indels 4;	Gaps 3;
QY	1 AAOHTTSANKWSQPFGTGPAVAAGOKVGTLLSATATGPHNSVSITAGKGASVSGGVATVPFV	60	:	: :	:
Dd	37 SAOQTINATWTDSSVSGSSTAMQKGLNIRLTGSHAGVYVGSDDTGSSGLIITPFK	96	:	: :	:
QY	61 DGGQQPVFRGRIOGANINDQANTGIDGLA--GWRVASSQETLNVPTTF-GKSTLPAGTF	117	:	: :	:
Dd	97 NTAGQVLFRGR-TNAEIQAWTTPIVGHSPGWHLFCTQDNFNLDIRAFQNANNIPAGEY	155	:	: :	:
QY	118 TATFYVQQYNQON	128	:	: :	:
Dd	156 TATFYIQQYOS	166	:	: :	:

```

RESULT 5
Q50012 ENTHI PRELIMINARY; PRT; 656 AA.
ID ID Q50012 ENTHI PRELIMINARY;
AC AC Q50012;
DT DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE DE Hypothetical protein.
GN GN ORFNames=347.t00008;
OS OS Entamoeba histolytica HM-1:IMSS.
OC OC Eukaryota; Entamoebidae; Entamoeba.
OX OX NCBI_TaxID=294381;
[1]
RN RN NUCLEOTIDE SEQUENCE.
RP RP STRAIN=HM-1:IMSS;
RC RC STRAIN=15729342; DOI=10.1038/nature03291;
RX RX PubMed=15729342;
RA RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
RA Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leipzig M.,
RA Hofer M., Bruchhaus I., Willhoef U., Bhattacharya A.,
RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,
RA Jagels K., Moule S., Mungall K., Ommond D., Squares R., Whitehead S.,
RA Quail M.A., Rabinowitz E., Norbertczak H., Price C., Wang Z.,
RA Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,
RA Foster P.G., Sichteriz-Ponten T., Weber C., Singh U., Mukherjee C.,
RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrall B.,
RA Fraser C.M., Hall N.;
RA "The genome of the protist parasite Entamoeba histolytica."
RL RL Nature 433:865-868(2005).
CC CC -!- CAUTION: The sequence shown here is derived from an
CC CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC CC preliminary data.

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Query Match      14.8%; Score 98; DB 2; Length 656;
Best Local Similarity 26.8%; Pred. No. 4.4;
Matches 33; Conservative 16; Mismatches 62; Indels 12; Gaps 2;

QY      15  GTPPAVAAQKVGTLSITATGPHNSVSIAGKASVSGCATVPFVGGQGPVFRIGG 74
          : : : : : : : : : : : : : : : : : : : : : : : :
DB      358 GHKPLGSLGSSGSGSSSTIGTSISTITGLS--TGSVGTSGSVGTSGSVGT 415
          : : : : : : : : : : : : : : : : : : : : : : : :

QY      75  ANINPQANTGIDGLAGRWVASSQETINVPVTFITGKSTLPAGTFTAT-----FVYQ 124
          : : : : : : : : : : : : : : : : : : : : : : : :

```

Db 416 STSSVNVNPFVNNGIGSVPYTQTPTFPVTFTVPNTSPBPVTFTVPNTVPWPSYYPQ 475

Qy 125 QXQ 127

Dd 476 QQQ 478

RESULT 6

QS4JUT4 DICDI PRELIMINARY; PRT; 1929 AA.

AC QS4JUT4;

DT 13-SEP-2005 (TrEMBLrel. 31, Created)

DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

DE Hypothetical protein.

GN ORFNames=DDB0215928;

OS Dictyostelium discoideum (Slime mold).

OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.

NCBI_TaxID=44689;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=AX4;

RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,

RA Suecang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,

RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,

RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,

RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,

RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,

RA Fabrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,

RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,

RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,

RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,

RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,

RA Loulsegé H., Mungall K., Oliver K., Price C., Quaile M.A., Sanders M.,

RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Tivey A.,

MA J.J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,

RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,

RA Shaulsky G., Schleicher M., Weinstein G., Rosenthal A., Cox E.C.,

RA Chisholm R.L., Gibbs R., Loomis W.F., Platzter M., Kay R.R.,

RA Williams J., Dear P.H., Noegel A.A., Bartell B., Kuspa A.,

RT "The genome of the social amoeba Dictyostelium discoideum.";

Nature 0:0-0(2005).

RL -! CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

DR EMBL; AAFI01000157; EAL63578.1; -; Genomic_DNA.

KW Hypothetical protein.

SQ SEQUENCE 1929 AA; 181152 MW; B3218ECD6787EF57 CRC64;

Query Match 14.3%; Score 94.5; DB 2; Length 1929;

Best Local Similarity 29.1%; Pred. No. 29;

Matches 34; Conservative 13; Mismatches 53; Indels 17; Gaps 3;

Qy 4 NTTSANWSQDPFGTGPAVAGKVGTLSTATGPHNSVSIAHGKASVSGGVATVPFDQG 63

Dd 323 STTTTSGSQSTGASTATASGQSQTASATTATA-SGSQSQTGSTATTSGGST----- 373

Qy 64 GQPVRGRIGQANINDQANTGIDGLAGRWAVASSQETLVNPPVTFKGSLTPAGTPTAT 120

Dd 374 -----GPISGASTTSMSTTTATG--SIPTTSGTSQTSGSYTTTGTSGTSTSGTYTTT 422

RESULT 7

KNAT3 ARATH STANDARD; PRT; 431 AA.

ID KNAT3 ARATH

AC P48000;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Homeobox protein knotted-1-like 3 (KNAT3).

GN Name=KNAT3; OrderedLocusNames=At5g25220; ORFNames=F21J6.18;

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
[1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97304677; PubMed=9161040;
RA Serikawa K.A., Martinez-Laborda A., Kim H.S., Zambryski P.C.;
RT "Localization of expression of KNAT3, a class 2 knotted-like gene."
RL Plant J. 11:853-861(1997).
[2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=cv. Columbia;
RX MEDLINE=21016721; PubMed=11130714; DOI=10.1038/35048507;
RA Tabata S., Kaneko T., Nakamura Y., Kotani H., Kato T., Asanizu E.,
RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,
RA Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakayama S.,
RA Nakazaki N., Naruo K., Okumura S., Shino S., Takeuchi C., Wada T.,
RA Nakanabe A., Yamada M., Yasuda M., Sato S., de la Bastide M.,
RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
RA Habermann K., Murray J., Johnson D., Rohlfing T., Nelson J.,
RA Stoneking T., Pepin K., Spieth J., Sekhon M., Armstrong J., Becker M.,
RA Belter E., Cordum H., Cordes M., Courtney L., Courtney W., Dante M.,
RA Du H., Edwards J., Fryman J., Haakensen B., Lamar E., Latreille P.,
RA Leonard S., Meyer R., Mulvaney E., Ozerky P., Riley A., Strowmatt C.,
RA Wagner-McPherson C., Wollam A., Yeakum M., Bell M., Dedhia N.,
RA Ramsperger U., Wedler E., Balke K., Wedler E., Peters S.,
RA van Staveren M., Dirke G., Moeljan P., Klein Lankhorst R.,
RA Weitzenecker T., Borkes W., Rose M., Hauf J., Bernerstor S., Hempel S.,
RA Feldpausch M., Lamberth S., Villarroel R., Gielen J., Ardiles W.,
RA Bents O., Lemcke K., Kolesov G., Mayer K.F.X., Rudd S., Schoof H.,
RA Schueller C., Zaccaria P., Mewes H.-W., Bevan M., Franz P.F.;
RT "Sequence and analysis of chromosome 5 of the plant Arabidopsis thaliana."
RL Nature 408:823-826(2000).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- SIMILARITY: Belongs to the TALE/KNOX homeobox family.
CC -1- SIMILARITY: Contains 1 ELK domain.
CC -1- SIMILARITY: Contains 1 homeobox DNA-binding domain.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

DR EMBL; X92392; CRA63130.1; -; mRNA.
DR EMBL; AC006259; AAC98441.1; -; Genomic_DNA.
DR TRANSFAC; T04044; -;
DR GeneFarm; 4056; 408.
DR InterPro; IPR005539; ELK.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR012287; Homeobox-rel.
DR InterPro; IPR005540; KNOX1.
DR InterPro; IPR005541; KNOX2.
DR Pfam; PF03789; ELK; 1.
DR Pfam; PF03790; KNOX1; 1.
DR Pfam; PF03791; KNOX2; 1.
DR ProDom; PD000010; Homeobox; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT DOMAIN 320 343 ELK.
FT DNA_BIND 344 406 Homeobox; TALE-type.
FT COMPBIAS 23 33 Poly-Pro.
FT COMPBIAS 34 37 Poly-Gln.
FT COMPBIAS 58 61 Poly-Asn.

FT COMPBIAS 84 90 Poly-Ala.
FT COMPBIAS 104 108 Poly-Asn.
SQ SEQUENCE 431 AA; 47600 MW; 5222B67AB54B9673 CRC64;
Query Match 14.1%; Score 93.5; DB 1; Length 431;
Best Local Similarity 33.3%; Pred. No. 6.9;
Matches 36; Conservative 14; Mismatches 47; Indels 11; Gaps 6;
Qy 1 AAQNTTSANWSQDPGFTGPAVAAGQKVG-TLSITATGPHNSVSIAGKGA-SVSGGVATVP 58
Db ATANTTTASSSDSPSSAAAAAANQWLSRSSFLQRNNNNASIVGDGIDDDVTGGADTMI 127
Qy 59 FVDCGQGPVFRGRIQGANINDQAN-TGIDGLAGWRVASSQ-ETLNVPV 104
Db 128 ----QGEKTKG---GENKNDGGGATADGVVSMQNRHAKAILSHPL 168
RESULT 8
ID Q8LDC1_ARATH PRELIMINARY; PRT; 431 AA.
AC Q8LDC1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DS KNAT3 homeodomain protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
[1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2208475; PubMed=12093376;
RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation."
RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AY086091; AAM63298.1; -; mRNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006355; P:transcription factor activity; IEA.
DR InterPro; IPR005539; ELK.
DR InterPro; IPR012287; Homeobox-rel.
DR InterPro; IPR005540; KNOX1.
DR InterPro; IPR005541; KNOX2.
DR Pfam; PF03789; ELK; 1.
DR Pfam; PF03790; KNOX1; 1.
DR Pfam; PF03791; KNOX2; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; UNKNOWN_1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 431 AA; 47557 MW; 5EP832F3CEB2E02B CRC64;
Query Match 14.1%; Score 93.5; DB 2; Length 431;
Best Local Similarity 33.3%; Pred. No. 6.9;
Matches 36; Conservative 14; Mismatches 47; Indels 11; Gaps 6;
Qy 1 AAQNTTSANWSQDPGFTGPAVAAGQKVG-TLSITATGPHNSVSIAGKGA-SVSGGVATVP 58
Db ATANTTTASSSDSPSSAAAAAANQWLSRSSFLQRNNNNASIVGDGIDDDVTGGADTMI 127
Qy 59 FVDCGQGPVFRGRIQGANINDQAN-TGIDGLAGWRVASSQ-ETLNVPV 104

Db 128 ----QGENKTTGG-----GENKNDDGGATAADGVVSWQNHAKBILSHPL 168

RESULT 9

Q6VA08_TREPA PRELIMINARY; PRT; 398 AA.
 AC Q6VA08;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE TprK (Fragment).
 GN Name=tprK;
 OS Treponema pallidum subsp. pallidum (syphilis treponeme).
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=161;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Sea81-4;
 RX DOI=10.1128/JB.185.21.6262-6268.2003;
 RA LaFond R.E., Centurion-Lara A., Godornes C., Rompalo A.M.,
 RA Van Voorhis W.C., Lukehart S.A.;
 RT "Sequence diversity of Treponema pallidum subsp. pallidum tprK in
 human syphilis lesions and rabbit-propagated isolates.";
 RL J. Bacteriol. 185:6262-6268(2003).
 DR EMBL; AY346070; AAQ23285.1; -; Genomic DNA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR003872; MOSP_C.
 DR InterPro; IPR003857; MOSP_Nterm.
 DR Pfam; PF02722; MOSP_C; 1.
 DR Pfam; PF02707; MOSP_N; 1.
 FT NON_TER 1 398
 FT NON_TER 398 398
 SQ SEQUENCE 398 AA; 43192 MW; C3E55C5467ADEBDB CRC64;

Query Match 14.0%; Score 93; DB 2; Length 398;
 Best Local Similarity 30.9%; Pred. No. 7;
 Matches 34; Conservative 12; Mismatches 44; Indels 20; Gaps 5;

Qy 13 DPGFTGPAVAAGQKVGTLTITATGPHNSVSIAGKASVSGVATVPFVDDGGQGVPRGRI 72
 Db 126 EPGFEG-----AGGKLG-----YKQTDIAGTGLTFDIAFKFASNTDWEKGP--NGNV 170

Qy 73 QGANINDQANTGIDGLAGW---RVASSQETLNVPVTTFGKSTLPAGTFTA 119
 Db 171 QAGANHSKYGLGGDILFGWERTREDGVQYIKVELT--GNSTLSSGYATA 218

RESULT 10

Q6VA13_TREPA PRELIMINARY; PRT; 400 AA.
 AC Q6VA13;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE TprK (Fragment).
 GN Name=tprK;
 OS Treponema pallidum subsp. pallidum (syphilis treponeme).
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=161;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Sea81-4;
 RX DOI=10.1128/JB.185.21.6262-6268.2003;
 RA LaFond R.E., Centurion-Lara A., Godornes C., Rompalo A.M.,
 RA Van Voorhis W.C., Lukehart S.A.;
 RT "Sequence diversity of Treponema pallidum subsp. pallidum tprK in
 human syphilis lesions and rabbit-propagated isolates.";
 RL J. Bacteriol. 185:6262-6268(2003).
 DR EMBL; AY346065; AAQ23280.1; -; Genomic DNA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR003872; MOSP_C.

DR InterPro; IPR003857; MOSP_Nterm.
 DR Pfam; PF02722; MOSP_C; 1.
 DR Pfam; PF02707; MOSP_N; 1.
 FT NON_TER 1 400
 FT NON_TER 400 400
 SQ SEQUENCE 400 AA; 43341 MW; AFC15CED22D44400 CRC64;

Query Match 14.0%; Score 93; DB 2; Length 400;
 Best Local Similarity 30.9%; Pred. No. 7.1;
 Matches 34; Conservative 12; Mismatches 44; Indels 20; Gaps 5;

Qy 13 DPGFTGPAVAAGQKVGTLTITATGPHNSVSIAGKASVSGVATVPFVDDGGQGVPRGRI 72
 Db 126 EPGFEG-----AGGKLG-----YKQTDIAGTGLTFDIAFKFASNTDWEKGP--NGNV 170

Qy 73 QGANINDQANTGIDGLAGW---RVASSQETLNVPVTTFGKSTLPAGTFTA 119
 Db 171 QAGANHSKYGLGGDILFGWERTREDGVQYIKVELT--GNSTLSSGYATA 218

RESULT 11

Q6VA23_TREPA PRELIMINARY; PRT; 401 AA.
 AC Q6VA23;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE TprK (Fragment).
 GN Name=tprK;
 OS Treponema pallidum subsp. pallidum (syphilis treponeme).
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=161;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Sea81-4;
 RX DOI=10.1128/JB.185.21.6262-6268.2003;
 RA LaFond R.E., Centurion-Lara A., Godornes C., Rompalo A.M.,
 RA Van Voorhis W.C., Lukehart S.A.;
 RT "Sequence diversity of Treponema pallidum subsp. pallidum tprK in
 human syphilis lesions and rabbit-propagated isolates.";
 RL J. Bacteriol. 185:6262-6268(2003).
 DR EMBL; AY346055; AAQ23270.1; -; Genomic DNA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR003872; MOSP_C.
 DR InterPro; IPR003857; MOSP_Nterm.
 DR Pfam; PF02722; MOSP_C; 1.
 DR Pfam; PF02707; MOSP_N; 1.
 FT NON_TER 1 401
 FT NON_TER 401 401
 SQ SEQUENCE 401 AA; 43276 MW; 2F9AB2730EC87499 CRC64;

Query Match 14.0%; Score 93; DB 2; Length 401;
 Best Local Similarity 30.9%; Pred. No. 7.1;
 Matches 34; Conservative 12; Mismatches 44; Indels 20; Gaps 5;

Qy 13 DPGFTGPAVAAGQKVGTLTITATGPHNSVSIAGKASVSGVATVPFVDDGGQGVPRGRI 72
 Db 126 EPGFEG-----AGGKLG-----YKQTDIAGTGLTFDIAFKFASNTDWEKGP--NGNV 170

Qy 73 QGANINDQANTGIDGLAGW---RVASSQETLNVPVTTFGKSTLPAGTFTA 119
 Db 171 QAGANHSKYGLGGDILFGWERTREDGVQYIKVELT--GNSTLSSGYATA 218

RESULT 12

Q6VA22_TREPA PRELIMINARY; PRT; 405 AA.
 AC Q6VA22;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE TprK (Fragment).


```

GN Name:tpkR;
OS Treponema pallidum subsp. pallidum (syphilis treponeme).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
ON NCBI_TaxID=161;
RX [1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=Sea81-4;
RR MEDLINE=22925844; PubMed=14563860;
RS DOI=10.1128/JB.185.21.6262-6268.2003;
RA LaFont R.E., Centurion-Lara A., Godornes C., Rompalo A.M.,
RV Van Voorhis W.C., Lukehart S.A.;
RT "Sequence diversity of Treponema pallidum subsp. pallidum tprK in
RI human syphilis lesions and rabbit-propagated isolates." ;
RL J. Bacteriol. 185:6262-6268(2003).
DR ENBL; AV346056; AAQ23271.1; -; Genomic DNA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR003872; MOSP_C.
DR InterPro; IPR003857; MOSP_Nterm.
DR Pfam; PF02722; MOSP_C; 1.
DR Pfam; PF02707; MOSP_N; 1.
FT NON_TER 1
FT TER 405
SQ SEQUENCE 405 AA; 43967 MW; AA8BA48BAE812ED5E CRC64;

Query Match      14.0%; Score 93; DB 2; Length 405;
Best Local Similarity 30.9%; Pred.No 7.2;
Matches 34; Conservative 12; Mismatches 44; Indels 20; Gaps 5;

QY    13 DRGFTGPAVAAQGVLTSLTATGPHNSVSITAGKGASVSGVAIVPFVDGGQGPVRGRI 72
Db     :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
       126 EPGFEG----AGGKLGI-----YKQTDIAGTLGTDFIAFKPASNTDWEKKP--NGNV 170

QY    73 QGANINDQANTGIDLAGW---RVASSOETLNPVTTFGKSTLPAGTFTA 119
Db     :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
       171 QAGANHSEKYGLCGDILFGWERTRENGVQEYIKVELT--GNSTLSGGYATA 218

RESULT 13
Q912M3 PSBAE
ID   Q912M3_PSEAE PRELIMINARY; PRT; 2468 AA.
AC   Q912M3;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DI   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
DS   OrderedLocusNames=PA1874;
OS   Pseudomonas aeruginosa.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
ON   NCBI_TaxID=287;
RX   [1]
RN   NUCLEOTIDE SEQUENCE.
RC   STRAIN=ATCC 15692 / PAOI;
RR   MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA   Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA   Hickey M.J., Brinkman F.S.L., Huffnagle W.O., Kowalik D.J., Lagrou M.,
RA   Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA   Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA   Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA   Reizer J., Saier M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;
RT   "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
RI opportunistic pathogen." ;
RL   Nature 406:959-964(2000).
DR   ENBL; AE004613; AAC05263.1; --; Genomic_DNA.
DR   PIR; A83412; ASW41.
DR   HSSP; P22629; 1SWH.
GO; GO:0005509; F:calcium ion binding; IEA.
DR   InterPro; IPR001343; Hemlyan_Ca_bind.
DR   InterPro; IPR006162; Pplantne_S.
DR   InterPro; IPR002035; VWF_A.
DR   PRINTS; PR00313; CAENDNGRPT.
DR   PRINTS; PR00453; VWFADOMAIN.
DR   PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN 1.

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RESULT 15

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Q4J4Q1.AZQVI
AC Q4J4Q1.AZQVI PRELIMINARY; PRT; 476 AA.
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DE Hypothetical protein.
GN ORFNames=AvindRAFT_6098;
OS Azotobacter vinelandii AvOP.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=322710;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Azotobacter vinelandii
RT AvOP.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Azotobacter vinelandii
RT AvOP.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAU03000001; EAM07440.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 49423 MW; 1025B18ADE1E6158 CRC64;

Query Match 13.6%; Score 90; DB 2; Length 476;
Best Local Similarity 28.9%; Pred. No. 16;
Matches 35; Conservative 9; Mismatches 43; Indels 34; Gaps 4;

QY 13 DPQFTG-----PAAAGQKVGTSITATGPHNSVIAGKGSVSGGV 54
DB 296 DPQGTGADGDLDMAVIAGVGTQVVAEQQTAEITGLVAAFQENTVLGGARGAEVIGGA 355
QY 55 A-----TVPFVDGQGPVFRGRIQGANINDQANTGIDGLAGWRVASSQETLNPVPTTF 107
DB 356 ADGKDQGVVFQFALGQGRALFLGR-----LGRQADT-----LVGPVQTAHAHAVLELVVPF 406
QY 108 G 108
DB 407 G 407

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Search completed: April 26, 2006, 17:04:38
 Job time : 77 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 26, 2006, 17:04:07 ; Search time 23 Seconds
(without alignments)
460.108 Million cell updates/sec

Title: US-10-018-892-3
Perfect score: 662
Sequence: 1 AAQNTTSANWSQDPGFTGPA.....KSTLPAGFTATFYVQYQN 128

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCRTUS COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	662	100.0	144	2	US-09-230-078A-6
2	662	100.0	144	2	US-09-230-078A-6
3	662	100.0	176	1	US-08-233-788A-40
4	662	100.0	180	2	US-08-449-922-1
5	646.5	97.7	143	2	US-09-230-078A-4
6	87.5	13.2	328	1	US-09-543-407-46
7	86.5	13.1	2736	2	US-08-229-287-4
8	83	12.5	549	2	US-09-252-991A-30227
9	82.5	12.5	1415	2	US-09-712-363-190
10	82.5	12.5	2763	2	US-09-252-991A-26438
11	81.5	12.3	693	2	US-08-496-344-2
12	79.5	12.0	1509	2	US-09-252-991A-19167
13	79	11.9	1481	1	US-09-676-519-27
14	79	11.9	1481	1	US-08-616-844-40
15	79	11.9	1481	1	US-08-599-654-40
16	79	11.9	1481	2	US-08-944-868A-40
17	79	11.9	1481	2	US-08-944-423A-40
18	78.5	11.9	281	2	US-08-944-496-40
19	78.5	11.9	281	2	US-09-512-251A-9
20	78.5	11.9	281	2	US-09-515-150A-9
21	78.5	11.9	281	2	US-09-196-281-12
22	78.5	11.9	512	2	US-10-336-324-9
23	78.5	11.9	522	2	US-09-107-532A-6559
24	78.5	11.9	613	2	US-09-902-540-12496
25	77	11.6	469	2	US-09-252-991A-20168
26	77	11.6	675	2	US-10-018-902-30
27	77	11.6	1569	2	US-10-104-047-3810
					US-09-711-164-312

28 76.5 11.6 617 2 US-10-104-047-2915 Sequence 2915, Ap
29 76.5 11.6 730 2 US-09-961-403-8 Sequence 8, Appli
30 76.5 11.6 731 1 US-08-911-364-1 Sequence 1, Appli
31 76.5 11.6 731 2 US-09-340-736B-1 Sequence 1, Appli
32 76.5 11.6 731 2 US-09-364-662-1 Sequence 1, Appli
33 76.5 11.6 733 2 US-08-464-700-2 Sequence 2, Appli
34 76.5 11.6 792 1 US-08-678-039A-40 Sequence 302, App
35 76.5 11.6 2383 2 US-09-492-709A-302 Sequence 40, Appl
36 75.5 11.4 1218 2 US-09-949-016-7065 Sequence 7065, Ap
37 75.5 11.4 1690 2 US-09-949-016-5884 Sequence 5884, Ap
38 75 11.3 214 2 US-09-252-991A-27795 Sequence 27795, A
39 75 11.3 910 2 US-09-902-540-10793 Sequence 10793, A
40 74.5 11.3 1034 2 US-09-252-991A-26658 Sequence 26658, A
41 74.5 11.3 1912 1 US-08-409-995-4 Sequence 4, Appli
42 74.5 11.3 1912 2 US-08-685-467-4 Sequence 4, Appli
43 74.5 11.3 2353 2 US-09-377-155-33 Sequence 33, Appli
44 74.5 11.3 2353 2 US-08-913-942-4 Sequence 4, Appli
45 74.5 11.3 2353 2 US-09-669-974-33 Sequence 33, Appli

ALIGNMENTS

RESULT 1

US-09-230-078A-6
; Sequence 6, Application US/09230078A
; Patent No. 6495334
; GENERAL INFORMATION:
; APPLICANT: Rajashekara, Gireesh
; APPLICANT: Kakambi, Nagarata V.
; APPLICANT: Kapur, Vivek
; TITLE OF INVENTION: RECOMBINANT SEF14 FIMBRIAL PROTEIN FROM SALMONELLA
; FILE REFERENCE: 600.335USWO
; CURRENT APPLICATION NUMBER: US/09/230,078A
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: PCT/US97/12639
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 60/022,191
; PRIOR FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Salmonella enteritidis
US-09-230-078A-6

Query Match 100.0%; Score 662; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 7.5e-62;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAQNTTSANWSQDPGFTGTPAAGQKVGTLSTATGPHNSVSIAGKASVSGGVATVPFV 60
Db 17 AAQNTTSANWSQDPGFTGTPAAGQKVGTLSTATGPHNSVSIAGKASVSGGVATVPFV 76
Qy 61 DQGGQVPRGRIOGANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTPTAT 120
Db 77 DQGGQVPRGRIOGANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTPTAT 136
Qy 121 FYVQYQN 128
Db 137 FYVQYQN 144

RESULT 2

US-08-233-788A-40
; Sequence 40, Application US/082333788A
; Patent No. 5635617
; GENERAL INFORMATION:
; APPLICANT: Doran, James L.
; APPLICANT: Kay, William W.
; APPLICANT: Collinson, Karen S.
; APPLICANT: Clouthier, Sharon C.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
 TITLE OF INVENTION: OF SALMONELLA

NUMBER OF SEQUENCES: 61
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Seed and Berry
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: U.S.A.
 ZIP: 98104-7092

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 FILING DATE: 26-APR-1994
 APPLICATION NUMBER: US/08/233,788A

CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: King, Joshua
 REGISTRATION NUMBER: 35,570
 REFERENCE/DOCKET NUMBER: 920043.403C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 TELEX: 3723836 SEEDANBERRY

INFORMATION FOR SEQ ID NO: 40:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 165 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-233-788A-40

Query Match 100.0%; Score 662; DB 1; Length 165;
 Best Local Similarity 100.0%; Pred. No. 8.9e-62;
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAQNTTSANWSQDPGFTGPAVAAGKVGTLSTATGPHNSVSIAGKGSVSGGVATVPFV 60
 Db 38 AAQNTTSANWSQDPGFTGPAVAAGKVGTLSTATGPHNSVSIAGKGSVSGGVATVPFV 97
 Qy 61 DGGQPVPRGRIQGANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTFTAT 120
 Db 98 DGGQPVPRGRIQGANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTFTAT 157
 Qy 121 FVQOYQN 128
 Db 158 FVQOYQN 165

RESULT 3
 US-08-449-922-1
 Sequence 1, Application US/08449922
 Patent No. 5510241
 GENERAL INFORMATION:
 APPLICANT: THORNS, CHRISTOPHER J
 TITLE OF INVENTION: METHOD OF TESTING FOR SALMONELLA
 NUMBER OF SEQUENCES: 1
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHYE, P C
 STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: USA
 ZIP: 22201
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/449,922
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08,030,208
 FILING DATE: 26-MAR-1993
 APPLICATION NUMBER: GB 9021290.3
 FILING DATE: 01-OCT-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9022570.7
 FILING DATE: 17-OCT-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9106546.6
 FILING DATE: 27-MAR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: CRAWFORD, ARTHUR R
 REGISTRATION NUMBER: 25,327
 REFERENCE/DOCKET NUMBER: 1498-30
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 176 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 ORIGINAL SOURCE:
 ORGANISM: Salmonella enteritidis/Salmonella dublin
 US-08-449-922-1

Query Match 100.0%; Score 662; DB 1; Length 176;
 Best Local Similarity 100.0%; Pred. No. 9.6e-62;
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAQNTTSANWSQDPGFTGPAVAAGKVGTLSTATGPHNSVSIAGKGSVSGGVATVPFV 60
 Db 49 AAQNTTSANWSQDPGFTGPAVAAGKVGTLSTATGPHNSVSIAGKGSVSGGVATVPFV 108
 Qy 61 DGGQPVPRGRIQGANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTFTAT 120
 Db 109 DGGQPVPRGRIQGANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTFTAT 168
 Qy 121 FVQOYQN 128
 Db 169 FVQOYQN 176

RESULT 4
 US-09-230-078A-4
 Sequence 4, Application US/09230078A
 Patent No. 6495334
 GENERAL INFORMATION:
 APPLICANT: Rajashekara, Gireesh
 APPLICANT: Kakambi, Nagarata V.
 APPLICANT: Kapur, Vivek
 TITLE OF INVENTION: RECOMBINANT SEF14 FIMBRIAL PROTEIN FROM SALMONELLA
 FILE REFERENCE: 600.33USNO
 CURRENT APPLICATION NUMBER: US/09/230,078A
 CURRENT FILING DATE: 1999-05-20
 PRIOR APPLICATION NUMBER: PCT/US97/12639
 PRIOR FILING DATE: 1997-07-18
 PRIOR APPLICATION NUMBER: 60/022,191
 PRIOR FILING DATE: 1996-07-19
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: Patent in Ver. 2.1
 SEQ ID NO 4
 LENGTH: 180
 TYPE: PRT
 ORGANISM: Salmonella enteritidis
 US-09-230-078A-4

Query Match 100.0%; Score 662; DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. No. 9.9e-62;
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AAQNTTSANWSODPGFTGPAVAAQCKVGTLSITATGPHNSVSIACKGASVSGGVATVPV	60
Db	53	AAQNTTSANWSODPGFTGPAVAAQCKVGTLSITATGPHNSVSIACKGASVSGGVATVPV	112
Qy	61	DGQQPVRGRIQANINDQANTGIDGLAGWRVASSQETLNPVPTVTFCKSTLPAGTFTAT	120
Db	113	DGQQPVRGRIQANINDQANTGIDGLAGWRVASSQETLNPVPTVTFCKSTLPAGTFTAT	172

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RESULT 5
US-09-543-407-46
; Sequence 46, Application US/09543407
; Patent No. 6864365
; GENERAL INFORMATION:
; APPLICANT: White, Aaron P.
; APPLICANT: Doran, James L.
; APPLICANT: Collinson, S. Karen
; APPLICANT: Kay, William W.
; TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
; TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
; FILE REFERENCE: 920043.406
; CURRENT APPLICATION NUMBER: US/09/543,407
; CURRENT FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Salmonella enteritidis
US-09-543-407-46

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Query Match	97.7%	Score 646.5	DB 2	Length 143
Best Local Similarity	99.2%	Pred. No. 3.1e-60		
Matches 127	Conservative	0	Mismatches 0	Indels 1
				Gaps 1

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RESULT 6
US-08-229-287-4
; Sequence 4, Application US/08229287
; Patent No. 5530193
; GENERAL INFORMATION:
; APPLICANT: Clark Jr., John M.
; APPLICANT: Milka, Joseph M.
; APPLICANT: Murry, Lynn E.
; APPLICANT: Scarafia, Lilliana E.
; TITLE OF INVENTION: VIRUS RESISTANT CORN PLANTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Sandoz Agro, Inc.
; STREET: 975 California Avenue
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/229,287
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/067,257
/ FILING DATE: 25-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/817,922
/ FILING DATE: 08-JAN-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Marcus-Wyner, Lynn
/ REGISTRATION NUMBER: 34,869
/ REFERENCE/DOCKET NUMBER: 135-1084/XCC
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415/354-3588
/ TELEFAX: 415/857-1125
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 328 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-229-287-4

Query Match 13.2%; Score 87.5; DB 1; Length 328;
Best Local Similarity 30.1%; Pred. No. 0.41;
Matches 31; Conservative 9; Mismatches 54; Indels 9; Gaps 2;

Qy 11 SDDPGFTGPAVAGQKVGTLSTATGPHNSVSIAGKGASVSGGVATVPFVDGQGPVFRG 70
Db 12 SGSQCTTPPTGSGAK-----PATSGAGSGGTGAGTGTGQARTGSGGTGTGSGATGG 65

Qy 71 RIQGANINDQANTGIDGLGWRVASSQETLNVPTTFGKSTLP 113
Db 66 QSGSGSGTGEQVNT---GSGATNATGQQRDDVDAGSTGKISVP 105

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RESULT 7
US-09-252-991A-30227
; Sequence 30227, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30227
; LENGTH: 2736
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30227

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Query Match      13.1%; Score 86.5; DB 2; Length 2736;
Best Local Similarity 22.8%; Pred. No. 7, 9;
Matches 33; Conservative 12; Mismatches 43; Indels 57; Gaps 6;

Qy 7 SANW-----SQDP-GFTGPAAAGQKVGTLSITATGPNHSVSIAGKGA 48
   |||||:|||||
Db 1306 SGNWTFTPATPLANGTVVNAVAQDPAGNTGPQ-----GSTTVDVAAPTVPVNPNGN 1358
   |||||:|||||

Qy 49 SVSGGV---ATVPFVDGGQGVFRGRIQGANINDQANTCIDGLAGHRVASSQETLN--- 101
   |||||:|||||
Db 1359 LINCTARGSGTIVTIDGNGNPT-----GOTTADGSGNWSFTPGSOLPNCITVV 1405
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QY 102 -----VPTTFKSTLPA 114
 DB 1406 NVTASDAAGNTSAPATTIVDSSLPS 1430

RESULT 8
 US-09-712-363-190
 ; Sequence 190, Application US/09712363
 ; Patent No. 6892139
 ; GENERAL INFORMATION:
 ; APPLICANT: Eisenberg, David
 ; APPLICANT: Rotstein, Sergio H.
 ; APPLICANT: Marcotte, Edward M.
 ; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
 ; FILE REFERENCE: 07419-032001
 ; CURRENT APPLICATION NUMBER: US/09/712,363
 ; CURRENT FILING DATE: 2000-11-13
 ; PRIOR APPLICATION NUMBER: PCT/US00/02246
 ; PRIOR FILING DATE: 2000-01-28
 ; PRIOR APPLICATION NUMBER: 60/179,531
 ; PRIOR FILING DATE: 2000-02-01
 ; PRIOR APPLICATION NUMBER: 60/117,844
 ; PRIOR FILING DATE: 1999-01-29
 ; PRIOR APPLICATION NUMBER: 60/118,206,
 ; PRIOR FILING DATE: 1999-02-01
 ; PRIOR APPLICATION NUMBER: 60/126,593
 ; PRIOR FILING DATE: 1999-03-26
 ; PRIOR APPLICATION NUMBER: 60/134,093
 ; PRIOR FILING DATE: 1999-05-14
 ; PRIOR APPLICATION NUMBER: 60/134,092
 ; PRIOR FILING DATE: 1999-05-14
 ; PRIOR APPLICATION NUMBER: 60/165,124
 ; PRIOR FILING DATE: 1999-11-12
 ; PRIOR APPLICATION NUMBER: 60/165,086
 ; PRIOR FILING DATE: 1999-11-12
 ; NUMBER OF SEQ ID NOS: 292
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 190
 ; LENGTH: 549
 ; TYPE: PRT
 ; ORGANISM: Mycobacterium tuberculosis
 ; US-09-712-363-190

Query Match 12.5%; Score 83; DB 2; Length 549;
 Best Local Similarity 25.6%; Pred. No. 2.4;
 Matches 34; Conservative 18; Mismatches 43; Indels 38; Gaps 5;
 QY 1 AAQNTTSANWSQDPGFTGPAVAAGKVGTLISITATGPHNSVSIAGK-----GASVS- 51
 DB 142 AAEKDGAGDPDPDPDRDPAALAA--LGTPLAAPAPHGALAGSGKLVGRDVLFGKVS 199
 QY 52 ---GGVATVPVDCGQGVFRGRIQGANINDQANTGIDGLAGWRVASSQBE---TLNVPVT 105
 DB 200 LALGILVAIALVTG-----GIGGVIGKRTAEVVDFTTSKVTLS 238
 QY 106 TFGKSTLPAGTFT 118
 DB 239 TTGNAQBPAGRFT 251

RESULT 9
 US-09-252-991A-26438
 ; Sequence 26438, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18

Query Match 12.5%; Score 82.5; DB 2; Length 2763;
 Best Local Similarity 29.1%; Pred. No. 21;
 Matches 30; Conservative 9; Mismatches 55; Indels 9; Gaps 2;
 QY 11 SQDPGFTGPAVAAGKVGTLISITATGPHNSVSIAGKASVSGGVATVPVDCGQGVFRG 70
 DB 2447 SGSQGTTPATGSGAK-----PATSGAGSGSDTGAGTGTGTSQARTGSGTGTSGATGG 2500
 QY 71 RIQGANINDQANTGIDGLAGWRVASSQETLNVPVTFGKSTLP 113

; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 26438
 ; LENGTH: 1415
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-26438

Query Match 12.5%; Score 82.5; DB 2; Length 1415;
 Best Local Similarity 28.8%; Pred. No. 8.9;
 Matches 34; Conservative 13; Mismatches 52; Indels 19; Gaps 6;
 QY 2 AQNTTSANWSQDPGFT-----GPAV--AAQKVGTLISITATGPHN-----SVSTAGKG 47
 DB 392 AQGPAGANASDSNGTIVQQQPAVDLAAGAN-GTSAVQSQGANIGSGANGISVVQSQNG 450
 QY 48 ASVSGGVATVPVDCGQGVFRGRIQGANI---NDQANTGIDGLAGWRVASSQETLN 102
 DB 451 ANIGAGASDISVVQSQNSPNTGSGVGTVVQSQGANIG-SGASGITVVQSQGANI 507

RESULT 10
 US-08-496-944-2
 ; Sequence 2, Application US/08496944
 ; Patent No. 6040496
 ; GENERAL INFORMATION:
 ; APPLICANT: Law, Marcus D
 ; APPLICANT: Dietz, Jon M
 ; TITLE OF INVENTION: Use of Translationally altered RNA to
 ; TITLE OF INVENTION: Confer Resistance to Maize Dwarf Mosaic Virus and Other
 ; TITLE OF INVENTION: Monocotyledonous Plant Viruses
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CIBA-Geigy Corporation
 ; STREET: 7 Skyline Drive
 ; CITY: Hawthorne
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10532
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30B
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/496,944
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Elmer, James Scott
 ; REGISTRATION NUMBER: 36,129
 ; REFERENCE/DOCKET NUMBER: CGC 1814
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2763 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-496-944-2

Query Match 12.5%; Score 82.5; DB 2; Length 2763;
 Best Local Similarity 29.1%; Pred. No. 21;
 Matches 30; Conservative 9; Mismatches 55; Indels 9; Gaps 2;
 QY 11 SQDPGFTGPAVAAGKVGTLISITATGPHNSVSIAGKASVSGGVATVPVDCGQGVFRG 70
 DB 2447 SGSQGTTPATGSGAK-----PATSGAGSGSDTGAGTGTGTSQARTGSGTGTSGATGG 2500
 QY 71 RIQGANINDQANTGIDGLAGWRVASSQETLNVPVTFGKSTLP 113

Db 2501 QSGSGTGEQVNT---GSAGTNATGGQRDRDNDAGSTGKISVP 2540

RESULT 11
US-09-252-991A-19167
; Sequence 19167, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19167
; LENGTH: 693
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19167

Query Match 12.3%; Score 81.5; DB 2; Length 693;
Best Local Similarity 28.3%; Pred. No. 4.6;
Matches 32; Conservative 17; Mismatches 51; Indels 13; Gaps 6;

Qy 15 GFTGPAVAAGQKVGTLSTATGPHNSVSIAGKAS--VSGGVATVPFVDGQG-QPVFRGR 71
Db 236 GLFGRHVGPAKVSFVSALMG-----ITGSGVANVVTGQFTIPLMKRFGYKPAFAGG 280

Qy 72 IQG-ANINDQANTGIDGLAGWRVASSQETLNVPTTFGKSTL-PAGTFTATFY 122
Db 281 VEATASMSQLMPPFVMGAVAFIMA---ETINVPYVYIAKAALIPALLYFGSVY 330

RESULT 12
US-09-676-519-27
; Sequence 27, Application US/09676519
; Patent No. 6737508
; GENERAL INFORMATION:
; APPLICANT: PELLETIER, JERRY
; APPLICANT: GROS, PHILIPPE
; APPLICANT: DUBOW, MICHAEL
; TITLE OF INVENTION: DNA SEQUENCES FROM STAPHYLOCOCCUS AUREUS BACTERIOPHAGES
; TITLE OF INVENTION: 3A, 77, AND 96 THAT ENCODE ANTI-MICROBIAL POLYPEPTIDES
; FILE REFERENCE: 073406-0404
; CURRENT APPLICATION NUMBER: US/09/676,519
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/407,804
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: 60/110,992
; PRIOR FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 27
; LENGTH: 1509
; TYPE: PRT
; ORGANISM: Staphylococcus bacteriophage
US-09-676-519-27

Query Match 12.0%; Score 79.5; DB 2; Length 1509;
Best Local Similarity 28.6%; Pred. No. 20;
Matches 28; Conservative 9; Mismatches 34; Indels 27; Gaps 3;

Qy 9 NWSQDPGFTGPAVAAGQKVGTLST--ATGPH-----NSVS 42
Db 1194 NFSKSP-SGTMVFKPGDVGLTGNTGFTGPHLHFEMRNGRHFDPFLRNKKGRLS 1252

Qy 43 IAGKASVSGGVATVPFVDGQGQPVFRGRIGANINDQ 80

Db 1253 IGGGATSGSGATYASRVIRQAQSILGGRYKGRKWIHQ 1290

RESULT 13
US-08-616-844-40
; Sequence 40, Application US/08616844
; Patent No. 5849578
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A.
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/616,844
; FILING DATE: 15-MAR-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/599,654
; FILING DATE: 09-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,573
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CORUZZI, LAURA A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1481 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-616-844-40

Query Match 11.9%; Score 79; DB 1; Length 1481;
Best Local Similarity 30.1%; Pred. No. 22;
Matches 44; Conservative 16; Mismatches 54; Indels 32; Gaps 8;

Qy 6 TSANWSQ-DPGFTGPAVAAGQKV---GTLSTITA---TGPHNSVSIAGKASVSGGVATV 57
Db 931 TSTNLAQMSPTFTTILKTSQPLMTTPGTLSTASLVTGPIAVQTTAGKQLSLTHPELV 990

Qy 58 PFVDGQGQ-PVFRGRIGGANINDQANTGIDGLAGWRVASSQETLNVPTV-----TFG 108
Db 991 PQISTEGGISTERNRV---IVD-ATTGLIPLTSVPTSAREMTTKLGVTAEYSPASRSLG 1045

Qy 109 KSTLPAGTF-----TATFYVQ 124

Db 1046 TSPSPQTTVVSTAEDLAPKSAFAVQ 1071

RESULT 14
US-08-599-654-40

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; Sequence 40, Application US/08599654
; Patent No. 5882925
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,654
; FILING DATE: 09-FEB-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,573
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CORUZZI, LAURA A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-041
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1481 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-599-654-40

Query Match 11.9%; Score 79; DB 1; Length 1481;
Best Local Similarity 30.1%; Pred. No. 22;
Matches 44; Conservative 16; Mismatches 54; Indels 32; Gaps 8;

Qy 6 TSANWSQ-DPGFTGPAVAAGKV-----GTLGITA---TGPHNSVSIAGKGASVSGGVATV 57
Db 931 TSTNLAQMSPTFTTILKTSQPLMTTPTGLSTASLTGPIAVQTAGKQLSLTHPEILV 990

Qy 58 PFVDGQGGQ-PVFRGRIQAGNINDQANTGIDGLAGMRVASSQETLNVPT-----TFG 108
Db 991 PQISTEGGISTERNRV-----IVD-ATTGLIPLTSTVPTSAKEMTTKLGVTAEYSPASRSLG 1045

Qy 109 KSTLPAGTF-----TATFYVQ 124
Db 1046 TSPSPQTTVVSTAEADLPKSNATFAVQ 1071

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RESULT 15
US-08-944-868A-40
; Sequence 40, Application US/08944868A
; Patent No. 6018025
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,868A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/599,654
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CORUZZI, LAURA A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-041
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1481 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-944-868A-40

Query Match 11.9%; Score 79; DB 2; Length 1481;
Best Local Similarity 30.1%; Pred. No. 22;
Matches 44; Conservative 16; Mismatches 54; Indels 32; Gaps 8;

Qy 6 TSANWSQ-DPGFTGPAVAAGKV-----GTLGITA---TGPHNSVSIAGKGASVSGGVATV 57
Db 931 TSTNLAQMSPTFTTILKTSQPLMTTPTGLSTASLTGPIAVQTAGKQLSLTHPEILV 990

Qy 58 PFVDGQGGQ-PVFRGRIQAGNINDQANTGIDGLAGMRVASSQETLNVPT-----TFG 108
Db 991 PQISTEGGISTERNRV-----IVD-ATTGLIPLTSTVPTSAKEMTTKLGVTAEYSPASRSLG 1045

Qy 109 KSTLPAGTF-----TATFYVQ 124
Db 1046 TSPSPQTTVVSTAEADLPKSNATFAVQ 1071

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Search completed: April 26, 2006, 17:06:55
Job time : 24 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 26, 2006, 17:04:53 ; Search time 64 Seconds
(without alignments)
835.659 Million cell updates/sec

Title: US-10-018-892-3
Perfect score: 662
Sequence: 1 AAQNTTSANWSQDPGFTGPA.....KSTLPAGTFTATFYVQYQN 128

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94	14.2	176	4	US-10-425-115-215192
2	94	14.2	233	4	US-10-425-115-215188
3	93.5	14.1	431	4	US-10-374-780A-1998
4	91.5	13.8	2468	4	US-10-246-330-4
5	91.5	13.8	2468	4	US-10-282-122A-66335
6	88.5	13.4	439	4	US-10-425-114-72872
7	87	13.1	609	4	US-10-156-761-10122
8	83.5	12.6	219	4	US-10-425-114-70608
9	83.5	12.6	230	4	US-10-425-115-269298
10	83	12.5	466	4	US-10-156-761-9303
11	83	12.5	524	4	US-10-282-122A-62373
12	83	12.5	549	3	US-09-712-363-190
13	83	12.5	549	4	US-10-282-122A-64511
14	83	12.5	549	4	US-10-432-934-62
15	83	12.5	660	6	US-11-053-710A-5
16	81.5	12.3	1721	4	US-10-282-122A-62548
17	81.5	12.3	2204	4	US-10-282-122A-64364
18	81.5	12.3	2694	4	US-10-184-644-207
19	81.5	12.3	2694	4	US-10-184-634-207
20	81	12.2	174	4	US-10-425-115-215193
21	81	12.2	329	4	US-10-029-386-32216
22	81	12.2	334	4	US-10-282-122A-47939
23	81	12.2	441	4	US-10-425-115-289415
24	81	12.2	605	4	US-10-094-749-3209
25	81	12.2	607	4	US-10-425-115-269306
26	81	12.2	827	4	US-10-282-122A-47312
27	80.5	12.2	139	4	US-10-437-963-183869

28	80.5	12.2	595	4	US-10-282-122A-47723	Sequence 47723, A
29	80.5	12.2	999	4	US-10-408-765A-2033	Sequence 2033, Ap
30	80.5	12.2	1862	4	US-10-282-122A-49757	Sequence 49757, A
31	80	12.1	176	4	US-10-767-701-38981	Sequence 38981, A
32	80	12.1	176	4	US-10-425-115-366647	Sequence 366647, A
33	80	12.1	205	4	US-10-425-115-269307	Sequence 269307, A
34	80	12.1	291	4	US-10-156-761-13735	Sequence 13735, A
35	79.5	12.0	342	4	US-10-156-761-12399	Sequence 12399, A
36	79.5	12.0	561	4	US-10-156-761-13274	Sequence 13274, A
37	79	11.9	367	4	US-10-282-122A-47588	Sequence 47588, A
38	79	11.9	654	4	US-10-467-490-6	Sequence 6, Appli
39	79	11.9	946	3	US-09-840-746-1	Sequence 1, Appli
40	79	11.9	1331	4	US-10-282-122A-47930	Sequence 47930, A
41	79	11.9	1481	3	US-09-371-900-40	Sequence 40, Appl
42	79	11.9	1481	3	US-09-924-417-60	Sequence 60, Appl
43	79	11.9	1481	4	US-10-186-950-40	Sequence 40, Appl
44	79	11.9	1481	4	US-10-653-872-60	Sequence 60, Appl
45	78.5	11.9	158	4	US-10-767-701-45705	Sequence 45705, A

ALIGNMENTS

RESULT 1
US-10-425-115-215192
; Sequence 215192, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 215192
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_127852C.1.pap
US-10-425-115-215192

Query Match	14.2%;	Score 94;	DB 4;	Length 176;
Best Local Similarity	29.5%;	Pred. No. 0.16;		
Matches	38;	Conservative 14;	Mismatches 41;	Indels 36; Gaps 6;
QY	1	AAQNTTSANWS-----QDPGFTGPAVAGQKVGTLISITAT-----G	36	
Db	55	ASNTSSTNFGAVVAIDPLTTGPTRAAGTGVRAQGYTFADQQTFGLLMVNMFVFTAG	114	
QY	37	PHN--SVSTAGKASGSGVATVPFVGGQ--PVPRGRIQGANINDQANTGIDGLACGRV	93	
Db	115	EHNGTSLSLGN--EVLSDVREMSIVGSGKFRMARGVQAHTIDSGATSG-----T	165	
QY	94	ASSQETLNV	102	
Db	166	TVQYTVNV	174	

RESULT 2
US-10-425-115-215188
; Sequence 215188, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

```

; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 215188
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_127849C.1.pep
US-10-425-115-215188

Query Match 14.2%; Score 94; DB 4; Length 233;
Best Local Similarity 29.5%; Pred. No. 0.22; Indels 36; Gaps 6;
Matches 36; Conservative 14; Mismatches 41; Indels 36; Gaps 6;

QY 1 AAQNTTSANWS-----ODPGFTGPAVAAAGKVG-TLSITATGPHNSVSIAGKGA-SVSGGVATVP 58
Db 112 ASNTSSTNFGAVVAIDDLTTGTTRAAGTEVGRAQGTTFADQQTGLLMMVNFVFTAG 171
QY 37 PHN--SVSIAGKASVSGGVATVPFVDGQGO-PVFRGRIQGANINDQANTGIDGLAGWRV 93
Db 172 EHNSTLSILGRN-EVLSDVREMSIVGSGKFRMARGVVOAHTIDSGATSG-----T 222
QY 94 ASQOETLNV 102
Db 223 TVVQYTVNV 231

RESULT 3
US-10-374-780A-1998
; Sequence 1998, Application US/10374780A
; Publication No. US20040019927A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, Bradley K
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Heard, Jacqueline E
; APPLICANT: Haake, Volker
; APPLICANT: Creelman, Robert A
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Adam, Luc J
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddle, James
; APPLICANT: Broun, Pierre E
; APPLICANT: Pilgrim, Marsha L
; APPLICANT: Dubell III, Arnold T
; APPLICANT: Pineda, Omaira
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
; FILE REFERENCE: MBI-0047 CIP
; CURRENT APPLICATION NUMBER: 2003-02-25
; PRIOR FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/837,944
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/934,455
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 10/225,066
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,067
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,068
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 2906

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1998
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G426 Paralogous to G427
US-10-374-780A-1998

Query Match 14.1%; Score 93.5; DB 4; Length 431;
Best Local Similarity 33.3%; Pred. No. 0.54; Indels 11; Gaps 6;
Matches 36; Conservative 14; Mismatches 47; Indels 11; Gaps 6;

QY 1 AAQNTTSANWSQDPGFTGPAVAAAGKVG-TLSITATGPHNSVSIAGKGA-SVSGGVATVP 58
Db 68 ATANTTTASSSDSSSSAAAAAANQWLSRSSFLQRNNNNASIVGDGDDVTGGADTMI 127
QY 59 FVDGQGOQPVFRGRIQGANINDOAN-TGIDGLAGWRVASSQ-ETLNVFV 104
Db 128 ----QGMKTGG---GENKNDGGGATAADGVVSMQNAHKAEILSHPL 168

RESULT 4
US-10-246-330-4
; Sequence 4, Application US/10246330
; Publication No. US20030166030A1
; GENERAL INFORMATION:
; APPLICANT: O'Toole, George A.
; APPLICANT: Mah, Thien-Fah
; TITLE OF INVENTION: METHODS TO STUDY AND MECHANISMS OF
; FILE REFERENCE: 14537-002001
; CURRENT APPLICATION NUMBER: US/10/246,330
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/323,241
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 2468
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-246-330-4

Query Match 13.8%; Score 91.5; DB 4; Length 2468;
Best Local Similarity 26.3%; Pred. No. 7.6; Indels 47; Gaps 7;
Matches 36; Conservative 11; Mismatches 43; Indels 47; Gaps 7;

QY 7 SANWS-----QDP-GFTGPAVAAAGKVG-TLSITATGPHNSVSIAGKGA 48
Db 1284 SGNWSFTPTGTPLANGTVVNAVAQDPAGNTGPO-----GSTTVDAAVAFNTPVVPSNGN 1336
QY 49 SVSGGV---ATVPFVDGQGOQPVFRGRIQGANINDQANTGIDGLAGWRVASSQETLN---V 102
Db 1337 LLNGTAEPGSTVTLTDGNGNPI-----GOTTADSGSNWSFTPGSQLPNGTVV 1383
QY 103 PVT---TFGKSTLPAGT 116
Db 1384 NVTASDAAGNTSLPAT 1400

RESULT 5
US-10-282-122A-66335
; Sequence 66335, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel

```

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; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66335
; LENGTH: 2468
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-66335

Query Match          13.8%; Score 91.5; DB 4; Length 2468;
Best Local Similarity 26.3%; Pred. No. 7.6;
Matches 36; Conservative 11; Mismatches 43; Indels 47; Gaps 7;

Qy 7 SANNS-----QDP-GFTGPAVAGQKVGTLSTITATGPHNSVIAGKGA 48
Db 1284 SGNWSFTPGTFLANGTVVNAVAQDPAGNTGQ-----GSTTVDVAVAPTFVVPNSGN 1336

Qy 49 SVSGGV---ATVPFVDSQGPVFRGRIQGANINDQANTGIDGLAGRWVASSOETLN---V 102
Db 1337 LLNGTAERGSIIVTLTDNGNPI-----GQTTADSGNWSFTPGSQLPNGTVV 1383

Qy 103 PVT---TFGKSTLPAGT 116
Db 1384 NVTASDAAGNTSLPATT 1400

RESULT 6
US-10-425-114-72872
; Sequence 72872, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, Steven E.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 72872
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; LENGTH: 439
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana columbia
; FEATURE:
; OTHER INFORMATION: Clone ID: JC-ATXLIB327421P4P06_FLI.pep
US-10-425-114-72872

Query Match          13.4%; Score 88.5; DB 4; Length 439;
Best Local Similarity 33.3%; Pred. No. 1.8;
Matches 36; Conservative 13; Mismatches 48; Indels 11; Gaps 6;

Qy 1 AAQNTTSANWSQDPGFTGPAVAGQKVG-TLSITATGPHNSVIAGKGA-SVSGGVATVP 58
Db 88 ATANTTTASSDPPSSAAAAAANQWLSPSSFLQRNNNNASIVGDDIVTGGADTMI 147

Qy 59 FVDGQGPVFRGRIQGANINDQAN-TGIDGLAGRWVASSO-ETLNVVP 104
Db 148 ----QGEMKTGG---GENKNDGGGATAADGVWSQWNAHKAELSHPL 188

RESULT 7
US-10-156-761-10122
; Sequence 10122, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 10122
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10122

Query Match          13.1%; Score 87; DB 4; Length 609;
Best Local Similarity 25.7%; Pred. No. 3.9;
Matches 35; Conservative 22; Mismatches 49; Indels 30; Gaps 6;

Qy 6 TSANWSQDPGFTGPAVAGQKVGTLSTITATGPHNSVIAGKGSVSGGVATVPFVDQGG 65
Db 161 TGAYYADDISLVGPGVDAGQPPAAPGLKAGTVTSTSVALSWSAVPGAT-----GY 211

Qy 66 PVFRGRIQGANINDQANTGIDGLA-----GWRVAS-----SOETLNVPTTF-----GK 109
Db 212 AIYRDGVKARSVTGTSAT-VTGLSPATAYGFQVAAVNDAGESAKSATVPATTSAGSGGGS 270

Qy 110 STLPA-----GTETATF 121
Db 271 TDLPAHALVGYLHASF 286

RESULT 8
US-10-425-114-70608
; Sequence 70608, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, Steven E.
; APPLICANT: Screen, Steven E.
```

APPLICANT: Tabaaka, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 70608
LENGTH: 219
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3600-056-H10_F11.pep
US-10-425-114-70608

Query Match 12.6%; Score 83.5; DB 4; Length 219;
Best Local Similarity 28.2%; Pred. No. 2.5;
Matches 40; Conservative 16; Mismatches 45; Indels 41; Gaps 6;
QY 1 AAQNTTSANWSQDPGFTGPAVAGQKVGTTLSITATGPHNSV-----SIAGKGSVSG--- 52
DB 53 AATSLVSAATSGSAASGTGAAA-----SVSAAGAAASVSASLTSVSAAGAAAGSAS 104
QY 53 -GVATVPFDGQGPVPRGRIQGANINDQANTGIDGLAGRWVASSQETLNVPTTFGKST 111
DB 105 LGSASVGSATASASLV-----SVSVASSTGSGSLA---TTTSVSTAGAAVSSFGVST 153
QY 112 LPA-----GTFTAT 120
DB 154 ABAASWAASSTGAAGVGTWIST 175

RESULT 9
US-10-425-115-269298
Sequence 269298, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 269298
LENGTH: 230
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MFT4577_177198C.1.pep
US-10-425-115-269298

Query Match 12.6%; Score 83.5; DB 4; Length 230;
Best Local Similarity 27.3%; Pred. No. 2.7;
Matches 41; Conservative 16; Mismatches 58; Indels 35; Gaps 5;
QY 1 AAQNTTSANWSQDPGFTGPAVAGQKVGTTLSITATGPHNSVSIAGKGSVSGVATVPFV 60
DB 50 AAASLVSAATSGSAASGTGAAA-----SVSAAGAAASVSASLTSVSAAGAAAGSASVPA 107
QY 61 DGQGP-----VPRGRIQGANINDQANTGIDGLAGRWVASSQETLNVPTTFGKST 111
DB 108 AGAVAPGSASLGSASVGSATASASLVSVASSTGTGSLA---TTTSVSTAGAAVSSFGVST 164
QY 112 LPA-----GTFTAT 120
DB 165 ABAASWAASSTGAAGVGTWIST 194

RESULT 10

US-10-156-761-9303
Sequence 9303, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9303
LENGTH: 466
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-9303

Query Match 12.5%; Score 83; DB 4; Length 466;
Best Local Similarity 28.9%; Pred. No. 7.3;
Matches 37; Conservative 11; Mismatches 68; Indels 12; Gaps 5;
QY 1 AAQNTTSANWSQDPGFTGPAVAGQKVGTTLSITATGPHNSVSIAGKGSVSGVATVPFV 60
DB 62 AGSGVSTANWQYDTGTSTPGGAANWGTGEV-TMTSSNNVSLDG-----NGNLRITPLR 115
QY 61 DGQGPVPRGRIQGANINDQANTGIDGLAGRWVASSQETLNVPTTFGKSTLPAGTFTAT 120
DB 116 DSAGNWT-SGRIETNRTDFQPPAG---GTLRVESRIQLPNV-TGAAGKGYWPAFWMLGA 169
QY 121 FYVQOYQN 128
DB 170 PYRGNQYQN 177

RESULT 11

US-10-122A-122A-62373
Sequence 62373, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zykkind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06

Matches 34; Conservative 18; Mismatches 43; Indels 38; Gaps 5;
QY 1 AAQNTTSANWSQDPGFTGPAVAAGKQVGTLSITATGPHNSVSIAGK-----GASVS- 51
Db 142 AAEKDGAGDPDPDRDPAALAA--LGTPLAALAPAPHGALAGSKLGVRDVLFGGKVS 199
QY 52 ---GGVATVPFVDGQGPVFRGRIQGANINDQANTGIDGLAGWRVASSQB---TLNVPT 105
Db 200 LALGILVALVALVIG-----GIGGVIGRKTAEVVDFTTSKVTLS 238
QY 106 TFGKSTLPACTFT 118
Db 239 TTGNAQEPAGRFT 251

RESULT 14
US-10-432-934-62
; Sequence 62, Application US/10432934
; Publication No. US20040110269A1
; GENERAL INFORMATION:
; APPLICANT: Vipond, Richard
; APPLICANT: Shuttleworth, Helen
; APPLICANT: Ambrose, Emma
; APPLICANT: Minton, Nigel Peter
; TITLE OF INVENTION: Protection against mycobacterial infections
; FILE REFERENCE: 1581.0970001
; CURRENT FILING DATE: 2003-05-28
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: PCT/GB01/05250
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB0028966.0
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-432-934-62

Query Match 12.5%; Score 83; DB 4; Length 549;
Best Local Similarity 25.6%; Pred. No. 8.9;
Matches 34; Conservative 18; Mismatches 43; Indels 38; Gaps 5;
QY 1 AAQNTTSANWSQDPGFTGPAVAAGKQVGTLSITATGPHNSVSIAGK-----GASVS- 51
Db 142 AAEKDGAGDPDPDRDPAALAA--LGTPLAALAPAPHGALAGSKLGVRDVLFGGKVS 199
QY 52 ---GGVATVPFVDGQGPVFRGRIQGANINDQANTGIDGLAGWRVASSQB---TLNVPT 105
Db 200 LALGILVALVALVIG-----GIGGVIGRKTAEVVDFTTSKVTLS 238
QY 106 TFGKSTLPACTFT 118
Db 239 TTGNAQEPAGRFT 251

RESULT 15
US-11-053-710A-5
; Sequence 5, Application US/11053710A
; Publication No. US20050204408A1
; GENERAL INFORMATION:
; APPLICANT: WEISS, ANTHONY S
; TITLE OF INVENTION: TROPOELASTIN DERIVATIVES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRIFFITH HACK
; STREET: 168 WALKER STREET
; CITY: NORTH SYDNEY
; STATE: NEW SOUTH WALES
; COUNTRY: AUSTRALIA
; ZIP: 2060

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC7DOS/MS7DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/053.710A
FILING DATE: 08-Feb-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P08117
FILING DATE: 18?JUL?1997
ATTORNEY/AGENT INFORMATION:
NAME: GUMLEY, THOMAS P
REFERENCE/DOCKET NUMBER: 04828ZK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 61 2 9957 5944
TELEFAX: 61 2 9957 6288
TELEX: 26547
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 660 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-11-053-710A-5
Query Match 12.5%; Score 83; DB 6; Length 660;
Best Local Similarity 33.8%; Pred. No. 11;
Matches 27; Conservative 6; Mismatches 33; Indels 14; Gaps 2;
QY 15 GFTGPAVAAGKQVGTLSITATGPHNSVSIAGKASVSG-----GVATVPFVDGQGPVFRG 70
Db 164 GYGPQGVAAAGKAGYPTGTGTGVPQAAAAAAAKAFGAGAGFGAIVGVGGAGVPGVPG 223
QY 71 RIQGANINDQANTGIDGLAG 90
Db 224 AI-----PGIGGIAG 233
Search completed: April 26, 2006, 17:06:07
Job time : 65 secs



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 185944

TO: Ginny Portner
Location: REM/3B02/3C18
Art Unit: 1645
Thursday, April 27, 2006

Case Serial Number: 10/018892

From: Paul Schulwitz
Location: Biotech-Chem Library
REM-1A65
Phone: 571-272-2527

Paul.schulwitz@uspto.gov

Search Notes

Examiner Portner,

Please review the attached search results.

If you have any questions or if you would like to refine the search query, please feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
REM-1A65
571-272-2527

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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OM protein - protein search, using sw model

Run on: April 26, 2006, 17:05:14 ; Search time 13 Seconds
(without alignments)
447.782 Million cell updates/sec

Title: US-10-018-892-3

Perfect score: 662

Sequence: 1 AAQNTTSANWSQDPGFTGPA.....KSTLPAGTTFATFVQVQYON 128

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 232119 seqs, 45477862 residues

Total number of hits satisfying chosen parameters: 232119

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA New:*
- 1: /SIDSS5/ptodata/2/pubpaa/US08 NEW PUB.pap.*
 - 2: /SIDSS5/ptodata/2/pubpaa/US06 NEW PUB.pap.*
 - 3: /SIDSS5/ptodata/2/pubpaa/US07 NEW PUB.pap.*
 - 4: /SIDSS5/ptodata/2/pubpaa/PCT_NEW PUB.pap.*
 - 5: /SIDSS5/ptodata/2/pubpaa/US09 NEW PUB.pap.*
 - 6: /SIDSS5/ptodata/2/pubpaa/US10 NEW PUB.pap.*
 - 7: /SIDSS5/ptodata/2/pubpaa/US11 NEW PUB.pap.*
 - 8: /SIDSS5/ptodata/2/pubpaa/US60 NEW PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	93.5	14.1	431	7	US-11-096-568A-33761
2	93	14.0	171	7	US-11-096-568A-24841
3	93	14.0	189	7	US-11-096-568A-24840
4	83.5	12.6	346	6	US-10-517-939-170
5	82	12.4	347	6	US-10-517-939-222
6	81.5	12.3	2204	7	US-11-052-554A-134
7	81	12.2	5712	7	US-11-143-980-47
8	80	12.1	176	7	US-11-096-568A-21627
9	80	12.1	208	7	US-11-096-568A-21626
10	79	11.9	654	7	US-11-169-041-186
11	77.5	11.7	591	6	US-10-510-386-22
12	77	11.6	675	7	US-11-072-512-3810
13	76.5	11.6	617	7	US-11-072-512-2915
14	76.5	11.6	757	6	US-10-509-472-2
15	75.5	11.4	1268	7	US-11-052-554A-1
16	75.5	11.4	1571	7	US-11-052-554A-2
17	75	11.3	148	7	US-11-096-568A-32672
18	75	11.3	235	7	US-11-096-568A-32671
19	75	11.3	282	7	US-11-096-568A-32670
20	74.5	11.3	431	7	US-11-052-554A-210
21	74.5	11.3	1345	7	US-11-052-554A-282
22	74	11.2	1049	7	US-11-051-720-1563
23	74	11.2	1049	7	US-11-051-720-1565
24	74	11.2	1521	7	US-11-051-720-1564
25	74	11.2	1526	7	US-11-051-720-1566

26	73.5	11.1	710	7	US-11-045-802-2	Sequence 2, Appli
27	73.5	11.1	710	7	US-11-045-802-19	Sequence 19, Appl
28	73.5	11.1	710	7	US-11-045-802-20	Sequence 20, Appl
29	73.5	11.1	803	7	US-11-188-298-2035	Sequence 2035, Ap
30	72	10.9	347	6	US-10-517-939-254	Sequence 254, App
31	72	10.9	478	7	US-11-096-568A-16409	Sequence 16409, A
32	72	10.9	493	7	US-11-096-568A-16408	Sequence 16408, A
33	72	10.9	542	7	US-11-096-568A-16407	Sequence 16407, A
34	72	10.9	634	6	US-10-632-150-26	Sequence 26, Appl
35	72	10.9	634	7	US-11-073-457-26	Sequence 26, Appl
36	72	10.9	634	7	US-11-073-460-26	Sequence 26, Appl
37	71.5	10.8	228	7	US-11-096-568A-9780	Sequence 9780, Ap
38	70.5	10.6	152	7	US-11-087-099-881	Sequence 881, App
39	70.5	10.6	710	7	US-11-045-802-22	Sequence 22, Appl
40	70.5	10.6	7465	7	US-11-087-099-7521	Sequence 7521, Ap
41	70	10.6	273	6	US-10-821-234-1203	Sequence 1203, Ap
42	70	10.6	360	7	US-11-079-463-10442	Sequence 10442, A
43	70	10.6	710	7	US-11-143-980-40	Sequence 40, Appl
44	70	10.6	949	7	US-11-052-554A-6	Sequence 6, Appli
45	70	10.6	1093	7	US-11-079-463-9529	Sequence 9529, Ap

ALIGNMENTS

RESULT 1

US-11-096-568A-33761
; Sequence 33761, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
; TITLE OF INVENTION: Theryby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 33761
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(431)
; OTHER INFORMATION: Ceres Seq. ID no. 13604019
US-11-096-568A-33761

Query Match	14.1%	Score 93.5;	DB 7;	Length 431;
Best Local Similarity	33.3%	Pred No. 0.15;		
Matches	36;	Conservative 14;	Mismatches 47;	Indels 11; Gaps 6;
Qy	1	AAQNTTSANWSQDPGFTGPAVAGQKVG-TLSITATGPHNSVSIAGKGA-SVSGGVATVP	58	
Db	68	ATANTTTASSDSPSAAAAAQAQWLSRSSFLQNNNNNASIVGDDVTGGADTMI	127	
Qy	59	FVDCGGQVFRGRQGANINDQAN-TGIDGLAGWRVASSQ-ETLVFV 104		
Db	128	-----QGMKMG---GENKNDGGGAATAADGVVSWQNAHKAILSHPL	168	

RESULT 2

US-11-096-568A-24841
; Sequence 24841, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
; TITLE OF INVENTION: Theryby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 24841

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; LENGTH: 171
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(171)
; OTHER INFORMATION: Ceres Seq. ID no. 12462325
; *FEATURE:
; NAME/KEY: misc feature
; LOCATION: (133)..(133)
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-11-096-568A-24841

Query Match      14.0%; Score 93; DB 7; Length 171;
Best Local Similarity 29.5%; Pred. No. 0.053;
Matches 38; Conservative 14; Mismatches 41; Indels 36; Gaps 6;

QY 1 AAQNTTSANWS-----QDPGFTGPAVAAGQKVGTLSTAT-----G 36
Db 50 ASNTSSNFGAVVAIDDLTTGPTRAAGTEVGRAQGYTFADQQTGGLLWMVNFVFTAG 109
QY 37 PHN--SVSIAGKASVSGGVATVPFDGQGO-PVFRGRIQGANINDQANTGIDGLAGWRV 93
Db 110 EHNGLTSLILGRN-EVLSDVREMSXVSGSGKFRMARGVYVQAHTIDSGATSG-----T 160
QY 94 ASSQETLNV 102
Db 161 TVVQYTVNV 169

RESULT 3
US-11-096-568A-24840
; Sequence 24840, Application US/11096568A
; Publication No. US2006048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 24840
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(189)
; OTHER INFORMATION: Ceres Seq. ID no. 12462324
; *FEATURE:
; NAME/KEY: misc feature
; LOCATION: (151)..(151)
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-11-096-568A-24840

Query Match      14.0%; Score 93; DB 7; Length 189;
Best Local Similarity 29.5%; Pred. No. 0.06;
Matches 38; Conservative 14; Mismatches 41; Indels 36; Gaps 6;

QY 1 AAQNTTSANWS-----QDPGFTGPAVAAGQKVGTLSTAT-----G 36
Db 68 ASNTSSNFGAVVAIDDLTTGPTRAAGTEVGRAQGYTFADQQTGGLLWMVNFVFTAG 127
QY 37 PHN--SVSIAGKASVSGGVATVPFDGQGO-PVFRGRIQGANINDQANTGIDGLAGWRV 93
Db 128 EHNGLTSLILGRN-EVLSDVREMSXVSGSGKFRMARGVYVQAHTIDSGATSG-----T 178
QY 94 ASSQETLNV 102
Db 179 TVVQYTVNV 187
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```

RESULT 4
US-10-517-939-170
; Sequence 170, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 170
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; NAME/KEY: SIGNAL
; LOCATION: (1)....(24)
US-10-517-939-170

Query Match      12.6%; Score 83.5; DB 6; Length 346;
Best Local Similarity 29.5%; Pred. No. 1.1;
Matches 26; Conservative 12; Mismatches 43; Indels 7; Gaps 2;

QY 25 QKVGTLSITATGPHNSVSIAGKASVSGGVATVPFDGQGO-PVFRGRIQGANINDQANTG 84
Db 205 QSSGSSDITVTGEGGSSSSSGGSGGSKSFTVRA-----RGTVGGENIQLVNN- 258
QY 85 IDGLAGWRVASSQETLNVPTTTFGKSTL 112
Db 259 -QTVASWNLTTSMQYNASTSLSGGITV 285

RESULT 5
US-10-517-939-222
; Sequence 222, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 222
; LENGTH: 347
; TYPE: PRT
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; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(24)
US-10-517-939-222

Query Match          12.4%; Score 82; DB 6; Length 347;
Best Local Similarity 30.3%; Pred. No. 1.5;
Matches 27; Conservative 13; Mismatches 41; Indels 8; Gaps 3;

Qy 25 QKVGLSLTAT-GPHNSVSIAGKASVSGGVATVPFDGQGQVFRGRIOGANINDQANT 83
Db 205 QSSGSDITVTEGGSSSSSGGSSGGSFTVRA-----RGTVGGENIQLVNN 259
Qy 84 GIDGLAGWRVASSQETLNPVTTGKSTL 112
Db 260 --QTVASWNLTTSMQNYNASTSLSGGITV 286

RESULT 6
US-11-052-554A-134
; Sequence 134, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; FILE REFERENCE: 30853/40359A
; CURRENT FILING DATE: 2005-02-07
; PRIOR FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 134
; LENGTH: 2204
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-134

Query Match          12.3%; Score 81.5; DB 7; Length 2204;
Best Local Similarity 24.8%; Pred. No. 17;
Matches 33; Conservative 18; Mismatches 51; Indels 31; Gaps 7;

Qy 17 TGPVAV---AAGQK-----VGTLSITATGPHNSVSIAGKASVS---GGVATVPFDGQGG 65
Db 367 TGDIVLSSIAQRAHFQPIIPNITVVGPTTVAIGGPNWTAITITGGAIRIPLISIPAA 426
Qy 66 PVFRGRIOGANINDQA---NTGIDGLAG-----WRVASSQETLN--VPVTTFGK 109
Db 427 PGP-----GNSTNPSSGFFNTGAGASGFGNGANGSFWNLASATSGASLLNVGALGS 482
Qy 110 STLPAQTFATFY 122
Db 483 GLANVGTTVSGFY 495

RESULT 7
US-11-143-980-47
; Sequence 47, Application US/11143980
; Publication No. US20050272133A1
; GENERAL INFORMATION:
; APPLICANT: He, Min
; APPLICANT: Hucul, John
; APPLICANT: Haitli, Bradley A.
; APPLICANT: Wagenaar, Melissa M.
; APPLICANT: Graziani, Edmund
; APPLICANT: Summers, Mia
; APPLICANT: Kulowski, Kerry
```

```
; APPLICANT: Pong, Kevin
; TITLE OF INVENTION: Biosynthetic Gene Cluster for the Production of a Complex
; FILE REFERENCE: AM-101426US
; CURRENT APPLICATION NUMBER: US/11/143,980
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 60/664,483
; PRIOR FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: US 60/576,895
; PRIOR FILING DATE: 2004-06-03
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 47
; LENGTH: 5712
; TYPE: PRT
; ORGANISM: Streptomyces sp.
US-11-143-980-47

Query Match          12.2%; Score 81; DB 7; Length 5712;
Best Local Similarity 29.0%; Pred. No. 61;
Matches 29; Conservative 15; Mismatches 52; Indels 4; Gaps 3;

Qy 5 TTSANWSQDPGFTGPAVAAQKVGTLG--ITATGPHNSVSIAGKASVSGGVATVPFY-D 61
Db 2910 TESAEWRQEGRRPRRAGVSAGVSGTNAHVILEQAPKHPAGVAAEGRKGRGEPPTVPWVLS 2969
Qy 62 GQGQPVFRGRIOGANINDQANTGIDGL-AGMRVASSQETL 100
Db 2970 GASEAGLRAQIEGLRAFADDNPTLDPADVGNLSLASTRALL 3009

RESULT 8
US-11-096-568A-21627
; Sequence 21627, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 21627
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(176)
; OTHER INFORMATION: Ceres Seq. ID no. 12405531
US-11-096-568A-21627

Query Match          12.1%; Score 80; DB 7; Length 176;
Best Local Similarity 28.8%; Pred. No. 1;
Matches 32; Conservative 14; Mismatches 37; Indels 28; Gaps 5;

Qy 1 AAQNTTSANWS-----QDPGFTGPAVAAQKVGTLGTLTAT-----G 36
Db 55 AASNTSSTSGFAMVAIDDLPTTGPTRAAGTGVGRAQGTVPADQQTFGLLMVMDFFVTAG 114
Qy 37 PH--NSVSIAGKASVSGGVATVPFDGQGG--PVFRGRIOGANINDQANTG 84
Db 115 EHKGSTLSILGRN-EVLSDVREMSIVGGSGKFRMARGVQVQHTIDSGFKSG 164

RESULT 9
US-11-096-568A-21626
; Sequence 21626, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
```


Query Match 11.6%; Score 77; DB 7; Length 675;
Best Local Similarity 26.0%; Pred. No. 11;
Matches 26; Conservative 17; Mismatches 41; Indels 16; Gaps 4;
QY 9 NWSQDPG-----FTGPAVAGQKVTLSITATGPHNSVSIAGKASVSGGVATVPFVDG 62
DB 476 SWEADGGIGLLFGSLVSGSTGRLLRLWAGVAVSELCKGSGARSS-----VPM 528
QY 63 QGQPVFRGRIQANINDQANTGIDG-LAG--WRVASSQBT 99
DB 529 EHELVDGANVVSASFDDSDVMGVGTGTAGTLNFWVSWAEGT 568

RESULT 13
US-11-072-512-2915
; Sequence 2915, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOKIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2915
; LENGTH: 617
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2915
Query Match 11.6%; Score 76.5; DB 7; Length 617;
Best Local Similarity 35.4%; Pred. No. 11;
Matches 28; Conservative 7; Mismatches 29; Indels 15; Gaps 4;
QY 14 PGFTGPAVAGQKVTLSITATGPHNSVSIAGKASV--SGGVATVPFVDGQGPVFRGR 71
DB 188 PG--GVAGAAG-KAGYPTGTGVGPQAAAAAATAKAFGAGAGVLPGVGGAGVGPVPGA 244
QY 72 IQGANINDQANTGIDGLAG 90
DB 245 I-----PGIGGIAG 253

RESULT 14
US-10-509-472-2
; Sequence 2, Application US/10509472
; Publication No. US20060079439A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; TITLE OF INVENTION: ELASTIN PREVENTS OCCLUSION OF BODY VESSELS BY VASCULAR SMOOTH
; TITLE OF INVENTION: MUSCLE CELLS

; FILE REFERENCE: HYDR-PWO-005
; CURRENT APPLICATION NUMBER: US/10/509,472
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/368084
; PRIOR FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LENGTH: 757
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-509-472-2
Query Match 11.6%; Score 76.5; DB 6; Length 757;
Best Local Similarity 35.4%; Pred. No. 14;
Matches 28; Conservative 7; Mismatches 29; Indels 15; Gaps 4;
QY 14 PGFTGPAVAGQKVTLSITATGPHNSVSIAGKASV--SGGVATVPFVDGQGPVFRGR 71
DB 232 PG--GVAGAAG-KAGYPTGTGVGPQAAAAAATAKAFGAGAGVLPGVGGAGVGPVPGA 288
QY 72 IQGANINDQANTGIDGLAG 90
DB 289 I-----PGIGGIAG 297

RESULT 15
US-11-052-554A-1
; Sequence 1, Application US/11052554A
; Publication No. US2005028866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1
; LENGTH: 1268
; TYPE: PRT
; ORGANISM: Escherichia coli 0157:H7
US-11-052-554A-1
Query Match 11.4%; Score 75.5; DB 7; Length 1268;
Best Local Similarity 31.1%; Pred. No. 32;
Matches 32; Conservative 13; Mismatches 45; Indels 13; Gaps 5;
QY 22 AAGQKVTLSITATGPHN--SVSIAGKASVSGGVATVPFVDGQ--QPVFRGRIQGAN 76
DB 216 AAGQVTG--SVSATSGRNGYSVDVAKLGMNANKISLSTKGVGVNVLGIAGGVNGVS 273
QY 77 INDQANTGIDGLAGWRVASSQBTLNVPVTTFGKSTLPAGTFTA 119
DB 274 IDSKGNL----LNSNAIQSASTIN--LTNGTLDNTTGTITS 310

Search completed: April 26, 2006, 17:06:26
Job time : 14 secs

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OM protein - protein search, using sw model

Run on: April 26, 2006, 17:06:19 ; Search time 186 Seconds
(without alignments)

302.368 Million cell updates/sec

Title: US-10-018-892-3

Perfect score: 128

Sequence: 1 AAQNTTSANWSQDFGTGPA.....KSTLPAGTFTATFYVQYQN 128

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size: 1

Total number of hits satisfying chosen parameters: 2441974

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

- 1: Geneseq 21:*
- 2: geneseq1980s:*
- 3: geneseq1990s:*
- 4: geneseq2000s:*
- 5: geneseq2001s:*
- 6: geneseq2002s:*
- 7: geneseq2003as:*
- 8: geneseq2003bs:*
- 9: geneseq2004s:*
- 9: geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	128	100.0	128	4 AAB31431	Aab31431 Amino aci
2	128	100.0	144	2 AAW47082	Aaw47082 Salmonell
3	128	100.0	165	2 AAW23571	Aaw23571 Salmonell
4	128	100.0	165	4 AAB31430	Aab31430 Amino aci
5	128	100.0	176	2 AAR23731	Aar23731 Fimbrial
6	128	100.0	176	2 AAR42173	Aar42173 SE fimbri
7	128	100.0	180	2 AAW47081	Aaw47081 Salmonell
8	66	51.6	165	2 AAR62752	Aar62752 Sefa sequ
9	8	6.2	225	8 ADJ51007	Adj51007 Human nov
10	8	6.2	345	6 ADA55453	Ada55453 Human pro
11	8	6.2	490	8 ADS43323	Ads43323 Bacterial
12	8	6.2	492	5 ABP69377	Abp69377 Human pol
13	8	6.2	494	9 ADY37608	Ady37608 lung canc
14	8	6.2	559	6 ABU62853	Abu62853 Novel end
15	8	6.2	574	4 ABG29271	Abg29271 Novel hum
16	8	6.2	599	7 ADC58096	Adc58096 Microtubu
17	8	6.2	705	6 AAE32112	Aae32112 Human cyt
18	7	5.5	17	4 AAB57669	Aab57669 CD148 PL
19	7	5.5	17	4 AAB57692	Aab57692 CD148 PL
20	7	5.5	17	4 AAB58079	Aab58079 CD148 PL
21	7	5.5	17	4 AAB58102	Aab58102 CD148 PL
22	7	5.5	17	4 AAB55830	Aab55830 PL peptid
23	7	5.5	17	4 AAB55807	Aab55807 PL peptid
24	7	5.5	17	5 ABJ05199	Abj05199 C-termina

25	7	5.5	17	5	ABJ05222	C-termina
26	7	5.5	17	5	ABP63217	CD148 PL
27	7	5.5	17	5	ABP63247	CD148 PL
28	7	5.5	55	3	AAG05854	Arabidops
29	7	5.5	58	7	ABR61594	Z. mays a
30	7	5.5	63	4	AAM25922	Human pro
31	7	5.5	63	4	AAM79596	Human pro
32	7	5.5	63	4	AAU56367	Propionib
33	7	5.5	63	6	ABM52886	Human rep
34	7	5.5	83	4	AAM95904	Human tes
35	7	5.5	83	4	ABB96435	Human tes
36	7	5.5	84	8	ADS07289	Staphyloc
37	7	5.5	86	3	AAG05852	Arabidops
38	7	5.5	87	4	AAM88979	Human imm
39	7	5.5	95	5	ABP10155	Human ORF
40	7	5.5	104	7	ADD36246	Frog orth
41	7	5.5	104	8	ADQ08869	Xenopus l
42	7	5.5	104	9	ADM46048	African c
43	7	5.5	114	4	AAE12624	Human gen
44	7	5.5	114	4	AAU04354	Mammalian
45	7	5.5	114	4	AAG93282	Human pro

ALIGNMENTS

RESULT 1

AAB31431
ID AAB31431 standard; peptide; 128 AA.

AC AAB31431;

DT 20-APR-2001 (first entry)

DE Amino acid sequence of the C128 fragment of the Sef14 antigen.

KW C128 fragment; fimbrial Sef14 antigen; fimbrial protein;
KW flagellin protein; poultry.

OS Salmonella enteritidis.

PN WO200078995-A1.

PD 28-DEC-2000.

PF 22-JUN-1999; 99WO-SG000061.

PR 22-JUN-1999; 99WO-SG000061.

XX (MOLE-) INST MOLECULAR AGROBIOLOGY.

XX Kwang H, Liu W, Low SS, Loh KYH;

XX WPI; 2001-071400/08.

PT New method for the specific detection of Salmonella enteritidis
PT infections of poultry comprises contacting a biological sample with
PT antigenic fragments of S. enteritidis fimbrial and/or flagellin proteins.

XX Claim 18; Page 42; 49pp; English.

CC The present sequence represents the C128 fragment of the fimbrial Sef14
CC antigen of Salmonella enteritidis. The specification describes a method
CC for detecting S. enteritidis in a biological sample obtained from
CC poultry. The method comprises contacting the sample with an antigenic
CC fragment of S. enteritidis fimbrial or flagellin protein and detecting
CC the formation of a complex, where the fragment is specifically recognized
CC by S. enteritidis antibodies. The antigenic fragments are specific to
CC Salmonella enteritidis and enable specific detection of S. enteritidis
CC even in the presence of other Salmonella spp. The methods are useful for
CC the specific detection of S. enteritidis infections in biological samples
CC derived from poultry

SQ Sequence 128 AA;
 Query Match 100.0%; Score 128; DB 4; Length 128;
 Best Local Similarity 100.0%; Pred. No. 2.4e-119;
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAOQNTTSANWSQDPGFTGPAVAAGQKVGTLSTATGPHNSVSIAGKGSVSGGVATVPFV 60
 DB 1 AAOQNTTSANWSQDPGFTGPAVAAGQKVGTLSTATGPHNSVSIAGKGSVSGGVATVPFV 60
 QY 61 DGQGPVFRGRIQGANINDQANTGIDGLAGRWVASSQETLNVPTTFGKSTLPAGTFTAT 120
 DB 61 DGQGPVFRGRIQGANINDQANTGIDGLAGRWVASSQETLNVPTTFGKSTLPAGTFTAT 120
 QY 121 FYVQOYQN 128
 DB 121 FYVQOYQN 128

RESULT 2
 AAW47082
 ID AAW47082 standard; protein; 144 AA.
 XX
 AC AAW47082;
 XX 25-JUN-1998 (first entry)
 DT Salmonella Sef14 protein fragment.
 DE
 KW Sefa gene; Sef14 protein; infection; bird; chicken; turkey;
 KW anti-Salmonella enteritidis antibody; vaccine; poultry.
 XX
 OS Salmonella enteritidis.
 XX WO9803656-A1.
 XX 29-JAN-1998.
 PD 18-JUL-1997; 97WO-US012639.
 PF 19-JUL-1996; 96US-0022191P.
 PR (MINU) UNIV MINNESOTA.
 PA Rajashekara G, Nagaraja KV, Kapur V;
 PI WPI; 1998-120780/11.
 DR N-PSDB; AAV13948.
 XX
 CC Detecting antibodies against Salmonella enteritidis using truncated
 PT fimbrial antigen Sef14 - in immunoassays, particularly for diagnosing
 PT infection in poultry, also new antigens.
 XX
 PS Claim 4; Page 23-24; 38pp; English.
 XX
 CC This sequence is a fragment of the Salmonella enteritidis (Se) Sef14
 CC protein, encoded by the sefa gene. The method of the invention is for
 CC detecting antibodies (Ab) against Se in an animal by treating a sample
 CC with a truncated Sef14 antigen (Ag), lacking at least the native Sef14
 CC signal peptide, and detecting any Ab-Ag complex formed. Detection (by
 CC enzyme-linked immunosorbent assay or agglutination tests) of the Ab is
 CC used to diagnose Se infection in birds, especially chickens and turkeys.
 CC The Ag can also be used in vaccines to protect poultry against Se
 CC infection. Detection of the Ab is a sensitive, specific method for
 CC reliable and routine screening of animals. The Ag are easily produced in
 CC large quantities, in pure form, without requiring special growing
 CC conditions, so are suitable for large scale screening of flocks
 XX
 SQ Sequence 144 AA;
 Query Match 100.0%; Score 128; DB 2; Length 144;
 Best Local Similarity 100.0%; Pred. No. 2.6e-119;
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAOQNTTSANWSQDPGFTGPAVAAGQKVGTLSTATGPHNSVSIAGKGSVSGGVATVPFV 60
 DB 17 AAOQNTTSANWSQDPGFTGPAVAAGQKVGTLSTATGPHNSVSIAGKGSVSGGVATVPFV 76
 QY 61 DGQGPVFRGRIQGANINDQANTGIDGLAGRWVASSQETLNVPTTFGKSTLPAGTFTAT 120
 DB 77 DGQGPVFRGRIQGANINDQANTGIDGLAGRWVASSQETLNVPTTFGKSTLPAGTFTAT 136
 QY 121 FYVQOYQN 128
 DB 137 FYVQOYQN 144

RESULT 3
 AAW23571
 ID AAW23571 standard; protein; 165 AA.
 XX
 AC AAW23571;
 XX 25-MAR-2003 (revised)
 DT 29-SEP-1997 (first entry)
 DE Salmonella enteritidis sefa.
 XX Enteropathogenic bacteria; enterobacteria; S. enteritidis; antibody.
 KW Salmonella enteritidis.
 OS US5635617-A.
 XX 03-JUN-1997.
 PD 26-APR-1994; 94US-00233788.
 PF 26-APR-1993; 93US-00054452.
 PR (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
 PA Collinson SK, Kay WW, Doran JL;
 PI WPI; 1997-309886/28.
 DR N-PSDB; AAT74143.
 XX
 CC Isolated Salmonella gene agfa - used for diagnosis of Salmonella or
 PT enteropathogenic bacteria of the Enterobacteria family.
 XX
 PS Example 9; Fig 2; 85pp; English.
 XX
 CC The present sequence represents sefa found in the sef gene cluster from
 CC Salmonella enteritidis. The nucleic acid can be used to provide
 CC diagnostic assays for Salmonella and/or enteropathogenic bacteria of the
 CC family Enterobacteria. It can also be used to provide proteins and
 CC antibodies which can be used for assays. The nucleic acid sequence can be
 CC used to provide probes or primers which can specifically hybridise to
 CC nucleic acid molecules from greater than 99% of Salmonella strains that
 CC are pathogenic to warm-blooded animals relative to nucleic acid molecules
 CC from virtually all other microbial organisms. (Updated on 25-MAR-2003 to
 CC correct PF field.)
 XX
 SQ Sequence 165 AA;
 Query Match 100.0%; Score 128; DB 2; Length 165;
 Best Local Similarity 100.0%; Pred. No. 2.9e-119;
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAOQNTTSANWSQDPGFTGPAVAAGQKVGTLSTATGPHNSVSIAGKGSVSGGVATVPFV 60
 DB 38 AAOQNTTSANWSQDPGFTGPAVAAGQKVGTLSTATGPHNSVSIAGKGSVSGGVATVPFV 97
 QY 61 DGQGPVFRGRIQGANINDQANTGIDGLAGRWVASSQETLNVPTTFGKSTLPAGTFTAT 120
 DB 98 DGQGPVFRGRIQGANINDQANTGIDGLAGRWVASSQETLNVPTTFGKSTLPAGTFTAT 157

Qy 121 FYVQYQN 128
 |||||
 Db 158 FYVQYQN 165

RESULT 4

AAB31430
 ID AAB31430 standard; protein; 165 AA.

XX AC AAB31430;

XX DT 20-APR-2001 (first entry)

XX DE Amino acid sequence of the Sef14 antigen.

XX KW C128 fragment; fimbrial Sef14 antigen; fimbrial protein;
 KW flagellin protein; poultry.

XX OS Salmonella enteritidis.

XX PN W0200078995-A1.

XX PD 28-DEC-2000.

XX PF 22-JUN-1999; 99WO-SG0000061.

XX PR 22-JUN-1999; 99WO-SG0000061.

XX PA (MOLE-) INST MOLECULAR AGROBIOLOGY.

XX PI Kwang H, Liu W, Low SS, Loh KYH;

XX DR WPI; 2001-071400/08.

XX DR N-PSDB; AAF24784.

XX PT New method for the specific detection of Salmonella enteritidis
 PT infections of poultry comprises contacting a biological sample with
 PT antigenic fragments of S. enteritidis fimbrial and/or flagellin proteins.

XX PS Disclosure; Page 42; 49pp; English.

XX CC The present sequence represents the fimbrial Sef14 antigen of Salmonella
 CC enteritidis. The specification describes a method for detecting S.
 CC enteritidis in a biological sample obtained from poultry. The method
 CC comprises contacting the sample with an antigenic fragment of S.
 CC enteritidis fimbrial or flagellin protein and detecting the formation of
 CC a complex, where the fragment is specifically recognized by S.
 CC enteritidis antibodies. The antigenic fragments are specific to
 CC Salmonella enteritidis and enable specific detection of S. enteritidis
 CC even in the presence of other Salmonella spp. The methods are useful for
 CC the specific detection of S. enteritidis infections in biological samples
 CC derived from poultry

XX SQ Sequence 165 AA;

Query Match 100.0%; Score 128; DB 4; Length 165;

Best Local Similarity 100.0%; Pred. No. 2.9e-119;

Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAOQNTTSANWSQDPGFTGPAVAAQKVGTLISITATGPHNSVSIAGKASVSGGVATVPFV 60

Db 38 AAOQNTTSANWSQDPGFTGPAVAAQKVGTLISITATGPHNSVSIAGKASVSGGVATVPFV 97

Qy 61 DGOQOPVPRGRIQGANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTFTAT 120

Db 98 DGOQOPVPRGRIQGANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTFTAT 157

Qy 121 FYVQYQN 128

|||||

Db 158 FYVQYQN 165

RESULT 5

AAR23731
 ID AAR23731 standard; protein; 176 AA.

XX AC AAR23731;

XX DT 25-MAR-2003 (revised)

DT 02-NOV-1992 (first entry)

DE Fimbrial antigen.

XX KW S. dublin; S. moscow; fimbria-like structure; epitope.

XX OS Salmonella enteritidis.

XX PN W09206198-A.

XX PD 16-APR-1992.

XX PF 01-OCT-1991; 91WO-GB001691.

XX PR 01-OCT-1990; 90GB-00021338.

XX PR 17-OCT-1990; 90GB-00022570.

XX PA (UKAG-) UK MIN AGRIC FISH.

XX PI Woodward MJ;

XX DR WPI; 1992-150883/18.

XX PT Detection and identification of salmonella - by using monoclonal
 PT antibodies to detect epitope(s) of these serotypes in culture.

XX PS Disclosure; Page 3; 48pp; English.

XX CC The sequence given is Salmonella enteritidis fimbrial antigen (SEFA).
 CC Salmonella organisms have fimbria-like structures on their surfaces and
 CC it has been suggested that there are antigenically distinct types of
 CC fimbria, ie. possessing specific epitopes on the fimbrial antigens. This
 CC sequence has an amino acid sequence which forms an epitope on the fimbria
 CC "in vivo" which is specifically encoded by DNA of the species S.
 CC enteritidis, and some strains of the species S. dublin and S. moscow but
 CC which is apparently absent in virtually all other serotypes. This
 CC antigen can be used for testing for the presence of Salmonella
 CC microorganisms in clinical samples such as animal remains or prods., food
 CC samples and infected environmental samples. (Updated on 25-MAR-2003 to
 CC correct PF field.)

XX SQ Sequence 176 AA;

Query Match 100.0%; Score 128; DB 2; Length 176;

Best Local Similarity 100.0%; Pred. No. 3.1e-119;

Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAOQNTTSANWSQDPGFTGPAVAAQKVGTLISITATGPHNSVSIAGKASVSGGVATVPFV 60

Db 49 AAOQNTTSANWSQDPGFTGPAVAAQKVGTLISITATGPHNSVSIAGKASVSGGVATVPFV 108

Qy 61 DGOQOPVPRGRIQGANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTFTAT 120

Db 109 DGOQOPVPRGRIQGANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTFTAT 168

Qy 121 FYVQYQN 128

|||||

Db 169 FYVQYQN 176

RESULT 6

AAR42173
 ID AAR42173 standard; protein; 176 AA.

XX AC AAR42173;

DT 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 03-MAY-1994 (first entry)
 XX SE fimbrial antigen (SEFA).
 XX Salmonella enteritidis fimbrial antigen; SEFA; Salmonella typhi;
 KW Salmonella dublin; serotype.
 XX Salmonella enteritidis.
 OS Salmonella typhi.
 XX WO9320231-A1.
 XX 14-OCT-1993.
 XX 29-MAR-1993; 93WO-GB000647.
 PF 31-MAR-1992; 92GB-00007069.
 PR (UKAG-) UK MIN FISHERIES & FOOD.
 XX Woodward MJ, Thorns CJ;
 XX WPI; 1993-336937/42.
 DR N-PSDB; AAQ49882.
 XX Testing for Salmonella serotypes, esp. S. Typhi - using test kit for
 PT detecting nucleic acid sequences specific to certain sero-types.
 PT Claim 2; Page 19-21; 37pp; English.
 XX DNA encoding SEFA is common to members of the enteritidis, dublin and
 CC typhi serogroups and can therefore be used in the detection of such
 CC organisms. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-
 CC AUG-2003 to correct OS field.)
 XX Sequence 176 AA;
 Query Match 100.0%; Score 128; DB 2; Length 176;
 Best Local Similarity 100.0%; Pred. No. 3.1e-119;
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAQNTTSANWSQDPGFTGPAVAAGKVGCTLSITATGPHNSVSIAGKGSVSGVATVPFV 60
 Db 49 AAQNTTSANWSQDPGFTGPAVAAGKVGCTLSITATGPHNSVSIAGKGSVSGVATVPFV 108
 QY 61 DGGQGPVFRGRIQGANINDOANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTFTAT 120
 Db 109 DGGQGPVFRGRIQGANINDOANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTFTAT 168
 QY 121 FYVQOYQN 128
 Db 169 FYVQOYQN 176
 RESULT 7
 ID AA47081
 XX AA47081 standard; protein; 180 AA.
 AC AA47081;
 XX 25-JUN-1998 (first entry)
 XX Salmonella Sef14 protein fragment.
 DE Sefa gene; Sef14 protein; infection; bird; chicken; turkey;
 KW anti-Salmonella enteritidis antibody; vaccine; poultry.
 XX Salmonella enteritidis.
 OS WO9803656-A1.
 PN 26-APR-1994; 94WO-IB000207.
 XX

PD 29-JAN-1998.
 XX 18-JUL-1997; 97WO-US012639.
 PF 19-JUL-1996; 96US-0022191P.
 XX (MINU) UNIV MINNESOTA.
 XX Rajashekara G, Nagaraja KV, Kapur V;
 PI WPI; 1998-120780/11.
 XX N-PSDB; AAV13974.
 DR Detecting antibodies against Salmonella enteritidis using truncated
 PT fimbrial antigen Sef14 - in immunoassays, particularly for diagnosing
 PT infection in poultry, also new antigens.
 XX Claim 3; Page 21-22; 38pp; English.
 XX This sequence is a fragment of the Salmonella enteritidis (Se) Sef14
 CC protein, encoded by the sefa gene. The method of the invention is for
 CC detecting antibodies (Ab) against Se in an animal by treating a sample
 CC with a truncated Sef14 antigen (Ag), lacking at least the native Sef14
 CC signal peptide, and detecting any Ab-Ag complex formed. Detection (by
 CC enzyme-linked immunosorbent assay or agglutination tests) of the Ab is
 CC used to diagnose Se infection in birds, especially chickens and turkeys.
 CC The Ag can also be used in vaccines to protect poultry against Se
 CC infection. Detection of the Ab is a sensitive, specific method for
 CC reliable and routine screening of animals. The Ag are easily produced in
 CC large quantities, in pure form, without requiring special growing
 CC conditions, so are suitable for large scale screening of flocks
 XX Sequence 180 AA;
 Query Match 100.0%; Score 128; DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. No. 3.2e-119;
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAQNTTSANWSQDPGFTGPAVAAGKVGCTLSITATGPHNSVSIAGKGSVSGVATVPFV 60
 Db 53 AAQNTTSANWSQDPGFTGPAVAAGKVGCTLSITATGPHNSVSIAGKGSVSGVATVPFV 112
 QY 61 DGGQGPVFRGRIQGANINDOANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTFTAT 120
 Db 113 DGGQGPVFRGRIQGANINDOANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTFTAT 172
 QY 121 FYVQOYQN 128
 Db 173 FYVQOYQN 180
 RESULT 8
 ID AAR62752
 XX AAR62752 standard; protein; 165 AA.
 AC AAR62752;
 XX 21-OCT-2004 (revised)
 DT 25-MAR-2003 (revised)
 DT 26-JUN-1995 (first entry)
 XX Sefa sequence.
 DE Salmonella; Sefa; vaccine.
 KW Salmonella sp.
 OS Unidentified.
 OS WO9425598-A2.
 PN 10-NOV-1994.
 PD 26-APR-1994; 94WO-IB000207.
 XX

XX 26-APR-1993; 93US-00054452.
 XX (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
 PA (KING/) KING J.
 XX Kay WW, Collinson SK, Clouthier SC, Doran JL;
 PI WPI; 1994-358275/44.
 DR N-PSDB; AAQ73061.
 XX
 PT Eliciting an immune response to Salmonella - using attenuated Salmonella
 PT strains, vector constructs, or compsns. contg. fimbrial type proteins.
 XX
 PS Disclosure; Fig 2A-2D; 95pp; English.
 XX
 CC The isolated Sefa protein may be used in a vaccine composition to elicit
 CC an immune response to Salmonella in animals (e.g. food producing animals)
 CC and humans. (Updated on 25-MAR-2003 to correct PN field.)
 CC
 CC Revised record issued on 21-OCT-2004 : Correction to OS line
 XX
 SQ Sequence 165 AA;

Query Match 51.6%; Score 66; DB 2; Length 165;
 Best Local Similarity 100.0%; Pred. No. 2.1e-57;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 63 QGQPVFRIGRIQGANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTTFATPY 122
 DB 100 QGQPVFRIGRIQGANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTTFATPY 159

QY 123 VQOYQN 128
 DB 160 VQOYQN 165

RESULT 9
 ADJ51007
 ID ADJ51007 standard; protein; 225 AA.
 AC ADJ51007;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human novel protein NOV30a.
 XX
 KW Human; NOVX; autoimmune disease; Alzheimer's disease; stroke; allergy;
 KW Parkinson's disease; Huntington's disease; multiple sclerosis; anxiety;
 KW pain; diabetes; graft versus host disease; pancreatitis; obesity; ulcer;
 KW anaemia; cancer; viral infection; bacterial infection;
 KW parasitic infection.
 XX
 OS Homo sapiens.
 XX
 XX US2004030096-A1.
 PN
 XX 12-FEB-2004.
 PD
 XX
 XX 01-AUG-2002; 2002US-00210281.
 PF
 XX
 PR 02-AUG-2001; 2001US-0309501P.
 PR 03-AUG-2001; 2001US-0310291P.
 PR 08-AUG-2001; 2001US-0310951P.
 PR 09-AUG-2001; 2001US-0311292P.
 PR 13-AUG-2001; 2001US-0311979P.
 PR 14-AUG-2001; 2001US-0312203P.
 PR 17-AUG-2001; 2001US-0313201P.
 PR 20-AUG-2001; 2001US-0313643P.
 PR 20-AUG-2001; 2001US-0313702P.
 PR 21-AUG-2001; 2001US-0314031P.
 PR 23-AUG-2001; 2001US-0314466P.
 PR 28-AUG-2001; 2001US-0315403P.

PR 29-AUG-2001; 2001US-0315853P.
 PR 05-MAR-2002; 2002US-0361775P.
 PR 05-MAR-2002; 2002US-0361832P.
 XX
 PA (GORM/) GORMAN L.
 PA (ZERH/) ZERHUSEN B D.
 PA (EDIN/) EDINGER S R.
 PA (PADI/) PADIGARU M.
 PA (GUOX/) GUO X.
 PA (KEKU/) KEKUDA R.
 PA (ZHON/) ZHONG M.
 PA (PATT/) PATTURAJAN M.
 PA (MILL/) MILLER C E.
 PA (JIWV/) JI W.
 PA (PENA/) PENA C E A.
 PA (BURG/) BURGESS C E.
 PA (SCIO/) SCIORE P.
 PA (STON/) STONE D J.
 PA (TAUP/) TAUPIER R J.
 PA (CASW/) CASMAN S J.
 PA (ROTH/) ROTHENBERG M E.
 PA (MALY/) MALYANKAR U M.
 PA (BOLD/) BOLDOG F L.
 XX
 PI Gorman L, Zerhusen BD, Edinger SR, Padigaru M, Guo X, Kékuda R;
 PI Zhong M, Patturajan M, Miller CE, Ji W, Pena CE, Burgess CE;
 PI Sciore P, Stone DJ, Taupier RJ, Casman SJ, Rothenberg ME;
 PI Malyankar UM, Boldog FL;
 XX
 DR WPI; 2004-168942/16.
 DR N-PSDB; ADJ51006.
 XX
 PT New NOVX polypeptides and polynucleotides, useful in diagnosing, treating
 PT or preventing diseases or conditions, e.g. autoimmune disease,
 PT Alzheimer's disease, diabetes, graft versus host disease, cancer or viral
 PT or bacterial infections.
 XX
 PS Claim 2; SEQ ID NO 72; 342pp; English.

XX The invention relates to an isolated NOVX polypeptide (of 44 disclosed)
 CC comprising its mature form, a sequence having at least 95% sequence
 CC identity to NOVX or a sequence comprising one or more conservative
 CC substitutions in the amino acid sequence of NOVX. Also included are a
 CC composition comprising NOVX and a carrier, a kit comprising, in one or
 CC more containers, the composition, a method of identifying an agent that
 CC binds to NOVX, a method for identifying a potential therapeutic agent for
 CC use in treatment of a pathology related to aberrant expression or
 CC aberrant physiological interactions of NOVX, a method for screening for a
 CC modulator of activity of or of latency or predisposition to a pathology
 CC associated with NOVX, a method for modulating the activity of NOVX, a
 CC method of treating or preventing a pathology associated with NOVX, a
 CC pathological state in a mammal, an isolated nucleic acid molecule
 CC encoding a NOVX protein, a vector comprising the nucleic acid molecule,
 CC a cell comprising the vector, an antibody that immunospecifically binds
 CC to NOVX, a method for determining the presence or amount of NOVX or the
 CC nucleic acid molecule in a sample, a method for determining the presence
 CC of or predisposition to a disease associated with altered levels of
 CC expression of NOVX or the nucleic acid molecule in a first mammalian
 CC subject and a method of producing NOVX (comprising culturing the cell
 CC under conditions that lead to expression of the polypeptide). NOVX is
 CC useful in the manufacture of a medicament for treating a syndrome
 CC associated with a human disease associated with NOVX. The polypeptides
 CC and nucleic acid molecules are useful in diagnosing, treating or
 CC preventing diseases or conditions, e.g. autoimmune disease, Alzheimer's
 CC disease, stroke, allergies, Parkinson's disease, Huntington's disease,
 CC multiple sclerosis, anxiety, pain, diabetes, graft versus host disease,
 CC pancreatitis, obesity, ulcers, anaemia, cancer, viral or bacterial and
 CC parasitic infections (many more diseases and disorders are listed in the
 CC specification). The present sequence represents a NOVX protein.

SQ Sequence 225 AA;

Query Match 6.2%; Score 8; DB 8; Length 225;

Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AGQKVGTL 30
|||||
Db 16 AGQKVGTL 23

RESULT 10
ADA55453
ID ADA55453 standard; protein; 345 AA.
XX
AC ADA55453;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human protein, SEQ ID 3021.
XX
KW Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
KW Gene Therapy; human; secretory protein; membrane proteins; cancer;
KW inflammatory disease; osteoporosis; neurological disease.
XX
OS Homo sapiens.
XX
PN EF1293569-A2.
XX
PD 19-MAR-2003.
XX
PP 21-MAR-2002; 2002EP-00006586.
XX
PR 14-SEP-2001; 2001JP-00328381.
XX
PR 24-JAN-2002; 2002US-0350435P.
XX
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Matsuho Y;
XX
DR WPI; 2003-395539/38.
DR N-PSDB; ADA53814.
XX
XX New polynucleotides encoding full-length polypeptides, e.g. secretory
PT and/or membrane proteins, useful for developing medicines for diseases in
PT which the gene is involved, or as target molecules for gene therapy.
XX
PS Claim 14; SEQ ID NO 3021; 205pp; English.
XX
CC The present invention relates to novel human secretory or membrane
CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
CC ADA54071). The coding sequences are useful in the gene therapy of
CC diseases caused by abnormalities of the proteins, e.g. cancer,
CC inflammatory diseases, osteoporosis or neurological disease.
XX
SQ Sequence 345 AA;
Query Match 6.2%; Score 8; DB 6; Length 345;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AGQKVGTL 30
|||||
Db 142 AGQKVGTL 149

RESULT 11
ADS43323
ID ADS43323 standard; protein; 490 AA.
XX
AC ADS43323;
XX
DT 02-DEC-2004 (first entry)

XX Bacterial polypeptide #21753.
DE
XX Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PP 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
FI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
DR WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 21753; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 490 AA;
Query Match 6.2%; Score 8; DB 8; Length 490;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 AVAAGQKV 27
|||||
Db 268 AVAAGQKV 275

RESULT 12

ABP69377
ID ABP69377 standard; protein; 492 AA.

XX AC ABP69377;

XX DT 20-JAN-2003 (first entry)

XX DE Human polypeptide SEQ ID NO 1424.

XX KW Human; genome mapping; gene therapy; food supplement; virus; fungus;
KW cell-proliferative disorder; neurodegenerative disease; bacterial;
KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
KW haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoasacide;
KW antiarthritic.

XX OS Homo sapiens.

XX PN WO200270539-A2.

XX PD 12-SEP-2002.

XX PF 05-MAR-2002; 2002WO-US005095.

XX PR 05-MAR-2001; 2001US-00799451.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
PI Wehrman T, Wang J, Wang D, Drmanac RT;

XX WPI; 2002-759812/82.

XX DR N-PSDB; ABZ11594.

XX PT New polynucleotides comprising sequences assembled from expressed
PT sequence tags (ESTs), useful for treating cell-proliferative,
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
PT or coagulation disorders.

XX PS Claim 9; SEQ ID NO 1424; 1012pp + Sequence Listing; English.

XX CC The invention relates to an isolated polynucleotide (I) comprising a
CC nucleotide sequence selected from any of 948 sequences (ABZ11119-
CC ABZ12066) or their mature protein coding portion, active domain coding
CC protein or complementary sequences. The polynucleotides are useful for
CC identifying expressed genes or for physical mapping of human genome. The
CC encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
CC markers, as a food supplement, for generating antibodies, in medical
CC imaging, screening and diagnostic assays and for treating cell-
CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
CC arthritis, etc. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 492 AA;

Query Match 6.2%; Score 8; DB 5; Length 492;

Best Local Similarity 100.0%; Pred. No. 42;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AGQKVGTL 30

|||||

Db 185 AGQKVGTL 192

RESULT 13

ADY37608
ID ADY37608 standard; protein; 494 AA.

XX AC ADY37608;

XX DT 19-MAY-2005 (first entry)

XX DE Lung cancer related protein, SEQ ID 84.

XX KW Cytostatic; lung tumor.

XX OS Homo sapiens.

XX PN US2005048589-A1.

XX PD 03-MAR-2005.

XX PF 25-AUG-2004; 2004US-00926543.

XX PR 25-AUG-2003; 2003US-0497790P.

XX PA (JEND/) JENDOUBI M.

XX PI Jendoubi M;

XX WPI; 2005-221517/23.

XX DR N-PSDB; ADY37562.

XX PT New antibody specific for an antigen differentially expressed between
PT lung cancer tissue and normal tissue, useful for diagnosing, treating or
PT preventing lung cancer.

XX PS Disclosure; SEQ ID NO 84; 171pp; English.

XX CC The present invention relates to an antibody (I) that binds to an antigen
CC that is differentially expressed between lung cancer tissue and normal
CC tissue, where the antigen is encoded by ADY37525. Also disclosed are
CC polypeptides (ADY37573-ADY37618) encoded by lung cancer related genes
CC (ADY37525-ADY37572), their fragments, analogs or derivatives; producing
CC lung cancer related polypeptides; and a diagnostic kit for detecting and
CC disease management of lung cancer. (I) is useful for characterizing and
CC analyzing biological activity and function of the lung cancer-specific
CC gene products in relation to cellular pathways and networks in normal and
CC disease states, purifying the cancer specific gene products, and
CC detecting lung cancer-specific gene products and their expression levels
CC in animal models of cancer. (I) is also useful for diagnosing, treating
CC or preventing lung cancer, and also disorders related to abnormal
CC cellular differentiation, proliferation or degeneration.

XX SQ Sequence 494 AA;

Query Match 6.2%; Score 8; DB 9; Length 494;

Best Local Similarity 100.0%; Pred. No. 42;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AGQKVGTL 30

|||||

Db 185 AGQKVGTL 192

RESULT 14

ABUG2853
ID ABUG2853 standard; protein; 559 AA.

XX AC ABUG2853;

XX DT 09-SEP-2003 (first entry)

XX DE Novel endochitinase.

XX KW Endochitinase; GM13 strain; chitin oligosaccharide; NAG; chitin.

OS Cellulomonas sp.
 XX RN2002075143-A.
 XX
 PD 04-OCT-2002.
 XX
 XX 23-MAR-2001; 2001KR-00015379.
 XX
 XX 23-MAR-2001; 2001KR-00015379.
 XX
 XX (AMIC-) AMICOGEN CO LTD.
 XX
 XX Choi YJ, Jun YJ, Jung GH, Shin YC;
 XX WPI; 2003-146028/14.
 XX N-PSDB; ACD26615.
 DR
 DR Novel endochitinase gene from cellulomonas sp. gml3 strain.
 PT
 XX Claim 2; Fig 2; 7pp; Korean.
 PS
 XX The invention describes the nucleotide sequence of a novel endochitinase
 CC gene derived from Cellulomonas sp. Gml3 strain. Also, provided is the
 CC amino acid sequence translated therefrom. Therefore, chitin
 CC oligosaccharide and NAG can be manufactured from chitin by using an
 CC endochitinase encoded by the novel endochitinase gene. This is the amino
 CC acid sequence of the novel endochitinase protein
 XX
 XX Sequence 559 AA;
 SQ
 Query Match 6.2%; Score 8; DB 6; Length 559;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 114 AGTGTATF 121
 DB 45 AGTGTATF 52
 RESULT 15
 ABG29271
 ID ABG29271 standard; protein; 574 AA.
 XX
 AC ABG29271;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #29262.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 XX WO200175067-A2.
 FN
 XX 11-OCT-2001.
 PD
 XX 30-MAR-2001; 2001WO-US008631.
 PF
 XX 31-MAR-2000; 2000US-00540217.
 XX
 PR 23-AUG-2000; 2000US-00649167.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX Drmanac RT, Liu C, Tang YT;
 XX
 XX WPI; 2001-639362/73.
 DR
 DR N-PSDB; AAS93458.
 XX
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess

PT biodiversity.
 XX
 PS Claim 20; SEQ ID NO 59630; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 574 AA;
 SQ
 Query Match 6.2%; Score 8; DB 4; Length 574;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 23 AGQKVGTL 30
 DB 308 AGQKVGTL 315
 Search completed: April 26, 2006, 17:09:41
 Job time : 189 secs

GenCore version 5.1.1.7
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OM protein - protein search, using sw model

Run on: April 26, 2006, 17:06:39 ; Search time 16 Seconds
(without alignments)
769.734 Million cell updates/sec

Title: US-10-018-892-3
Perfect score: 128
Sequence: 1 AAQNTTSANWSQDPGFTGPA.....KSTLPAGTFTATFYVQYQN 128
Scoring Table: ~~obscure~~
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues
Word size: 1
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Listing first 45 summaries

Database : PIR_80.*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	128	100.0	165	A40618	fimbrin, SEF14 - S
2	7	5.5	100	C64431	conserved hypothetical
3	7	5.5	104	JC7376	hardening-inducibl
4	7	5.5	188	H95348	nitric-oxide reduc
5	7	5.5	242	C84380	hypothetical prote
6	7	5.5	247	A55208	short-chain alcoh
7	7	5.5	248	T12632	water channel prot
8	7	5.5	248	T01648	probable tonoplast
9	7	5.5	248	T07819	hypothetical water cha
10	7	5.5	277	E82739	hypothetical prote
11	7	5.5	292	H87260	asparaginase famil
12	7	5.5	338	T32972	hypothetical prote
13	7	5.5	369	AE2345	phospho-N-acetylmu
14	7	5.5	390	F95350	VirB10 transmembra
15	7	5.5	398	AI3231	conjugal transfer
16	7	5.5	417	E95327	conserved hypothet
17	7	5.5	434	T47772	hypothetical prote
18	7	5.5	454	AI1278	anthranilate synth
19	7	5.5	454	AI1641	anthranilate synth
20	7	5.5	471	T41407	hypothetical prote
21	7	5.5	497	A29055	aldehyde dehydroge
22	7	5.5	512	H86206	hypothetical prote
23	7	5.5	513	I45456	NADH2 dehydrogenas
24	7	5.5	515	E84577	probable cyclokinin
25	7	5.5	526	C70539	hypothetical prote
26	7	5.5	534	F84398	phosphate ABC tran
27	7	5.5	543	T32109	hypothetical prote
28	7	5.5	580	S56645	chaperonin 60 alph
29	7	5.5	594	C96525	protein Tln15.25 [

30 7 5.5 594 2 T33686 hypothetical prote
31 7 5.5 715 2 S76492 lipoprotein nlPD -
32 7 5.5 721 2 D83110 exodeoxyribonuclea
33 7 5.5 802 2 AF1227 phenylalanyl-tRNA
34 7 5.5 802 2 AH1580 phenylalanyl-tRNA
35 7 5.5 808 2 F84038 phenylalanyl-tRNA
36 7 5.5 818 2 T33689 hypothetical prote
37 7 5.5 818 2 T33687 hypothetical prote
38 7 5.5 826 1 D64978 probable outer mem
39 7 5.5 826 2 C90993 probable outer mem
40 7 5.5 826 2 F85838 probable outer mem
41 7 5.5 863 2 S37088 phycobilisome anch
42 7 5.5 1018 2 H83135 probable adhesin P
43 7 5.5 1167 2 B75258 probable S-layer p
44 7 5.5 1336 2 T17479 hypothetical prote
45 7 5.5 1337 1 I38670 protein-tyrosine-p

ALIGNMENTS

RESULT 1

A40618
fimbrin, SEF14 - Salmonella enteritidis
N:Alternate names: fimbrin, Sefa
C:Species: Salmonella enteritidis
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A40618, A25034
R:Clouthier, S.C.; Muller, K.H.; Doran, J.L.; Collinson, S.K.; Kay, W.W.
J. Bacteriol. 175, 2523-2533, 1993
A:Title: Characterization of three fimbrial genes, sefABC, of Salmonella enteritidis.
A:Reference number: A40618; MUID:93239677; PMID:8097515
A:Contents: 27655-3b
A:Accession: A40618
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-165 <CLO>
A:Cross-references: UNIPROT:PI2061; UNIPARC:UPI00001135BD; GB:L11008; NID:g310645; PID
A:Note: sequence extracted from NCBI backbone (NCBI:130387, NCBIP:130395)
R:Feutrier, J.; Kay, W.W.; frust, T.J.
J. Bacteriol. 168, 221-227, 1986
A:Title: Purification and characterization of fimbriae from Salmonella enteritidis.
A:Reference number: A25034; MUID:87008384; PMID:2875990
A:Accession: A25034
A:Molecule type: protein
A:Residues: 22-78, 'X', 80-82, 'XQ', 128 <FEU>
A:Cross-references: UNIPARC:UPI00001798D8

Query Match 100.0%; Score 128; DB 2; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.5e-119; Indels 0; Gaps 0;
Matches 128; Conservative 0; Mismatches 0;

QY 1 AAQNTTSANWSQDPGFTGPAVAAQKVGFTLSITATGPHNSVSIAGKASVSGGVATVPFV 60
Db 38 AAQNTTSANWSQDPGFTGPAVAAQKVGFTLSITATGPHNSVSIAGKASVSGGVATVPFV 97
QY 61 DQCGQPVFRGRIQGANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTPTAT 120
Db 98 DQCGQPVFRGRIQGANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTPTAT 157
QY 121 FVQOQYQN 128
Db 158 FVQOQYQN 165

RESULT 2

C64431
conserved hypothetical protein MJ1052 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: C64431
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A

rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.

Science 273, 1058-1073, 1996

A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.

A:Title: Complete genome sequence of the methanogenic archaeon, *Methanococcus jannaschii*

A:Reference number: A64300; MUID:96337999; PMID:8698087

A:Accession: C64431

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-100 <BUL>

A:Cross-references: UNIPROT:Q58452; UNIPARC:UPI0000139F75; GB:U67548; GB:L77117; NID:928

C:Genetics:

A:Map position: REV989804-989502

A:Start codon: GNG

C:Superfamily: *Methanococcus jannaschii* conserved hypothetical protein MJ1052

Query Match 5.5%; Score 7; DB 2; Length 100;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 45 GKGSVS 51

Db 17 GKGSVS 23

RESULT 3

JC7376

hardening-inducible protein HIC12 - *Chlorella vulgaris*

C:Species: *Chlorella vulgaris*

C:Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004

C:Accession: JC7376

R:Honjoh, K.; Matsumoto, H.; Shimizu, H.; Ooyama, K.; Tanaka, K.; Oda, Y.; Takata, R.; J

BioSci. Biotechnol. Biochem. 64, 1656-1663, 2000

A:Title: Cryoprotective activities of group 3 late embryogenesis abundant proteins from

A:Reference number: JC7376

A:Accession: JC7376

A:Molecule type: mRNA

A:Residues: 1-104 <HON>

A:Cross-references: UNIPROT:Q9SLP7; UNIPARC:UPI00000A7366; DDBJ:AB035642

A:Experimental source: strain IAM C-27

C:Comment: This protein, homolog of group 3 late embryogenesis abundant protein, has eff

C:Genetics:

A:Gene: hic12

Query Match 5.5%; Score 7; DB 2; Length 104;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 AAGQKVG 28

Db 17 AAGQKVG 23

RESULT 4

H95348

nitric-oxide reductase (EC 1.7.99.7) NorE [imported] - *Sinorhizobium meliloti* (strain 10

C:Species: *Sinorhizobium meliloti*

C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

C:Accession: H95348

R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe

; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.

Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9886, 2001

A:Title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meliloti*

A:Reference number: A95262; MUID:21396509; PMID:11481432

A:Accession: H95348

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-188 <KUR>

A:Cross-references: UNIPROT:Q92214; UNIPARC:UPI00000CB18E; GB:AE006469; PIDN:AAK65354.1;

A:Experimental source: strain 1021, megaplasmid pSymA

R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,

pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;

L.; Hymen, R.W.; Jones, T.

Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure

hebaute, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.

A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.

A:Reference number: A96039; MUID:21368234; PMID:11474104

A:Contents: annotation

C:Genetics:

A:Gene: norE

A:Genome: plasmid

C:Keywords: oxidoreductase

Query Match 5.5%; Score 7; DB 2; Length 188;

Best Local Similarity 100.0%; Pred. No. 28;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 44 AGKGASV 50

Db 84 AGKGASV 90

RESULT 5

C84380

hypothetical protein hisA [imported] - *Halobacterium* sp. NRC-1

C:Species: *Halobacterium* sp. NRC-1

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: C84380

R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Laaky,

Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; I

A:Title: Genome sequence of *Halobacterium* species NRC-1.

A:Reference number: A84160; MUID:20504483; PMID:11016950

A:Accession: C84380

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-242 <STO>

A:Cross-references: UNIPROT:Q9HN14; UNIPARC:UPI000012C7C5; GB:AE004437; NID:gl0581706;

C:Genetics:

A:Gene: hisA

Query Match 5.5%; Score 7; DB 2; Length 242;

Best Local Similarity 100.0%; Pred. No. 35;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 SGGVATV 57

Db 200 SGGVATV 206

RESULT 6

A55208

short-chain alcohol dehydrogenase homolog socA1 - *Myxococcus xanthus*

C:Species: *Myxococcus xanthus*

C:Date: 05-May-1995 #sequence_revision 05-May-1995 #text_change 05-Oct-2004

C:Accession: A55208

J:Ree, K.; Shinkets, L.J.

J. Bacteriol. 176, 2200-2209, 1994

A:Title: Cloning and characterization of the socA locus which restores development to

A:Reference number: A55208; MUID:94209218; PMID:8157590

A:Accession: A55208

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-247 <LEB>

A:Cross-references: UNIPROT:Q7M0Y6; UNIPARC:UPI0000174E88; GB:L27430

C:Genetics:

A:Gene: socA1

C:Superfamily: short-chain dehydrogenase; short-chain alcohol dehydrogenase homology

C:Keywords: alcohol metabolism

F:17-187/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 5.5%; Score 7; DB 2; Length 247;

Best Local Similarity 100.0%; Pred. No. 35;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TGPAAVAA 23
 |||||
 Db 197 TGPAAVAA 203

RESULT 7

T12632
 water channel protein - common sunflower
 N:Alternate names: aquaporin; tonoplast intrinsic protein homolog
 C:Species: Helianthus annuus (common sunflower)
 C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 05-Oct-2004
 C:Accession: T12632
 R:Sarda, X.; Tusch, D.; Ferrare, K.; Legrand, E.; Dupuis, J.M.; Casse-Delbart, P.; Lama
 Plant J. 12, 1103-1111, 1997
 A>Title: Two TIP-like genes encoding aquaporins are expressed in sunflower guard cells.
 A:Reference number: Z17561; MUID:98079246; PMID:9418051
 A:Accession: T12632
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-248 <SAR>
 A:Cross-references: UNIPROT:Q39935; UNIPARC:UPI00000AB8DF; EMBL:X95952; NID:g1212914; PI
 A:Experimental source: root
 C:Superfamily: aquaporin
 C:Keywords: channel-forming protein; transmembrane protein

Query Match 5.5%; Score 7; DB 2; Length 248;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 GPAVAA 24
 |||||
 Db 203 GPAVAA 209

RESULT 8

T01648
 Probable tonoplast aquaporin - maize
 C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 05-Oct-2004
 R:Finkelstein, D. B.; Drew, M.C.; Jordan, W.J.; Wing, R.A.; Mullet, J.E.; Morgan, P.W.
 submitted to the EMBL Data Library, April 1998
 A:Reference number: Z14367
 A:Accession: T01648
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-248 <PIN>
 A:Cross-references: UNIPROT:O81216; UNIPARC:UPI00000ACCBF; EMBL:AF057183; NID:g3264595;
 A:Experimental source: strain TX5855
 C:Superfamily: aquaporin

Query Match 5.5%; Score 7; DB 2; Length 248;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 GPAVAA 24
 |||||
 Db 202 GPAVAA 208

RESULT 9

T07819
 probable water channel protein delta-VM23 - radish
 C:Species: Raphanus sativus (radish)
 C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 05-Oct-2004
 C:Accession: T07819
 R:Higuchi, T.; Suga, S.; Teuchiya, T.; Hisada, H.; Morishima, S.; Okada, Y.; Maeshima, M.
 Plant Cell Physiol. 39, 905-913, 1998
 A>Title: Molecular cloning, water channel activity and tissue specific expression of two
 A:Reference number: Z16148; MUID:99033463; PMID:9816675
 A:Accession: T07819
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
 A:Residues: 1-248 <HIG>
 A:Cross-references: UNIPROT:O82142; UNIPARC:UPI00000A5347; EMBL:AB010416; NID:g3298326
 A:Experimental source: cultivar Tokinashidaikon
 C:Genetics:
 A:Gene: VIP3
 C:Superfamily: aquaporin
 C:Keywords: water channel

Query Match 5.5%; Score 7; DB 2; Length 248;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 GPAVAA 24
 |||||
 Db 203 GPAVAA 209

RESULT 10

E82739
 hypothetical protein XF0968 [imported] - Xylella fastidiosa (strain 9a5c)
 C:Species: Xylella fastidiosa
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C:Accession: E82739
 R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequ
 Nature 406, 151-157, 2000
 A>Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A:Reference number: A82515; MUID:20365717; PMID:10910347
 A>Note: for a complete list of authors see reference number A59328 below
 A:Accession: E82739
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-277 <SIM>
 A:Cross-references: UNIPROT:Q9PER0; UNIPARC:UPI00000C25A7; GB:AE003935; GB:AE003849; N
 A:Experimental source: strain 9a5c
 R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer,
 as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fro
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Lai
 Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins,
 A:Authors: Martins, E.M.P.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, B.C.; Miyaki, C.Y.
 , P.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawas
 A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silve
 M.; Teshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;
 A:Reference number: A59328
 A:Contents: annotation
 C:Genetics:
 A:Gene: XF0968

Query Match 5.5%; Score 7; DB 2; Length 277;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AONTTSA 8
 |||||
 Db 83 AONTTSA 89

RESULT 11

H87260
 asparaginase family protein [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C:Accession: H87260
 R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, M.
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kol
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A>Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; MUID:21173698; PMID:11259647

A;Accession: H87260
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-292 <STO>
A;Cross-references: UNIPROT:Q9ABX3; UNIPARC:UPI000000C6F20; GB:AE005673; NID:gl3421200; F
C;Genetics:
A;Gene: CC0097
C;Superfamily: ybiK protein

Query Match 5.5%; Score 7; DB 2; Length 292;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 IAGKGAS 49
|||||
Db 64 IAGKGAS 70

RESULT 12
T32972
hypothetical protein F58H7.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T32972
R;Graves, T.
submitted to the EMBL Data Library, February 1998
A;Description: The sequence of C. elegans cosmid F58H7.
A;Reference number: T32972
A;Accession: T32972
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-338 <GRA>
A;Cross-references: UNIPROT:O45094; UNIPARC:UPI000007F204; EMBL:AF045643; PIDN:AAC02595.
A;Experimental source: strain Bristol N2; clone F58H7
C;Genetics:
A;Gene: CESP:F58H7.8
A;Map position: 4
A;Introns: 31/2
C;Superfamily: Caenorhabditis elegans hypothetical protein F42G2.3

Query Match 5.5%; Score 7; DB 2; Length 338;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KVGTLIS 32
|||||
Db 183 KVGTLIS 189

RESULT 13
AE2345
phospho-N-acetylmuramoyl-pentapeptide-transferase e [imported] - Nostoc sp. (strain PCC 7
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AE2345
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE2345
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-369 <KUR>
A;Cross-references: UNIPROT:Q8YP83; UNIPARC:UPI000012F50C; GB:BA000019; PIDN:BAE76015-1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all4316
C;Superfamily: phospho-N-acetylmuramoyl-pentapeptide-transferase

Query Match 5.5%; Score 7; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 50;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 84 GIDGLAG 90
|||||
Db 214 GIDGLAG 220

RESULT 14
F95350
VirB10 transmembrane type IV secretion protein [imported] - Sinorhizobium meliloti (str
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: F95350
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Boy
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.
Proc. Natl. Acad. Sci. U.S.A. 98, 9893-9898, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilo
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: F95350
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-390 <KUR>
A;Cross-references: UNIPROT:Q92202; UNIPARC:UPI00000CB19A; GB:AE006469; PIDN:AAK65368.
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lela
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, I
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: virB10
A;Genome: plasmid
C;Superfamily: tumor-inducing plasmid pTiC58 virB10 protein

Query Match 5.5%; Score 7; DB 2; Length 390;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AQTNTSA 8
|||||
Db 314 AQTNTSA 320

RESULT 15
AI3231
conjugal transfer protein trbL [imported] - Agrobacterium tumefaciens (strain C58, Dup
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AI3231
R;Wood, D.W.; Stetshak, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl
.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AI3231
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-398 <KUR>
A;Cross-references: UNIPROT:O61175; UNIPARC:UPI00000D1462; GB:AE008690; PIDN:AAL46271.
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: trbL
A;Genome: plasmid

Query Match 5.5%; Score 7; DB 2; Length 398;
Best Local Similarity 100.0%; Pred. No. 53;

Matches	7;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	47	GASVSGG	53						
Db	282	GASVSGG	288						

Search completed: April 26, 2006, 17:10:01
Job time : 18 secs

GenCore version 5.1.7

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OM protein - protein search, using sw model

Run on: April 26, 2006, 17:06:38 ; Search time 163 Seconds
(without alignments)

554.034 Million cell updates/sec

Title: US-10-018-892-3

Perfect score: 128

Sequence: 1 AAQNTTSANWSQDPFGTGA.....KSTLPAGTATTATFYVQYQN 128

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word-size: 1

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	128	100.0	165	1 FM_SALEN	P12061 salmonella
2	73	57.0	165	2 Q5PM43 SALPA	Q5pm43 salmonella
3	10	7.8	30	2 Q94V0 SALEN	Q94v0 salmonella
4	9	7.0	606	2 Q82KE7 STRAW	Q82ke7 streptomyces
5	9	7.0	725	2 Q8XZRI RALSO	Q8xzi1 ralestonia s
6	9	7.0	741	2 Q9K6X9 BURPI	Q9k6x9 burkholderi
7	8	6.2	187	2 Q4PLV2 USTMA	Q4ply2 ustilago ma
8	8	6.2	205	2 Q73TEI MYCPA	Q73tei mycobacteri
9	8	6.2	310	2 Q6ZLKI ORYSA	Q6zlk1 oryza sativ
10	8	6.2	329	2 Q88SS6 LACPL	Q88ss6 lactobacill
11	8	6.2	355	2 Q92BD2 TREDE	Q92bd2 treponema d
12	8	6.2	411	2 Q95LJ3 MACFA	Q95lj3 macaca fasc
13	8	6.2	453	2 Q8DVF8 STRMU	Q8dvf8 streptococc
14	8	6.2	456	2 Q5LYI2 STRT1	Q5lyi2 streptococc
15	8	6.2	456	2 Q5M345 STRT2	Q5m345 streptococc
16	8	6.2	512	2 Q4HZE9 GIBZE	Q4hze9 gibberella
17	8	6.2	528	2 Q6LRK8 PHOPR	Q6lrk8 photobacter
18	8	6.2	558	2 Q4R6U5 MACFA	Q4r6u5 macaca fasc
19	8	6.2	559	2 Q4BN2_9CELL	Q4bn2 cellulomona
20	8	6.2	579	1 ESR1_SPAAU	Q9pvz9 sparus aura
21	8	6.2	583	2 Q804Q6 ACASC	Q804q6 acanthopagr
22	8	6.2	587	2 Q74KW2 LACJO	Q74kw2 lactobacill
23	8	6.2	599	1 RSNL2 RAT	Q6hds5 rattus norv
24	8	6.2	614	2 Q4ZFY2 HUMAN	Q4zfy2 homo sapien
25	8	6.2	639	2 Q8VP60 TREDE	Q8vp60 treponema d
26	8	6.2	704	1 RSNL2 MOUSE	Q8ci96 mus musculu
27	8	6.2	705	1 RSNL2 HUMAN	Q8n3c7 homo sapien
28	8	6.2	716	2 Q4SK06 TETNG	Q4sk06 tetraodon n
29	8	6.2	724	2 Q59GR7 HUMAN	Q59gr7 homo sapien
30	7	5.5	26	2 Q9QRU9_9HEPC	Q9qru9 hepatitis c
31	7	5.5	26	2 Q9QRV0_9HEPC	Q9qrv0 hepatitis c

```

32 7 5.5 66 2 Q6Z7W2 ORYSA
33 7 5.5 69 2 Q67TN3 ORYZA
34 7 5.5 86 2 Q6K202 ORYZA
35 7 5.5 94 2 Q6LD31 LYMDI
36 7 5.5 100 1 Y1052 METJA
37 7 5.5 104 2 Q9SLP7 CHLVU
38 7 5.5 106 2 P95679 COXBU
39 7 5.5 106 2 Q8GM40 LEGFN
40 7 5.5 114 1 CT149_HUMAN
41 7 5.5 115 1 CT149_MOUSE
42 7 5.5 115 2 Q5PRO1 RAT
43 7 5.5 115 2 Q58EU5 MOUSE
44 7 5.5 120 2 Q6DIQ8 ERWCT
45 7 5.5 121 1 CHA9_LYMDI

```

ALIGNMENTS

```

RESULT 1
FM_SALEN
ID_ FM_SALEN STANDARD; PRT; 165 AA.
AC P12061;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Fimbrial protein precursor.
GN Name=sefA; Synonyms=sef14;
OS Salmonella enteritidis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=592;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=27655-3B;
RA MEDLINE=93239677; PubMed=8097515;
RX Clouthier S.C., Mueller K.-H., Doran J.L., Collinson S.K., Kay W.W.;
RT "Characterization of three fimbrial genes, sefABC, of Salmonella
   enteritidis."
RL J. Bacteriol. 175:2523-2533 (1993).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91072589; PubMed=1701443;
RA Thorns C.J., Sojka M.G., Chasey D.C.;
RT "Detection of a novel fimbrial structure on the surface of Salmonella
   enteritidis by using a monoclonal antibody."
RL J. Clin. Microbiol. 28:2409-2414 (1990).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Ogumiyi A.D., Kotlarski I., Morona R., Manning P.A.;
RT Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP PROTEIN SEQUENCE OF 22-85.
RX MEDLINE=87008384; PubMed=2875990;
RA Feutrier J., Kay W.W., Trust T.J.;
RT "Purification and characterization of fimbriae from Salmonella
   enteritidis."
RL J. Bacteriol. 168:221-227 (1986).
CC -!- FUNCTION: Structural subunit of the sef14 fimbriae (S.enteritidis
   filamentous fimbriae).
CC -!- SUBCELLULAR LOCATION: Fimbria.

```

```

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
   between the Swiss Institute of Bioinformatics and the EMBL outstation -
   the European Bioinformatics Institute. There are no restrictions on its
   use as long as its content is in no way modified and this statement is not
   removed.
CC -----
CC EMBL; L11008; AAA27219.1; -; Genomic DNA.
CC EMBL; L03833; AAA71892.1; -; Unassigned DNA.
CC EMBL; X98516; CAA67141.1; -; Genomic DNA.
CC PIR; A40618; A40618.
CC PDB; 1LU0; Model; A=1-165.

```

```

DR InterPro; IPR010498; SEF14 adhesin.
DR Pfam; PF06443; SEF14 adhesin; 1.
KW 3D-structure; Direct protein sequencing; Fimbria; Signal.
FT SIGNAL 1 21
FT CHAIN 22 165 Fimbrial protein.
FT FT CHAIN 30 30 V -> B (in Ref. 2 and 3).
FT CONFLICT 30 30 V -> B (in Ref. 2 and 3).
FT CONFLICT 84 85 GA -> QW (in Ref. 4).
FT SEQUENCE 165 AA; 16477 MW; 5B33798A3F0F9091 CRC64;
SQ
Query Match
Best Local Similarity 100.0%; Score 128; DB 1; Length 165;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAQNTTSANWSQDPTGTPAAGQKVGTLISITATGPHNSVSIAGKASVSGGVATVPFV 60
Db 38 AAQNTTSANWSQDPTGTPAAGQKVGTLISITATGPHNSVSIAGKASVSGGVATVPFV 97

Qy 61 DGGQQPVRGRICQANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTTAT 120
Db 98 DGGQQPVRGRICQANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTTAT 157

Qy 121 FYVQOYQN 128
Db 158 FYVQOYQN 165

RESULT 2
QSPM43 SALPA
ID QSPM43 SALPA PRELIMINARY; PRT; 165 AA.
AC QSPM43;
DT 01-FEB-2005 (Tremblrel. 29, Created)
DT 01-FEB-2005 (Tremblrel. 29, Last sequence update)
DE Fimbrial structural protein.
GN Name=sefA; OrderedLocNames=SPA4304;
OS Salmonella paratyphi-a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=54388;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 9150;
RX PubMed=15531882; DOI=10.1038/ng1470;
RA McClelland M., Sanderson K.E., Clifton S.W., Latreille P.,
RA Porwollik S., Sabo A., Meyer R., Bieri T., Ozersky P., McLellan M.,
RA Harkins C.R., Wang C., Nguyen C., Berghoff A., Elliott G.,
RA Kohlberg S., Strong C., Du F., Carter J., Kremizki C., Layman D.,
RA Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P.,
RA Delehaanty K., Fronick C., Megrini V., Nhan M., Warren W., Florea L.,
RA Spieth J., Wilson R.K.;
RT "Comparison of genome degradation in Paratyphi A and Typhi, human-
RT restricted serovars of Salmonella enterica that cause typhoid.";
RL Nat. Genet. 36:1268-1274(2004).
DR EMBL; CP000026; ANV80033.1; -; Genomic_DNA.
DR InterPro; IPR010498; SEF14 adhesin.
DR Pfam; PF06443; SEF14 adhesin; 1.
KW Complete proteome.
SQ SEQUENCE 165 AA; 16665 MW; 8A32BE3F43C91520 CRC64;

Query Match
Best Local Similarity 100.0%; Score 73; DB 2; Length 165;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAQNTTSANWSQDPTGTPAAGQKVGTLISITATGPHNSVSIAGKASVSGGVATVPFV 60
Db 38 AAQNTTSANWSQDPTGTPAAGQKVGTLISITATGPHNSVSIAGKASVSGGVATVPFV 97

Qy 61 DGGQQPVRGRIRIQ 73
Db 98 DGGQQPVRGRIRIQ 110

RESULT 3

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```

Q9R4V0 SALEN
ID Q9R4V0 SALEN PRELIMINARY; PRT; 30 AA.
AC Q9R4V0;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Fimbrial protein SEF14 (Pragmat).
OS Salmonella enteritidis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=592;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=95048770; PubMed=7960117;
RA Ogunniyi A.D., Manning P.A., Kotlarski I.;
RT "A Salmonella enteritidis 11RX pilin induces strong T-lymphocyte
RT responses.";
RL Infect. Immun. 62:5376-5383(1994).
DR InterPro; IPR010498; SEF14 adhesin.
DR Pfam; PF06443; SEF14 adhesin; 1.
SQ SEQUENCE 30 AA; 3074 MW; AE75376BE8860C34 CRC64;

Query Match
Best Local Similarity 100.0%; Score 10; DB 2; Length 30;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAQNTTSANW 10
Db 17 AAQNTTSANW 26

RESULT 4
Q82KE7 STRAW
ID Q82KE7 STRAW PRELIMINARY; PRT; 606 AA.
AC Q82KE7;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=SAV2456;
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562; DOI=10.1038/nbt820;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.21143198;
RA Shinoe S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinoe M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
DR EMBL; BA000030; BAC70167.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 606 AA; 64012 MW; F6DBC9DE2B621818 CRC64;

Query Match
Best Local Similarity 100.0%; Score 9; DB 2; Length 606;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 49 SVSGGVATV 57

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Db 73 SVSGGVATV 81

|||||

RESULT 5

Q8XZRL1_RALSO Q8XZRL1_RALSO PRELIMINARY; PRT; 725 AA.

AC Q8XZRL1

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE PROBABLE D-3-HYDROXYBUTYRATE OLIGOMER HYDROLASE LIPOPROTEIN

DE TRANSMEMBRANE (BC 3.1.1.-.-).

GN OrderedLocusNames=RSC1334; ORFNames=RS02856;

OS Ralstonia solanacearum (Pseudomonas solanacearum).

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

OC Burkholderiaceae; Ralstonia.

OX NCBI_TaxID=305;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=GMI1000;

RC MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;

RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,

RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,

RA Chander M., Choise N., Claudel-Renard C., Cumnac S., Demange N.,

RA Gaiglin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,

RA Guiguer P., Thebaud P., Whalen M., Wincker P., Levy M.,

RA Weissbach J., Boucher C.A.;

RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";

RL Nature 415:497-502(2002).

RE EMBL; AL646064; CAD15036.1; -; Genomic DNA.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0016787; F:hydrolase activity; IEA.

KW Complete proteome; Hydrolase; Lipoprotein; Transmembrane.

SQ SEQUENCE 725 AA; 73528 MW; 78B9A592B5C66293 CRC64;

Query Match 7.0%; Score 9; DB 2; Length 725;

Best Local Similarity 100.0%; Pred. No. 6.9;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 SVSGGVATV 57

|||||

Db 713 SVSGGVATV 721

RESULT 6

Q9X6X9_BURPI Q9X6X9_BURPI PRELIMINARY; PRT; 741 AA.

AC Q9X6X9

DT 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE D(-)-3-hydroxybutyrate oligomer hydrolase.

OS Burkholderia pickettii (Pseudomonas pickettii).

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

OC Burkholderiaceae; Ralstonia.

OX NCBI_TaxID=329;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=TI;

RC MEDLINE=89123016; PubMed=2644188;

RA Saito T., Suzuki K., Yamamoto J., Fukui T., Miwa K., Tomita K.,

RA Nakanishi S., Odani S., Suzuki J.-I., Ishikawa K.;

RT "Cloning, nucleotide sequence, and expression in Escherichia coli of

RT the gene for poly(3-hydroxybutyrate) depolymerase from Alcaligenes

RT faecalis.";

RT J. Bacteriol. 171:184-189(1989).

RN [2]

RL NUCLEOTIDE SEQUENCE.

RC STRAIN=TI;

RA Saito T.;

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; J04223; AAD36989.1; -; Genomic DNA.

DR GO; GO:0016787; F:hydrolase activity; IEA.

SQ SEQUENCE 741 AA; 75590 MW; 68E13C032382B373 CRC64;

Query Match 7.0%; Score 9; DB 2; Length 741;

Best Local Similarity 100.0%; Pred. No. 7.1;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 SVSGGVATV 57

|||||

Db 729 SVSGGVATV 737

RESULT 7

Q4PIY2_USTMA Q4PIY2_USTMA PRELIMINARY; PRT; 187 AA.

AC Q4PIY2

DT 13-SEP-2005 (TrEMBLrel. 31, Created)

DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

DE Hypothetical protein.

GN ORFNames=UM05881.1;

OS Ustilago maydis 521.

OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;

OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.

OX NCBI_TaxID=237631;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=521;

RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya B.,

RA Ait-zahra H., Allen T., Allen T., An P., Anderson M., Anderson S.,

RA Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,

RA Bayul T., Blitshteyn B., Bloom T., Blye J., Boguslavsky L.,

RA Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,

RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,

RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,

RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,

RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,

RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,

RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,

RA Ginzke A., Goyette A., Graham J., Grandbois E., Gyalteen K., Hafez N.,

RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,

RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Huby E., Iliev I.,

RA Jaffe D., Jones C., Kamal M., Kamat A., Kamvyselis M., Karlsson E.,

RA Kells C., Kieu A., Kisner P., Kodira C., Kulbokas E., Labutti K.,

RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,

RA Lindblad-ton K., Liu X., Lokitsang T., Lokitsang Y., Lucien O.,

RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,

RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,

RA McCarthy M., McDonough S., McGhee T., Meldrum J., Menues L.,

RA Mesirov J., Mihalev A., Mihova T., Mikkelsen T., Menga V., Moru K.,

RA Mores J., Mulrain L., Munson G., Naylor J., Neues C., Nguyen C.,

RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,

RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,

RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Pignani B.,

RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,

RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,

RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,

RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,

RA Stetson K., Stalker J., Stange-thomann N., Stavropoulos S.,

RA Stetson K., Stone S., Stone S., Stubbs M., Talamas J., Tchuinga P.,

RA Tenzing P., Testaye S., Theodore J., Thoulutsang Y., Topham K.,

RA Towey S., Teamla T., Tsomo N., Vallee D., Vassiliev H.,

RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,

RA Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,

RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,

RA Zimmer A., Zody M., Lander E.;

RT "The genome sequence of Ustilago maydis.";

RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

CC -! CAUTION: The sequence shown here is derived from an

CC preliminary data.

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

DR EMBL; AACP01000215; EAK86826.1; -; Genomic DNA.

KW Hypothetical protein.
 SQ SEQUENCE 187 AA; 20885 MW; AF688CB7C85D14E2 CRC64;

Query Match 6.2%; Score 8; DB 2; Length 187;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 VSIAGKGA 48
 |||||
 Db 40 VSIAGKGA 47

RESULT 8
 Q73TEL_MYCPA
 ID Q73TEL_MYCPA PRELIMINARY; PRT; 205 AA.
 AC Q73TEL;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocNames=MAP3777;
 OS Mycobacterium paratuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;
 OC Mycobacterium avium complex (MAC).
 OX NCBI_TaxID=1770;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=k10;
 RA Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
 RL Submitted (SFP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017240; AAS06327.1; -; Genomic_DNA.
 DR InterPro; IPR011610; Mtu_fam_121.
 DR InterPro; IPR003455; Ont_N.
 DR Pfam; PF02409; Ont_N; 1.
 DR TIGRFAMs; TIGR00027; mthyl_TIGR00027; 1.
 DR Complete proteome; Hypothetical protein.
 KW SEQUENCE 205 AA; 22413 MW; 80A09C606237F10 CRC64;

Query Match 6.2%; Score 8; DB 2; Length 205;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 TGIDGLAG 90
 |||||
 Db 100 TGIDGLAG 107

RESULT 9
 Q6ZLKI_ORYSA
 ID Q6ZLKI_ORYSA PRELIMINARY; PRT; 310 AA.
 AC Q6ZLKI;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Membrane transporter PFB0275w-like protein.
 GN Name=QJ1136_A05.20;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzoae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC clone:QJ1136_A05.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP003748; BAC82966.1; -; Genomic_DNA.
 DR Gramene; O6ZLKI; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR011701; MFS_1.

DR Pfam; PF07690; MFS_1; 1.
 SQ SEQUENCE 310 AA; 34286 MW; B69FC90CFFAFD5EC CRC64;

Query Match 6.2%; Score 8; DB 2; Length 310;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 GLAGWRVA 94
 |||||
 Db 8 GLAGWRVA 15

RESULT 10
 Q8SS56_LACPL
 ID Q8SS56_LACPL PRELIMINARY; PRT; 329 AA.
 AC Q8SS56;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Esterase (Putative).
 GN OrderedLocNames=lp_3312;
 OS Lactobacillus plantarum.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID=1590;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NCIMB 8826 / WCFS1;
 RA MEDLINE=22480296; PubMed=12566566; DOI=10.1073/pnas.0337704100;
 RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
 RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
 RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
 RA Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
 RA De Vos W.M., Siezen K.J.;
 RT "Complete genome sequence of Lactobacillus plantarum WCFS1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
 DR EMBL; AL935261; CAD65434.1; -; Genomic DNA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0046677; P:response to antibiotic; IEA.
 DR InterPro; IPR001466; Beta_lactamase.
 DR Pfam; PF00144; Beta_lactamase; 1.
 KW Complete proteome.
 SQ SEQUENCE 329 AA; 37332 MW; FC66021317FCC1B7 CRC64;

Query Match 6.2%; Score 8; DB 2; Length 329;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GFTGPAVA 22
 |||||
 Db 283 GFTGPAVA 290

RESULT 11
 Q9ZBD2_TREDE
 ID Q9ZBD2_TREDE PRELIMINARY; PRT; 355 AA.
 AC Q9ZBD2;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE 43kDa protein.
 OS Treponema denticola.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=158;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC35405;
 RA MEDLINE=97101036; PubMed=8945563;
 RA Ishihara K., Miura T., Kuramitsu H.K., Oduda K.;
 RT "Characterization of the Treponema denticola prtp gene encoding a
 RT prolyl-phenylalanine-specific protease (denticillin).";
 RL Infect. Immun. 64:5178-5186(1996).
 RN [2]

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC35405;
RA Ishihara K., Miura T., Kuramitsu H.K., Okuda K.;
RT "Characterization of the Treponema denticola ptp gene expressing a
  prolyl-phenylalanine specific protease (dentilisin).";
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; D83264; BAAL1873.1; -; Genomic DNA.
SQ SEQUENCE 355 AA; 38855 MW; 29DD36C1B9551A8 CRC64;

Query Match      6.2%; Score 8; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      61 DGGQGPVF 68
DB      188 DGGQGPVF 195

RESULT 12
Q95LJ3 MACFA
ID Q95LJ3_MACFA PRELIMINARY; PRT; 411 AA.
AC Q95LJ3;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RA Osada N., Hida M., Kusuda J., Tanuma R., Hirata M., Suto Y., Hirai M.,
RA Terao K., Sugano S., Hashimoto K.;
RT "Cynomolgus monkey testicular cDNAs for discovery of novel human genes
  in the human genome sequence.";
RL BMC Genomics 3:36-36(2002).
DR EMBL; AB072795; BAB69764.1; -; mRNA.
DR HSSP; Q20728; 1LPL.
DR SMR; Q95LJ3; 159-247.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000938; CAP-Gly.
DR Pfam; PF00023; ANK; 3.
DR Pfam; PF01302; CAP_GLY; 2.
DR SMART; SM00248; ANK; 2.
DR PROSITE; PS50297; ANK_REPEAT; 1.
DR PROSITE; PS00888; ANK_REPEAT; 1.
DR PROSITE; PS00845; CAP_GLY_1; 1.
DR PROSITE; PS0245; CAP_GLY_2; 2.
DR ANK repeat; Hypothetical protein; Repeat.
KW ANK repeat; Hypothetical protein; Repeat.
SQ SEQUENCE 411 AA; 44660 MW; AA0D8543701FD11B CRC64;

Query Match      6.2%; Score 8; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      23 AGQKVGTL 30
DB      185 AGQKVGTL 192

RESULT 13
Q8DVFB STRMU
ID Q8DVFB_STRMU PRELIMINARY; PRT; 453 AA.
AC Q8DVFB;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Putative anthranilate synthase, alpha subunit (EC 4.1.3.27).
GN Name=trpE; OrderedLocNames=SMU.532;
OS Streptococcus mutans.

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OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1309;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=UAI59 / ATCC 700610 / Serotype c;
RX MEDLINE=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;
RA Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.,
RA Qian Y., Li S., Zhu H., Najjar F.Z., Lai H., White J., Roe B.A.,
RA Ferretti J.J.;
RT "Genome sequence of Streptococcus mutans UAI59, a cariogenic dental
  pathogen.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
DR EMBL; AE014898; AAN58275.1; -; Genomic DNA.
DR HSSP; P05041; 1KOG.
DR GO; GO:0004049; P:anthranilate synthase activity; IEA.
DR GO; GO:0009058; P:biogenesis; IEA.
DR GO; GO:0000162; P:tryptophan biosynthesis; IEA.
DR InterPro; IPR005256; Anth_synth.
DR InterPro; IPR005801; Anth_synth_chor.
DR InterPro; IPR006805; Anth_synth_I_N.
DR Pfam; PF04715; Anth_synth_I_N; 1.
DR Pfam; PF00425; Chorismate_Bind; 1.
DR PRINTS; PR00095; ANTSNTHASEI.
DR ProDom; PD000779; Anth_synth_chor; 1.
DR TIGRPFAMs; TIGR00564; trpE_most; 1.
DR Complete proteome.
KW Complete proteome.
SQ SEQUENCE 453 AA; 51042 MW; DECDA467AB4ABA0D CRC64;

Query Match      6.2%; Score 8; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      109 KSTLPAGT 116
DB      358 KSTLPAGT 365

RESULT 14
Q5LYI2 STRT1
ID Q5LYI2_STRT1 PRELIMINARY; PRT; 456 AA.
AC Q5LYI2;
DT 01-FEB-2005 (TRENBLrel. 29, Created)
DT 01-FEB-2005 (TRENBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)
DE Anthranilate synthase component I.
GN Name=trpE; OrderedLocNames=stl1593;
OS Streptococcus thermophilus (strain CNRZ 1066).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=299768;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
EX PubMed=15543133; DOI=10.1038/nbt1034;
RA Bolotin A., Quinquin B., Renault P., Sorokin A., Ehrlich S.D.,
RA Kulakauskas S., Lapidus A., Goldsman E., Mazur M., Pusch G.D.,
RA Fonstein M., Overbeek R., Kyprides N., Purnelle B., Prozzi D.,
RA Ngui K., Masuy D., Hancy F., Burtreau S., Boutry M., Delcours J.,
RA Goffeau A., Hols P.;
RT "Complete sequence and comparative genome analysis of the dairy
  bacterium Streptococcus thermophilus.";
RL Nat. Biotechnol. 22:1554-1558(2004).
DR EMBL; CP000024; AAV63123.1; -; Genomic DNA.
DR GO; GO:0004049; P:anthranilate synthase activity; IEA.
DR GO; GO:0009058; P:biogenesis; IEA.
DR GO; GO:0000162; P:tryptophan biosynthesis; IEA.
DR InterPro; IPR005256; Anth_synth.
DR InterPro; IPR005801; Anth_synth_chor.
DR InterPro; IPR006805; Anth_synth_I_N.
DR Pfam; PF04715; Anth_synth_I_N; 1.
DR Pfam; PF00425; Chorismate_Bind; 1.
DR PRINTS; PR00095; ANTSNTHASEI.

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DR ProDom; PD000779; Anth_synth_chor; 1.
DR TIGRFAMs; TIGR00564; trpE_most; 1.
KW Complete proteome.
SQ SEQUENCE 456 AA; 51170 MW; 5968B272A684A1A6 CRC64;

Query Match      6.2%; Score 8; DB 2; Length 456;
Best Local Similarity 100.0%; Pred.No. 46;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 KSTLPAGT 116
Db 361 KSTLPAGT 368

RESULT 15
Q5M345_STRT2
ID Q5M345_STRT2 PRELIMINARY; PRT; 456 AA.
AC Q5M345;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Anthranilate synthase component I.
GN Name=trpE; OrderedLocNames=stul593;
OS Streptococcus thermophilus (strain ATCC BAA-250 / LMG 18311).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=264199;
RN [1]
RT "Complete sequence and comparative genome analysis of the dairy
   bacterium Streptococcus thermophilus."
RL Nat. Biotechnol. 22:1554-1558 (2004).
DR EMBL; CP000023; AAV61196.1; -; Genomic DNA.
DR GO; GO:0004049; P:anthranilate synthase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR GO; GO:0000162; P:tryptophan biosynthesis; IEA.
DR InterPro; IPR005256; Anth_synthI.
DR InterPro; IPR005801; Anth_synth_chor.
DR InterPro; IPR006805; Anth_synth_I_N.
DR Pfam; PF04715; Anth_synth_I_N; 1.
DR Pfam; PF00425; Chorismate bind; 1.
DR PRINTS; PR00095; ANTSYNTHASEI.
DR ProDom; PD000779; Anth_synth_chor; 1.
DR TIGRFAMs; TIGR00564; trpE_most; 1.
KW Complete proteome.
SQ SEQUENCE 456 AA; 51170 MW; 5968B272A684A1A6 CRC64;

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Query Match      6.2%; Score 8; DB 2; Length 456;
Best Local Similarity 100.0%; Pred.No. 46;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 109 KSTLPAGT 116
Db 361 KSTLPAGT 368

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Search completed: April 26, 2006, 17:09:49
Job time : 164 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 26, 2006, 17:07:08 ; Search time 47 Seconds
(without alignments)
225.159 Million cell updates/sec

Title: US-10-018-892-3

Perfect score: 128

Sequence: 1 AAQNTTSANWSQDPGFTGPA.....KSTLPAGTFTATFYVQYQN 128

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 1

Total number of hits satisfying chosen parameters: 566820

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA: *
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2: /cgm2_6/ptodata/1/iaa/6 COMB.pep.*
3: /cgm2_6/ptodata/1/iaa/H COMB.pep.*
4: /cgm2_6/ptodata/1/iaa/PCTUS COMB.pep.*
5: /cgm2_6/ptodata/1/iaa/RE COMB.pep.*
6: /cgm2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	128	100.0	144	2	US-09-230-078A-6
2	128	100.0	165	1	US-08-233-788A-40
3	128	100.0	176	1	US-08-449-922-1
4	128	100.0	180	2	US-09-230-078A-4
5	115	89.8	143	2	US-09-543-407-46
6	7	5.5	17	2	US-09-688-017-194
7	7	5.5	17	2	US-09-688-017-217
8	7	5.5	114	2	US-09-443-184-53
9	7	5.5	132	2	US-09-125-642C-15
10	7	5.5	132	2	US-09-431-888-11
11	7	5.5	143	1	US-08-470-179-28
12	7	5.5	239	2	US-09-372-422A-42
13	7	5.5	245	2	US-09-902-540-13474
14	7	5.5	247	2	US-09-372-422A-48
15	7	5.5	249	2	US-09-372-422A-22
16	7	5.5	256	2	US-09-902-540-11830
17	7	5.5	376	2	US-09-056-556-202
18	7	5.5	376	2	US-09-072-596-197
19	7	5.5	376	2	US-09-072-967-202
20	7	5.5	376	2	US-10-193-002-197
21	7	5.5	376	2	US-10-084-843-202
22	7	5.5	452	2	US-09-252-991A-25818
23	7	5.5	611	2	US-09-252-991A-32402
24	7	5.5	739	2	US-09-413-814-86
25	7	5.5	757	2	US-09-413-814-84
26	7	5.5	791	2	US-09-252-991A-23201
27	7	5.5	826	2	US-09-492-709A-286

28 7 5.5 1034 2 US-09-252-991A-26658 Sequence 26658, A
29 7 5.5 1195 2 US-09-902-540-11967 Sequence 11967, A
30 7 5.5 1337 2 US-08-854-585-2 Sequence 2, Appli
31 7 5.5 1337 2 US-09-447-533-2 Sequence 2, Appli
32 7 5.5 1337 4 PCT-US95-05512-2 Sequence 2, Appli
33 6 4.7 21 2 US-09-010-317-20 Sequence 20, Appli
34 6 4.7 43 2 US-09-057-363C-62 Sequence 62, Appli
35 6 4.7 43 2 US-09-265-107-62 Sequence 62, Appli
36 6 4.7 54 2 US-09-621-976-5718 Sequence 5718, Ap
37 6 4.7 66 2 US-09-107-433-2721 Sequence 2721, Ap
38 6 4.7 67 2 US-09-270-767-58893 Sequence 58893, A
39 6 4.7 73 2 US-09-270-767-40382 Sequence 40382, A
40 6 4.7 73 2 US-09-270-767-55598 Sequence 55598, A
41 6 4.7 77 2 US-09-252-991A-19887 Sequence 19887, A
42 6 4.7 85 2 US-09-484-577A-67 Sequence 67, Appl
43 6 4.7 88 2 US-09-107-532A-4811 Sequence 4811, Ap
44 6 4.7 92 2 US-08-905-223-408 Sequence 408, App
45 6 4.7 95 2 US-09-540-236-2993 Sequence 2993, Ap

ALIGNMENTS

RESULT 1
US-09-230-078A-6
; Sequence 6, Application US/09230078A
; Patent No. 6495334
; GENERAL INFORMATION:
; APPLICANT: Rajashekara, Gireesh
; APPLICANT: Kakambi, Nagarata V.
; APPLICANT: Kapur, Vivek
; TITLE OF INVENTION: RECOMBINANT SEF14 FIMBRIAL PROTEIN FROM SALMONELLA
; FILE REFERENCE: 600.335USWO
; CURRENT APPLICATION NUMBER: US/09/230, 078A
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: PCT/US97/12639
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 60/022,191
; PRIOR FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Salmonella enteritidis
US-09-230-078A-6

Query Match 100.0%; Score 128; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 4.9e-115; Mismatches 0; Indels 0; Gaps 0;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAQNTTSANWSQDPGFTGPAVAGQKVGTLSTATGPHNSVSIAGKASVSGGVATVPFV 60
Db 17 AAQNTTSANWSQDPGFTGPAVAGQKVGTLSTATGPHNSVSIAGKASVSGGVATVPFV 76
QY 61 DQGGQPVFRGRITQGANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTPTAT 120
Db 77 DQGGQPVFRGRITQGANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTPTAT 136
QY 121 FVYQYQYQN 128
Db 137 FVYQYQYQN 144

RESULT 2
US-08-233-788A-40
; Sequence 40, Application US/08233788A
; Patent No. 5635617
; GENERAL INFORMATION:
; APPLICANT: Doran, James L.
; APPLICANT: Kay, William W.
; APPLICANT: Collinson, Karen S.
; APPLICANT: Clouthier, Sharon C.

;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
;; TITLE OF INVENTION: OF SALMONELLA
;; NUMBER OF SEQUENCES: 61
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Seed and Bexry
;; STREET: 6300 Columbia Center, 701 Fifth Avenue
;; CITY: Seattle
;; STATE: Washington
;; COUNTRY: U.S.A.
;; ZIP: 98104-7092
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/233,788A
;; FILING DATE: 26-APR-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: King, Joshua
;; REGISTRATION NUMBER: 35,570
;; REFERENCE/DOCKET NUMBER: 920043.403C2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 622-4900
;; TELEFAX: (206) 682-6031
;; TELEX: 3723836 SEEDANBERRY
;; INFORMATION FOR SEQ ID NO: 40:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 165 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-233-788A-40

Query Match 100.0%; Score 128; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 5.5e-115;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAQNTTSANWSQDPGFTGPAVAAGQKVGTLSITATGPHNSVSIAGKGASVSGGVATVPFV 60
DB 38 AAQNTTSANWSQDPGFTGPAVAAGQKVGTLSITATGPHNSVSIAGKGASVSGGVATVPFV 97

QY 61 DQGGQPVFRGRIQGANINDQANTGIDGLAGNRVASSQETLNPVTTFGKSTLPAGTFTAT 120
DB 98 DQGGQPVFRGRIQGANINDQANTGIDGLAGNRVASSQETLNPVTTFGKSTLPAGTFTAT 157

QY 121 FYVQYQN 128
DB 158 FYVQYQN 165

RESULT 3
US-08-449-922-1
; Sequence 1, Application US/08449922
; Patent No. 5510241
; GENERAL INFORMATION:
; APPLICANT: THORNS, CHRISTOPHER J
; TITLE OF INVENTION: METHOD OF TESTING FOR SALMONELLA
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE, P C
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/449,922
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08,030,208
;; FILING DATE: 26-MAR-1993
;; APPLICATION NUMBER: GB 9021290.3
;; FILING DATE: 01-OCT-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9022570.7
;; FILING DATE: 17-OCT-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9106546.6
;; FILING DATE: 27-MAR-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CRAWFORD, ARTHUR R
;; REGISTRATION NUMBER: 25,327
;; REFERENCE/DOCKET NUMBER: 1498-30
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 176 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; ORIGINAL SOURCE:
;; ORGANISM: Salmonella enteritidis/Salmonella dublin
;; US-08-449-922-1

Query Match 100.0%; Score 128; DB 1; Length 176;
Best Local Similarity 100.0%; Pred. No. 5.9e-115;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAQNTTSANWSQDPGFTGPAVAAGQKVGTLSITATGPHNSVSIAGKGASVSGGVATVPFV 60
DB 49 AAQNTTSANWSQDPGFTGPAVAAGQKVGTLSITATGPHNSVSIAGKGASVSGGVATVPFV 108

QY 61 DQGGQPVFRGRIQGANINDQANTGIDGLAGNRVASSQETLNPVTTFGKSTLPAGTFTAT 120
DB 109 DQGGQPVFRGRIQGANINDQANTGIDGLAGNRVASSQETLNPVTTFGKSTLPAGTFTAT 168

QY 121 FYVQYQN 128
DB 169 FYVQYQN 176

RESULT 4
US-09-230-078A-4
; Sequence 4, Application US/09230078A
; Patent No. 6495334
; GENERAL INFORMATION:
; APPLICANT: Rajashekara, Gireesh
; APPLICANT: Kakambi, Nagarata V.
; APPLICANT: Kapur, Vivek
; TITLE OF INVENTION: RECOMBINANT SEF14 FIMBRIAL PROTEIN FROM SALMONELLA
; FILE REFERENCE: 600.335USWO
; CURRENT APPLICATION NUMBER: US/09/230,078A
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: PCT/US97/12639
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 60/022,191
; PRIOR FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 4
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Salmonella enteritidis
; US-09-230-078A-4

Query Match 100.0%; Score 128; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 6e-115;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAQNTTSANWSQDPGFTGPAVAGKQVGTLSITATGPHNSVSIAGKGASVSGVATVPFV 60
Db 53 AAQNTTSANWSQDPGFTGPAVAGKQVGTLSITATGPHNSVSIAGKGASVSGVATVPFV 112
QY 61 DQGGQPVFRGRIOGANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTFTAT 120
Db 113 DQGGQPVFRGRIOGANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTFTAT 172

QY 121 FVVOQYQN 128

Db 173 FVVOQYQN 180

RESULT 5

US-09-543-407-46
; Sequence 46, Application US/09543407
; Patent No. 6864365
; GENERAL INFORMATION:
; APPLICANT: White, Aaron P.
; APPLICANT: Doran, James L.
; APPLICANT: Collinson, S. Karen
; APPLICANT: Kay, William W.
; TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
; PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
; FILE REFERENCE: 920043.406
; CURRENT APPLICATION NUMBER: US/09/543,407
; CURRENT FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Salmonella enteritidis
US-09-543-407-46

Query Match 89.8%; Score 115; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.4e-102; Mismatches 0; Indels 0; Gaps 0;
Matches 115; Conservative 0;

QY 1 AAQNTTSANWSQDPGFTGPAVAGKQVGTLSITATGPHNSVSIAGKGASVSGVATVPFV 60

Db 17 AAQNTTSANWSQDPGFTGPAVAGKQVGTLSITATGPHNSVSIAGKGASVSGVATVPFV 76

QY 61 DQGGQPVFRGRIOGANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAG 115

Db 77 DQGGQPVFRGRIOGANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAG 131

RESULT 6

US-09-688-017-194
; Sequence 194, Application US/09688017
; Patent No. 6942981
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Hematopoietic
; Cells
; FILE REFERENCE: 020054-001110US
; CURRENT APPLICATION NUMBER: US/09/688,017
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/134,114
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,117
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,118
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/160,860
; PRIOR FILING DATE: 1999-10-21
; PRIOR APPLICATION NUMBER: US 60/162,498
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/170,453

; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: US 60/176,195
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/182,296
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: US 60/196,267
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 60/196,460
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 60/196,527
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 60/196,528
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 383
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 194
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AA19L CD148 PL peptide
US-09-688-017-194

Query Match 5.5%; Score 7; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 PVTTFGK 109

Db 5 PVTTFGK 11

RESULT 7

US-09-688-017-217
; Sequence 217, Application US/09688017
; Patent No. 6942981
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Hematopoietic
; Cells
; FILE REFERENCE: 020054-001110US
; CURRENT APPLICATION NUMBER: US/09/688,017
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/134,114
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,117
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,118
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/160,860
; PRIOR FILING DATE: 1999-10-21
; PRIOR APPLICATION NUMBER: US 60/162,498
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/170,453
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: US 60/176,195
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/182,296
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: US 60/196,267
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 60/196,460
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 60/196,527
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 60/196,528
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 383
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 217

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; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AA55L CD148 PL peptide
US-09-688-017-217

Query Match          5.5%; Score 7; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 PVTTFGK 109
DB 8 PVTTFGK 14

RESULT 8
US-09-443-184-53
; Sequence 53, Application US/09443184A
; Patent No. 6372431
; GENERAL INFORMATION:
; APPLICANT: Cunningham, Mary Jane
; APPLICANT: Zweiger, Gary
; APPLICANT: Kaser, Matthew R.
; APPLICANT: Panzer, Scott
; APPLICANT: Seilhammer, Jeffrey J.
; APPLICANT: Yue, Henry
; APPLICANT: Baughn, Mariah
; APPLICANT: Azimzai, Valda
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: MAMMALIAN TOXICOLOGICAL RESPONSE MARKERS
; FILE REFERENCE: PC-0007 US
; CURRENT APPLICATION NUMBER: US/09/443,184A
; CURRENT FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 53
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6372431 3123954CD1
US-09-443-184-53

Query Match          5.5%; Score 7; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 FGKSTLP 113
DB 60 FGKSTLP 66

RESULT 9
US-09-125-642C-15
; Sequence 15, Application US/09125642C
; Patent No. 6365393
; GENERAL INFORMATION:
; APPLICANT: BAYER AG
; TITLE OF INVENTION: Parapoxviruses Which Contain Foreign DNA, and
; Their Production and Their Use in Vaccines
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; CITY: Pittsburgh
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 15205-9741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/125,642C
; FILING DATE: 20-Aug-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP97/00729,
; FILING DATE: 17-Feb-97
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Parapox ovis
; STRAIN: D1701 VEGF- Protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-125-642C-15

Query Match          5.5%; Score 7; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 GASVSGG 53
DB 91 GASVSGG 97

RESULT 10
US-09-431-888-11
; Sequence 11, Application US/09431888A
; Patent No. 6541008
; GENERAL INFORMATION:
; APPLICANT: Wise, Lyn M
; APPLICANT: Mercer, Andrew A
; APPLICANT: Savory, Loreen J
; APPLICANT: Fleming, Stephen B
; APPLICANT: Stacker, Stephen
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF
; TITLE OF INVENTION: VIRUS NZ2 BINDS AND ACTIVATES MAMMALIAN VEGF
; TITLE OF INVENTION: RECEPTOR-2, AND USES THEREOF
; FILE REFERENCE: Sequence Listing for 09/431,833
; Patent No. 6541008
; CURRENT APPLICATION NUMBER: US/09/431,888A
; CURRENT FILING DATE: 1999-11-02
; EARLIER APPLICATION NUMBER: 60/106,689
; EARLIER FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/106,800
; EARLIER FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Orf virus
US-09-431-888-11

Query Match          5.5%; Score 7; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 GASVSGG 53
DB 91 GASVSGG 97

RESULT 11
US-08-470-179-28
; Sequence 28, Application US/08470179

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; Patent No. 5645994
; GENERAL INFORMATION:
; APPLICANT: Huang Ph.D, Wai Mun
; TITLE OF INVENTION: Method and Compositions for
; TITLE OF INVENTION: Identification of Species in a Sample
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Trask, Britt and Rossa
; STREET: P.O. Box 2550
; CITY: Salt Lake City
; STATE: Utah
; COUNTRY: USA
; ZIP: 84110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,179
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sweigert Ph.D, Susan E.
; REGISTRATION NUMBER: 36,289
; REFERENCE/DOCKET NUMBER: 2601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 801-532-1922
; TELEFAX: 801-531-9168
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 143 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Legionella pneumoniae
US-08-470-179-28

Query Match 5.5%; Score 7; DB 1; Length 143;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 PFVDGQG 64
| | | | |
DB 64 PFVDGQG 70

RESULT 12
US-09-372-422A-42
; Sequence 42, Application US/09372422A
; Patent No. 6313375
; GENERAL INFORMATION:
; APPLICANT: Rudolf Jung
; APPLICANT: Francois Barrieu
; TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
; FILE REFERENCE: 0919
; CURRENT APPLICATION NUMBER: US/09/372,422A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: US 60/098,692
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Zea mays
US-09-372-422A-42

Query Match 5.5%; Score 7; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GPAVAA 24
| | | | |
DB 189 GPAVAA 195
| | | | |

RESULT 13
US-09-902-540-13474
; Sequence 13474, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13474
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13474

Query Match 5.5%; Score 7; DB 2; Length 245;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGPAAVAA 23
| | | | |
DB 195 TGPAAVAA 201

RESULT 14
US-09-372-422A-48
; Sequence 48, Application US/09372422A
; Patent No. 6313375
; GENERAL INFORMATION:
; APPLICANT: Rudolf Jung
; APPLICANT: Francois Barrieu
; TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
; FILE REFERENCE: 0919
; CURRENT APPLICATION NUMBER: US/09/372,422A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: US 60/098,692
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Zea mays
US-09-372-422A-48

Query Match 5.5%; Score 7; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GPAVAA 24
| | | | |
DB 201 GPAVAA 207

RESULT 15
US-09-372-422A-22
; Sequence 22, Application US/09372422A

; Patent No. 6313375
; GENERAL INFORMATION:
; APPLICANT: Rudolf Jung
; APPLICANT: Francois Barrieu
; TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
; FILE REFERENCE: 0919
; CURRENT APPLICATION NUMBER: US/09/372,422A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: US 60/098,692
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 249
; TYPE: FRT
; ORGANISM: Zea mays
US-09-372-422A-22

Query Match 5.5%; Score 7; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 GPAVAAAG 24
| | | | |
Db 202 GPAVAAAG 208

Search completed: April 26, 2006, 17:10:48
Job time : 48 secs

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OM protein - protein search, using sw model

Run on: April 26, 2006, 17:10:03 ; Search time 117 Seconds
(without alignments)
457.112 Million cell updates/sec

Title: US-10-018-892-3

Perfect score: 128

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Scoring table: 0.128

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Word size: 1

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	9	7.0	606	4	US-10-156-761-9993
2	8	6.2	194	4	US-10-437-963-150729
3	8	6.2	225	4	US-10-210-281-72
4	8	6.2	345	4	US-10-094-749-3021
5	8	6.2	490	4	US-10-369-493-21753
6	8	6.2	494	5	US-10-926-543-84
7	8	6.2	574	5	US-10-450-763-59630
8	8	6.2	705	4	US-10-473-574-10
9	7	5.5	17	5	US-10-938-249-427
10	7	5.5	17	5	US-10-938-249-457
11	7	5.5	17	6	US-11-131-054-194
12	7	5.5	17	6	US-11-131-054-217
13	7	5.5	17	6	US-11-131-042-194
14	7	5.5	17	6	US-11-131-042-217
15	7	5.5	58	4	US-10-403-701-17
16	7	5.5	63	4	US-10-296-115-1437
17	7	5.5	75	4	US-10-424-599-276075
18	7	5.5	78	4	US-10-425-115-238006
19	7	5.5	83	3	US-09-764-891-4562
20	7	5.5	84	4	US-10-724-972A-6584
21	7	5.5	84	4	US-10-425-115-320280
22	7	5.5	85	4	US-10-437-963-161218
23	7	5.5	104	4	US-10-317-832-54
24	7	5.5	104	5	US-10-733-878-54
25	7	5.5	104	5	US-10-601-072-54
26	7	5.5	114	3	US-09-890-688-66
27	7	5.5	114	4	US-10-333-900-20

Sequence 54316, A
Sequence 314419, A
Sequence 24, Appl
Sequence 33366, A
Sequence 151, App
Sequence 11, Appl
Sequence 30, Appl
Sequence 259533, A
Sequence 44321, A
Sequence 673, App
Sequence 673, App
Sequence 147994, A
Sequence 164998, A
Sequence 62343, A
Sequence 216265, A
Sequence 115691, A
Sequence 33534, A
Sequence 39996, A

28 7 5.5 121 4 US-10-767-701-54316
29 7 5.5 128 4 US-10-425-115-314419
30 7 5.5 130 3 US-09-805-290A-24
31 7 5.5 131 4 US-10-767-701-33366
32 7 5.5 132 3 US-09-795-006A-151
33 7 5.5 132 4 US-10-352-153-11
34 7 5.5 132 5 US-10-772-927A-30
35 7 5.5 134 4 US-10-424-599-259533
36 7 5.5 134 4 US-10-767-701-44321
37 7 5.5 139 3 US-09-925-298-673
38 7 5.5 139 4 US-10-102-806-673
39 7 5.5 143 4 US-10-437-963-147994
40 7 5.5 171 4 US-10-424-599-164998
41 7 5.5 174 4 US-10-382-122A-62343
42 7 5.5 179 4 US-10-424-599-216265
43 7 5.5 196 4 US-10-437-963-115691
44 7 5.5 196 5 US-10-450-763-33534
45 7 5.5 201 4 US-10-767-701-39996

ALIGNMENTS

RESULT 1
US-10-156-761-9993
; Sequence 9993, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9993
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9993

Query Match 7.0%; Score 9; DB 4; Length 606;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 SVSGGVATV 57
DB 73 SVSGGVATV 81

RESULT 2
US-10-437-963-150729
; Sequence 150729, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 150729
 ; LENGTH: 194
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_5093C.1.bep
 US-10-437-963-150729

Query Match 6.2%; Score 8; DB 4; Length 194;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 GLAGWRVA 94
 Db 138 GLAGWRVA 145

RESULT 3
 US-10-210-281-72
 ; Sequence 72, Application US/10210281
 ; Publication No. US20040030096A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gorman, Linda
 ; APPLICANT: Zerhusen, Bryan D.
 ; APPLICANT: Edinger, Shlomit R.
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Guo, Xiaojia
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Zhong, Mei
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Miller, Charles E.
 ; APPLICANT: Ji, Weizhen
 ; APPLICANT: Pena, Carol E.A.
 ; APPLICANT: Burgess, Catherine E.
 ; APPLICANT: Sciore, Paul
 ; APPLICANT: Stone, David J.
 ; APPLICANT: Taupier, Raymond J., Jr.
 ; APPLICANT: Casman, Stacie
 ; APPLICANT: Rothenberg, Mark E.
 ; APPLICANT: Malyankar, Uriel M.
 ; APPLICANT: Boldog, Ferenc L.
 ; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS
 ; TITLE OF INVENTION: THE SAME
 ; FILE REFERENCE: 21402-416D
 ; CURRENT APPLICATION NUMBER: US/10/210,281
 ; CURRENT FILING DATE: 2003-02-05
 ; PRIOR APPLICATION NUMBER: 60/309,501
 ; PRIOR FILING DATE: 2001-08-02
 ; PRIOR APPLICATION NUMBER: 60/310,291
 ; PRIOR FILING DATE: 2001-08-03
 ; PRIOR APPLICATION NUMBER: 60/361,775
 ; PRIOR FILING DATE: 2002-03-05
 ; PRIOR APPLICATION NUMBER: 60/310,951
 ; PRIOR FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: 60/361,832
 ; PRIOR FILING DATE: 2002-03-05
 ; PRIOR APPLICATION NUMBER: 60/311,292
 ; PRIOR FILING DATE: 2001-08-09
 ; PRIOR APPLICATION NUMBER: 60/311,979
 ; PRIOR FILING DATE: 2001-08-13
 ; PRIOR APPLICATION NUMBER: 60/312,203
 ; PRIOR FILING DATE: 2001-08-14
 ; PRIOR APPLICATION NUMBER: 60/313,201
 ; PRIOR FILING DATE: 2001-08-17
 ; PRIOR APPLICATION NUMBER: 60/313,702
 ; PRIOR FILING DATE: 2001-08-20
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 191

; SOFTWARE: CuraSeqList version 0.1
 ; SEQ ID NO 72
 ; LENGTH: 225
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-210-281-72

Query Match 6.2%; Score 8; DB 4; Length 225;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 AGQKVGTL 30
 Db 16 AGQKVGTL 23

RESULT 4
 US-10-094-749-3021
 ; Sequence 3021, Application US/10094749
 ; Publication No. US20030219741A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ISOGAI, TAKAO
 ; APPLICANT: SUGIYAMA, TOMOYASU
 ; APPLICANT: OTSUKI, TETSUJI
 ; APPLICANT: WAKAMATSU, AI
 ; APPLICANT: SATO, HIROYUKI
 ; APPLICANT: ISHII, SHIZUKO
 ; APPLICANT: YAMAMOTO, JUN-ICHI
 ; APPLICANT: ISONO, YUUKO
 ; APPLICANT: HIO, YURI
 ; APPLICANT: OTSUKA, KAORU
 ; APPLICANT: NAGAI, KEIICHI
 ; APPLICANT: IRIE, RYOTARO
 ; APPLICANT: TAMECHIKA, ICHIRO
 ; APPLICANT: SEKI, NAOHICO
 ; APPLICANT: YOSHIKAWA, TSUTOMU
 ; APPLICANT: OTSUKA, MOTYUYUKI
 ; APPLICANT: NAGAHARI, KENJI
 ; APPLICANT: MASUHO, YASUHIKO
 ; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
 ; FILE REFERENCE: 084335/0160
 ; CURRENT APPLICATION NUMBER: US/10/094,749
 ; CURRENT FILING DATE: 2002-03-12
 ; PRIOR APPLICATION NUMBER: 60/350,435
 ; PRIOR FILING DATE: 2002-01-24
 ; PRIOR APPLICATION NUMBER: JP 2001-328381
 ; PRIOR FILING DATE: 2001-09-14
 ; NUMBER OF SEQ ID NOS: 3381
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3021
 ; LENGTH: 345
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-094-749-3021

Query Match 6.2%; Score 8; DB 4; Length 345;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 AGQKVGTL 30
 Db 142 AGQKVGTL 149

RESULT 5
 US-10-369-493-21753
 ; Sequence 21753, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.


```
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 21753
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Rhodobacter capsulatus
US-10-369-493-21753

Query Match      6.2%; Score 8; DB 4; Length 490;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 AVAAGQKV 27
      |||||
Db 268 AVAAGQKV 275

RESULT 6
US-10-926-543-84
; Sequence 84, Application US/10926543
; Publication No. US2005004858A1
; GENERAL INFORMATION:
; APPLICANT: Jendoubi, Moncef
; TITLE OF INVENTION: LUNG CANCER SPECIFIC GENE PRODUCTS: THEIR CODING SEQUENCE, THEIR
; TITLE OF INVENTION: ANTIBODIES AND THEIR USE IN DIAGNOSTIC, THERAPEUTIC AND DISEASE
; TITLE OF INVENTION: MANAGEMENT OF LUNG CANCER
; FILE REFERENCE: 705403.4004
; CURRENT APPLICATION NUMBER: US/10/926,543
; CURRENT FILING DATE: 2004-08-25
; PRIOR APPLICATION NUMBER: US 60/497,790
; PRIOR FILING DATE: 2003-08-25
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 84
; LENGTH: 494
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-926-543-84

Query Match      6.2%; Score 8; DB 5; Length 494;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AGQKVGT 30
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Db 185 AGQKVGT 192

RESULT 7
US-10-450-763-59630
; Sequence 59630, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
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; SEQ ID NO 59630
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (326)..(351)
; OTHER INFORMATION: CAP-Gly domain proteins domain identified by eMATRIX,
; OTHER INFORMATION: accession number BL00845, p-value=9.820e-19, raw score of 16.43
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (319)..(367)
; OTHER INFORMATION: CAP-Gly domain identified by Pfam, accession name CAP_GLY, E-
; OTHER INFORMATION: value=1.1e-15, Pfam score of 65.6
US-10-450-763-59630

Query Match      6.2%; Score 8; DB 5; Length 574;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AGQKVGT 30
      |||||
Db 308 AGQKVGT 315

RESULT 8
US-10-473-574-10
; Sequence 10, Application US/10473574
; Publication No. US20040116670A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; HAPALIA, April J.A.;
; APPLICANT: TANG, Y. Tom; YUE, Henry;
; APPLICANT: KHAN, Farrah A.; ISON, Craig H.;
; APPLICANT: BAUGHN, Mariah R.; WARREN, Bridget A.;
; APPLICANT: DUGGAN, Brendan M.; THANGAVELU, Kavitha;
; APPLICANT: HONCHELL, Cynthia D.; AZIMZAI, Yalda;
; APPLICANT: ELLIOTT, Vicki S.; BURFORD, Neil;
; APPLICANT: DING, Li; YUE, Huibin;
; APPLICANT: BECHA, Shanya; EMERLING, Brooke M.;
; APPLICANT: RICHARDSON, Thomas W.; LEE, Soo Yeun;
; APPLICANT: BANDMAN, Olga; LAL, Preeti G.;
; APPLICANT: LEE, Sally; GIETZEN, Kimberly J.;
; APPLICANT: CHAWLA, Narinder K.; GRIFFIN, Jennifer A.;
; APPLICANT: LEE, Ernestine A.; SWARNAKAR, Anita;
; APPLICANT: KING, Huijun Z.; JONES, Karen Anne
; TITLE OF INVENTION: CYTOSKELETON-ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0918 USN
; CURRENT APPLICATION NUMBER: US/10/473,574
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: PCT/US02/09288
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US 60/294,451
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/291,870
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/290,518
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 60/288,609
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/283,769
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/281,323
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/280,508
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PERL Program
; SEQ ID NO 10
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
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; OTHER INFORMATION: Incyte ID No: 1683662CD1
US-10-473-574-10

Query Match 6.2%; Score 8; DB 4; Length 705;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AGQKVGTL 30
| | | | | | | |
DB 292 AGQKVGTL 299

RESULT 9
US-10-938-249-427
; Sequence 427, Application US/10938249
; Publication No. US20050037969A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Hematopoietic
; FILE REFERENCE: 020054-001130US
; CURRENT APPLICATION NUMBER: US/10/938,249
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US/09/724,553
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/134,114
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,117
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/160,860
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/176,195
; PRIOR FILING DATE: 1999-10-21
; PRIOR APPLICATION NUMBER: US 60/170,453
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/162,498
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: US 60/134,118
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,117
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/160,860
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/182,296
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/196,267
; PRIOR FILING DATE: 2000-04-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 543
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 427
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PL peptide
US-10-938-249-427

Query Match 5.5%; Score 7; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 PVTTFGK 109
| | | | | | | |
DB 5 PVTTFGK 11

RESULT 10
US-10-938-249-457
; Sequence 457, Application US/10938249
; Publication No. US20050037969A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.

; APPLICANT: Schweizer, Johannes
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Hematopoietic
; FILE REFERENCE: 020054-001130US
; CURRENT APPLICATION NUMBER: US/10/938,249
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US/09/724,553
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/134,114
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,117
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,118
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/160,860
; PRIOR FILING DATE: 1999-10-21
; PRIOR APPLICATION NUMBER: US 60/162,498
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/170,453
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: US 60/176,195
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/182,296
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: US 60/196,267
; PRIOR FILING DATE: 2000-04-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 543
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 457
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PL peptide
US-10-938-249-457

Query Match 5.5%; Score 7; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 PVTTFGK 109
| | | | | | | |
DB 8 PVTTFGK 14

RESULT 11
US-11-131-054-194
; Sequence 194, Application US/11131054
; Publication No. US20050214869A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Hematopoietic
; FILE REFERENCE: 020054-001110US
; CURRENT APPLICATION NUMBER: US/11/131,054
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: US/09/688,017
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/134,114
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,117
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,118
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/160,860
; PRIOR FILING DATE: 1999-10-21
; PRIOR APPLICATION NUMBER: US 60/162,498
; PRIOR FILING DATE: 1999-10-29

;; PRIOR APPLICATION NUMBER: US 60/170,453
;; PRIOR FILING DATE: 1999-12-13
;; PRIOR APPLICATION NUMBER: US 60/176,195
;; PRIOR FILING DATE: 2000-01-14
;; PRIOR APPLICATION NUMBER: US 60/182,296
;; PRIOR FILING DATE: 2000-02-14
;; PRIOR APPLICATION NUMBER: US 60/196,267
;; PRIOR FILING DATE: 2000-04-11
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 383
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 194
;; LENGTH: 17
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: AA19L CD148 PL peptide
US-11-131-054-194

Query Match 5.5%; Score 7; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 PVTTFGK 109
Db 5 PVTTFGK 11

RESULT 12
US-11-131-054-217
;; Sequence 217, Application US/11131054
;; Publication No. US20050214869A1
;; GENERAL INFORMATION:
;; APPLICANT: Lu, Peter S.
;; APPLICANT: Rabinowitz, Joshua D.
;; APPLICANT: Schweizer, Johannes
;; APPLICANT: Arbor Vita Corporation
;; TITLE OF INVENTION: Molecular Interactions in Hematopoietic
;; TITLE OF INVENTION: Cells
;; FILE REFERENCE: 020054-001110US
;; CURRENT APPLICATION NUMBER: US/11/131,054
;; CURRENT FILING DATE: 2005-05-16
;; PRIOR APPLICATION NUMBER: US/09/688,017
;; PRIOR FILING DATE: 2000-10-13
;; PRIOR APPLICATION NUMBER: US 60/134,114
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: US 60/160,860
;; PRIOR FILING DATE: 1999-10-21
;; PRIOR APPLICATION NUMBER: US 60/170,453
;; PRIOR FILING DATE: 1999-10-29
;; PRIOR APPLICATION NUMBER: US 60/176,195
;; PRIOR FILING DATE: 2000-01-14
;; PRIOR APPLICATION NUMBER: US 60/182,296
;; PRIOR FILING DATE: 1999-10-29
;; PRIOR APPLICATION NUMBER: US 60/170,453
;; PRIOR FILING DATE: 1999-12-13
;; PRIOR APPLICATION NUMBER: US 60/176,195
;; PRIOR FILING DATE: 2000-01-14
;; PRIOR APPLICATION NUMBER: US 60/182,296
;; PRIOR FILING DATE: 2000-02-14
;; PRIOR APPLICATION NUMBER: US 60/196,267
;; PRIOR FILING DATE: 2000-04-11
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 383
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 217
;; LENGTH: 17
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: AA55L CD148 PL peptide
US-11-131-054-217

Query Match 5.5%; Score 7; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 PVTTFGK 109
Db 8 PVTTFGK 14

RESULT 13
US-11-131-042-194
;; Sequence 194, Application US/11131042
;; Publication No. US20050221388A1
;; GENERAL INFORMATION:
;; APPLICANT: Lu, Peter S.
;; APPLICANT: Rabinowitz, Joshua D.
;; APPLICANT: Schweizer, Johannes
;; APPLICANT: Arbor Vita Corporation
;; TITLE OF INVENTION: Molecular Interactions in Hematopoietic
;; TITLE OF INVENTION: Cells
;; FILE REFERENCE: 020054-001110US
;; CURRENT APPLICATION NUMBER: US/11/131,042
;; CURRENT FILING DATE: 2005-05-16
;; PRIOR APPLICATION NUMBER: US/09/688,017
;; PRIOR FILING DATE: 2000-10-13
;; PRIOR APPLICATION NUMBER: US 60/134,114
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: US 60/134,117
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: US 60/134,118
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: US 60/160,860
;; PRIOR FILING DATE: 1999-10-21
;; PRIOR APPLICATION NUMBER: US 60/162,498
;; PRIOR FILING DATE: 1999-10-29
;; PRIOR APPLICATION NUMBER: US 60/170,453
;; PRIOR FILING DATE: 1999-12-13
;; PRIOR APPLICATION NUMBER: US 60/176,195
;; PRIOR FILING DATE: 2000-01-14
;; PRIOR APPLICATION NUMBER: US 60/182,296
;; PRIOR FILING DATE: 2000-02-14
;; PRIOR APPLICATION NUMBER: US 60/196,267
;; PRIOR FILING DATE: 2000-04-11
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 383
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 194
;; LENGTH: 17
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: AA19L CD148 PL peptide
US-11-131-042-194

Query Match 5.5%; Score 7; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 PVTTFGK 109
Db 5 PVTTFGK 11

RESULT 14
US-11-131-042-217
;; Sequence 217, Application US/11131042
;; Publication No. US20050221388A1
;; GENERAL INFORMATION:
;; APPLICANT: Lu, Peter S.
;; APPLICANT: Rabinowitz, Joshua D.
;; APPLICANT: Schweizer, Johannes
;; APPLICANT: Arbor Vita Corporation
;; TITLE OF INVENTION: Molecular Interactions in Hematopoietic

Search completed: April 26, 2006, 17:12:57
Job time : 118 secs

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; TITLE OF INVENTION: Cells
; FILE REFERENCE: 020054-001110US
; CURRENT APPLICATION NUMBER: US/11/131,042
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: US/09/688,017
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/134,114
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,117
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,118
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/160,860
; PRIOR FILING DATE: 1999-10-21
; PRIOR APPLICATION NUMBER: US 60/162,498
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/170,453
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: US 60/176,195
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/182,296
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: US 60/196,267
; PRIOR FILING DATE: 2000-04-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 217
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AA55L CD148 PL peptide
US-11-131-042-217

Query Match      5.5%; Score 7; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 PVTTEGK 109
Db 8 PVTTEGK 14

RESULT 15
US-10-409-701-17
; Sequence 17, Application US/10409701
; Publication No. US20030221224A1
; GENERAL INFORMATION:
; APPLICANT: Zinselmeier, Chris
; TITLE OF INVENTION: Enhanced Silk Exsersion Under Stress
; FILE REFERENCE: 1421
; CURRENT APPLICATION NUMBER: US/10/409,701
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 60/370,796
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Zea mays
US-10-409-701-17

Query Match      5.5%; Score 7; DB 4; Length 58;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GPAVAAG 24
Db 8 GPAVAAG 14

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Run on: April 26, 2006, 17:10:00 ; Search time 13 Seconds
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Title: US-10-018-892-3

Perfect score: 128

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Gapop 60.0 , Gapext 60.0

Searched: 232119 seqs, 45477862 residues

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	5.5	132	7 US-11-073-605-15	Sequence 15, Appl
2	7	5.5	132	7 US-11-064-774A-151	Sequence 151, Appl
3	7	5.5	132	7 US-11-075-400-22	Sequence 22, Appl
4	7	5.5	132	7 US-11-075-047A-93	Sequence 93, Appl
5	7	5.5	137	6 US-10-995-561-853	Sequence 853, Appl
6	7	5.5	247	7 US-11-087-099-5549	Sequence 5549, Appl
7	7	5.5	292	7 US-11-087-099-9937	Sequence 9937, Appl
8	7	5.5	329	7 US-11-096-568A-347	Sequence 347, Appl
9	7	5.5	331	7 US-11-096-568A-346	Sequence 346, Appl
10	7	5.5	420	7 US-11-188-298-15565	Sequence 15565, A
11	7	5.5	454	7 US-11-045-004-1402	Sequence 1402, Ap
12	7	5.5	479	7 US-11-188-298-12225	Sequence 12225, A
13	7	5.5	497	7 US-11-188-298-7036	Sequence 7036, Ap
14	7	5.5	497	7 US-11-188-298-13926	Sequence 13926, A
15	7	5.5	497	7 US-11-188-298-15143	Sequence 15143, A
16	7	5.5	497	7 US-11-188-298-21056	Sequence 21056, A
17	7	5.5	501	7 US-11-094-917-36	Sequence 36, Appl
18	7	5.5	555	7 US-11-096-568A-21949	Sequence 21949, A
19	7	5.5	802	7 US-11-045-004-1971	Sequence 1971, Ap
20	7	5.5	827	7 US-11-079-463-5812	Sequence 5812, Ap
21	7	5.5	1075	7 US-11-079-463-6009	Sequence 6009, Ap
22	7	5.5	1178	6 US-10-995-561-851	Sequence 851, Appl
23	7	5.5	1337	7 US-11-112-304A-33	Sequence 33, Appl
24	7	5.5	2117	7 US-11-087-099-9594	Sequence 9594, Ap
25	7	5.5	2117	7 US-11-188-298-8910	Sequence 8910, Ap

26	7	5.5	2132	7 US-11-087-099-2434	Sequence 2434, Ap
27	7	5.5	2132	7 US-11-188-298-2344	Sequence 2344, Ap
28	7	5.5	2160	7 US-11-087-099-819	Sequence 819, App
29	7	5.5	2160	7 US-11-087-099-5017	Sequence 5017, Ap
30	6	4.7	99	6 US-10-467-657-6714	Sequence 6714, Ap
31	6	4.7	99	6 US-10-467-657-7862	Sequence 7862, Ap
32	6	4.7	102	7 US-11-045-004-2066	Sequence 2066, Ap
33	6	4.7	105	7 US-11-096-568A-24144	Sequence 24144, A
34	6	4.7	125	6 US-10-821-234-1508	Sequence 1508, Ap
35	6	4.7	128	7 US-11-079-463-9556	Sequence 9556, Ap
36	6	4.7	140	7 US-11-188-298-1495	Sequence 1495, Ap
37	6	4.7	141	7 US-11-096-568A-14453	Sequence 14453, A
38	6	4.7	144	7 US-11-096-568A-16767	Sequence 16767, A
39	6	4.7	145	7 US-11-051-720-1294	Sequence 1294, Ap
40	6	4.7	149	7 US-11-096-568A-24143	Sequence 24143, A
41	6	4.7	152	6 US-10-957-569-38	Sequence 38, Appl
42	6	4.7	152	6 US-10-523-503-6	Sequence 6, Appl
43	6	4.7	152	7 US-11-097-589-37	Sequence 37, Appl
44	6	4.7	158	7 US-11-226-869-508	Sequence 508, App
45	6	4.7	161	7 US-11-096-568A-16766	Sequence 16766, A

ALIGNMENTS

RESULT 1
; Sequence 15, Application US/11073605
; Publication No. US20050260161A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, ULF
; APPLICANT: ALITALO, KARI
; APPLICANT: UUTELA, MARKO
; TITLE OF INVENTION: METHOD FOR MODULATING REGULATING AND/OR STABILIZING
; FILE REFERENCE: 029065.53347US
; CURRENT APPLICATION NUMBER: US/11/073,605
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: 60/550,327
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 15
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Orf virus
US-11-073-605-15

Query Match 5.5%; Score 7; DB 7; Length 132;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 47 GASVSGG 53
Db 91 GASVSGG 97

RESULT 2
US-11-064-774A-151
; Sequence 151, Application US/11064774A
; Publication No. US20050267024A1
; GENERAL INFORMATION:
; APPLICANT: Alicata et al.
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR ENDOTHELIAL GRO
; FILE REFERENCE: 28967/3597B2
; CURRENT APPLICATION NUMBER: US/11/064,774A
; CURRENT FILING DATE: 2005-02-24
; PRIOR APPLICATION NUMBER: 09/795,006
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205

; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 1212
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 151
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Orf virus
US-11-064-774A-151

Query Match 5.5%; Score 7; DB 7; Length 132;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 GASVSGG 53
Db 91 GASVSGG 97

RESULT 3

US-11-075-400-22
; Sequence 22, Application US/11075400
; Publication No. US2005028223A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSON, et al.
; TITLE OF INVENTION: MULTIVALENT ANTIBODY MATERIALS AND METHODS FOR VEGF/PDGF FAMILY OR
; TITLE OF INVENTION: GROWTH FACTORS
; FILE REFERENCE: 28967/39820B
; CURRENT APPLICATION NUMBER: US/11/075,400
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/550,511
; PRIOR FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: US 60/586,662
; PRIOR FILING DATE: 2004-07-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Orf Virus
US-11-075-400-22

Query Match 5.5%; Score 7; DB 7; Length 132;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 GASVSGG 53
Db 91 GASVSGG 97

RESULT 4

US-11-075-047A-93
; Sequence 93, Application US/11075047A
; Publication No. US20060030000A1
; GENERAL INFORMATION:
; APPLICANT: ALITALO, et al.
; TITLE OF INVENTION: GROWTH FACTOR BINDING CONSTRUCTS MATERIALS AND METHODS
; FILE REFERENCE: 28967/39700A
; CURRENT APPLICATION NUMBER: US/11/075,047A
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/550,907
; PRIOR FILING DATE: 2004-03-07
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 93
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Orf virus
US-11-075-047A-93

Query Match 5.5%; Score 7; DB 7; Length 132;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 GASVSGG 53
Db 91 GASVSGG 97

RESULT 5

US-10-995-561-853
; Sequence 853, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 853
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-853

Query Match 5.5%; Score 7; DB 6; Length 137;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 PVTTFGK 109
Db 49 PVTTFGK 55

RESULT 6

US-11-087-099-5549
; Sequence 5549, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 5549
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-11-087-099-5549

Query Match 5.5%; Score 7; DB 7; Length 247;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGPAAVA 23
Db 197 TGPAAVA 203

RESULT 7

US-11-087-099-9937
; Sequence 9937, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9937

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; LENGTH: 292
; TYPE: PRT
; ORGANISM: Caulobacter crescentus CB15
US-11-087-099-9937

Query Match      5.5%; Score 7; DB 7; Length 292;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      43 IAGKGAS 49
Db      64 IAGKGAS 70

RESULT 8
US-11-096-568A-347
; Sequence 347, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 347
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(329)
; OTHER INFORMATION: Ceres Seq. ID no. 15180143
US-11-096-568A-347

Query Match      5.5%; Score 7; DB 7; Length 329;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      37 PHNSVSI 43
Db      117 PHNSVSI 123

RESULT 9
US-11-096-568A-346
; Sequence 346, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 346
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(331)
; OTHER INFORMATION: Ceres Seq. ID no. 15180142
US-11-096-568A-346

Query Match      5.5%; Score 7; DB 7; Length 331;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      37 PHNSVSI 43
Db      117 PHNSVSI 123

; LENGTH: 292
; TYPE: PRT
; ORGANISM: Caulobacter crescentus CB15
US-11-087-099-9937

Query Match      5.5%; Score 7; DB 7; Length 292;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      43 IAGKGAS 49
Db      64 IAGKGAS 70

RESULT 10
US-11-188-298-15565
; Sequence 15565, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 15565
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Haemophilus somnus 129PT
US-11-188-298-15565

Query Match      5.5%; Score 7; DB 7; Length 420;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      111 TLPAGTF 117
Db      400 TLPAGTF 406

RESULT 11
US-11-045-004-1402
; Sequence 1402, Application US/11045004
; Publication No. US20060078901A1
; GENERAL INFORMATION:
; APPLICANT: BUCHRIER, CARMEN
; APPLICANT: FRANGEUL, LIONEL
; APPLICANT: COUVE, ELISABETH
; APPLICANT: RUSNIOK, CHRISTOPHE
; APPLICANT: FSIHI, HAFIDA
; APPLICANT: DEHOUX, PIERRE
; APPLICANT: DUSSURGET, OLIVIER
; APPLICANT: CHETOUANI, FARID
; APPLICANT: NEDJARI, HAFED
; APPLICANT: GLASER, PHILIPPE
; APPLICANT: KUNST, FRANCK
; APPLICANT: COSSART, PASCALE
; APPLICANT: DANIELS, JUSTIN
; APPLICANT: GOEBEL, WERNER
; APPLICANT: KREFT, JURGEN
; APPLICANT: KUHN, MICHAEL
; APPLICANT: NG, EVA
; APPLICANT: VAZQUEZ-BOLAND, ANTONIO
; APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
; APPLICANT: GARRIDO-GARCIA, PATRICIA
; APPLICANT: TIERREZ-MARTINEZ, ALBERTO
; APPLICANT: AMEND, ALEXANDRA
; APPLICANT: CHAKRABORTY, TRINAD
; APPLICANT: DOMANN, EUGEN
; APPLICANT: HAIN, THORSTEN
; APPLICANT: BERCHE, PATRICK
; APPLICANT: CHARBIT, ALAIN
; APPLICANT: DURANT, LIONEL
; APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
; APPLICANT: BAQUERO, FERNANDO
; APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
; APPLICANT: GOMEZ-LOPEZ, NURIA
; APPLICANT: MADUENIO, ENCARNA
; APPLICANT: PABLOS, BETRIZ DE
; APPLICANT: WEHLAND, JURGEN
; APPLICANT: KARST, UWE
; APPLICANT: ENTIAN, KARL-DIETER
```

```
; APPLICANT: HAUF, JORG
; APPLICANT: ROSE, MATTHIAS
; APPLICANT: VOSS, HAMUT
; TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
; CURRENT APPLICATION NUMBER: US/11/045,004
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: 10/637,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: 10/257,023
; PRIOR FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: PCT/FR01/01118
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: FR 00/04,629
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 2854
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1402
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
; US-11-045-004-1402

Query Match      5.5%; Score 7; DB 7; Length 454;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      110 STLPAGT 116
Db      362 STLPAGT 368

RESULT 12
US-11-188-298-12225
; Sequence 12225, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 12225
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Streptomyces coelicolor A3(2)
; US-11-188-298-12225

Query Match      5.5%; Score 7; DB 7; Length 479;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      18 GPAVAAAG 24
Db      163 GPAVAAAG 169

RESULT 13
US-11-188-298-7036
; Sequence 7036, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569

; APPLICANT: HAUF, JORG
; APPLICANT: ROSE, MATTHIAS
; APPLICANT: VOSS, HAMUT
; TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
; CURRENT APPLICATION NUMBER: US/11/045,004
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: 10/637,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: 10/257,023
; PRIOR FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: PCT/FR01/01118
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: FR 00/04,629
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 2854
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1402
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
; US-11-045-004-1402

Query Match      5.5%; Score 7; DB 7; Length 497;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      18 GPAVAAAG 24
Db      176 GPAVAAAG 182

RESULT 14
US-11-188-298-13926
; Sequence 13926, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 13926
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Emericella nidulans
; US-11-188-298-13926

Query Match      5.5%; Score 7; DB 7; Length 497;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      18 GPAVAAAG 24
Db      176 GPAVAAAG 182

RESULT 15
US-11-188-298-15143
; Sequence 15143, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 15143
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Emericella nidulans
; US-11-188-298-15143

Query Match      5.5%; Score 7; DB 7; Length 497;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      18 GPAVAAAG 24
Db      176 GPAVAAAG 182

Search completed: April 26, 2006, 17:10:21
Job time : 14 secs
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OM protein - protein search, using sw model

Run on: April 26, 2006, 17:03:33 ; Search time 15 Seconds
(without alignments)
821.050 Million cell updates/sec

Title: US-10-018-892-3
Perfect score: 662
Sequence: 1 AAQNTTSANWSQDPGFTGPA.....KSTLPAGTFTATFYVQYQN 128

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80: *
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	662	100.0	165	2 A40618	fimbrin, SEF14 - S
2	91.5	13.8	319	2 T43040	hypothetical prote
3	91.5	13.8	2468	2 A83412	hypothetical prote
4	87.5	13.2	380	1 GNV5MB	genome polyprotein
5	85	12.8	786	2 T16509	hypothetical prote
6	84	12.7	591	2 AC3528	extracellular seri
7	83	12.5	549	2 B70508	probable htrA prot
8	83	12.5	1844	2 T51890	related to Nup98-N
9	82.5	12.5	1045	2 A39199	endoglucanase B (E
10	81.5	12.3	674	2 B82954	conserved hypothet
11	81.5	12.3	1373	1 A43291	collagen alpha 2(I
12	81.5	12.3	2204	2 A70524	probable PPS prote
13	79.5	12.0	1286	2 S28634	adhesin AIDA-1 pre
14	79.5	12.0	1509	2 B89985	hypothetical prote
15	78.5	11.9	320	2 G97016	comE-like protein,
16	78.5	11.9	645	1 SUBSMP	serine proteinase
17	78.5	11.9	1417	2 A83080	hypothetical prote
18	78.5	11.9	1615	2 B49502	protein-tyrosine-p
19	78.5	11.9	1651	2 JC1340	outer membrane pro
20	78.5	11.9	1767	2 A49502	protein-tyrosine-p
21	78	11.8	445	2 T34352	hypothetical prote
22	78	11.8	751	2 S64741	cuticle collagen -
23	77.5	11.7	180	2 AC0208	probable fimbrin
24	77.5	11.7	1109	2 A56143	surface-array prot
25	77.5	11.7	1665	2 T29008	hypothetical prote
26	77	11.6	469	2 A35789	glutamate-1-semial
27	77	11.6	1024	2 H87599	TonB-dependent rec
28	77	11.6	1569	2 A65044	hypothetical prote
29	76.5	11.6	255	2 T50916	hypothetical prote

30	76.5	11.6	713	1 UMMS	period clock prote
31	76.5	11.6	792	1 EAHU	elastin precursor,
32	76.5	11.6	1335	2 G90975	probable factor li
33	76.5	11.6	2383	2 D64962	probable membrane
34	76.5	11.6	2660	2 E85822	probable invasin Z
35	76	11.5	327	2 C97057	spore protease (im
36	76	11.5	395	2 AG2606	conserved hypothet
37	76	11.5	395	2 F97388	probable lipase (A
38	76	11.5	1052	2 AF2959	conserved hypothet
39	76	11.5	1219	2 T14578	nucleoporin Nup153
40	76	11.5	1341	2 H98323	hypothetical prote
41	75.5	11.4	309	1 KIECRB	ribokinase (SC 2.7
42	75.5	11.4	309	2 F91215	ribokinase (import
43	75.5	11.4	309	2 G86061	ribokinase (import
44	75.5	11.4	673	1 VCPVB5	coat protein VP1 -
45	75.5	11.4	1145	2 B75625	hypothetical prote

ALIGNMENTS

RESULT 1

A40618
fimbrin, SEF14 - Salmonella enteritidis
N:Alternate names: fimbrin, Sefa
C:Species: Salmonella enteritidis
C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A40618; A25034
R:Clouthier, S.C.; Muller, K.H.; Doran, J.L.; Collinson, S.K.; Kay, W.W.
J. Bacteriol. 175, 2523-2533, 1993
A:Title: Characterization of three fimbrial genes, sefABC, of Salmonella enteritidis.
A:Reference number: A40618; MUID:93239677; PMID:8097515
A:Contents: 27655-3b
A:Accession: A40618
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-165 <CLO>
A:Cross-references: UNIPROT:P12061; UNIPARC:UPI00001135BD; GB:L11008; NID:g310645; PID:130395
A>Note: sequence extracted from NCBI backbone (NCBIN:130387, NCBIP:130395)
R:Feutrier, J.; Kay, W.W.; Trust, T.J.
J. Bacteriol. 168, 221-227, 1986
A:Title: Purification and characterization of fimbriae from Salmonella enteritidis.
A:Reference number: A25034; MUID:87008384; PMID:2875990
A:Accession: A25034
A:Molecule type: protein

A:Residues: 22-78, 'X', '80-82, 'XQ', 128 <PFU>
A:Cross-references: UNIPARC:UPI0000179BD8
Query Match 100.0%; Score 662; DB 2; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.6e-50;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAQNTTSANWSQDPGFTGPAAGQKVGTLSTATGPHNSVSIAGKASVSGGVATVPFV 60
|||||

Db 38 AAQNTTSANWSQDPGFTGPAAGQKVGTLSTATGPHNSVSIAGKASVSGGVATVPFV 97
|||||

QY 61 DQCGQPVFRGRTOGANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTFTAT 120
|||||

Db 98 DQCGQPVFRGRTOGANINDQANTGIDGLAGWRVASSQETLNVPVTTFGKSTLPAGTFTAT 157
|||||

QY 121 FYVQYQYN 128
|||||

Db 158 FYVQYQYN 165
|||||

RESULT 2

T43040
hypothetical protein - fission yeast (Schizosaccharomyces pombe) (fragment)

C:Species: Schizosaccharomyces pombe

C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C:Accession: T43040

R:Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.

DNA Res. 4, 363-369, 1997

A;Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.

A;Reference number: Z1723; MUID:98162722; PMID:950191
A;Accession: T43040
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-319 <YOS>
A;Cross-references: UNIPROT:Q8TFG9; UNIPARC:UPI00000698D1; EMBL:D89219; NID:gi749645; P1
A;Experimental source: strain PR745

Query Match 13.8%; Score 91.5; DB 2; Length 319;
Best Local Similarity 23.5%; Pred. No. 1.1;
Matches 36; Conservative 15; Mismatches 57; Indels 45; Gaps 5;

QY 4 NTTSANWSQDPGFTGPAVAAGQKVGTLISITATGPHNSVSIAGKASVSGGVATV----- 57

DB 120 NPTAAPNE-----PVTVTGTEGVSVTTEPTTSTFSFTTIIIGTTIIPVPG 173

QY 58 -----PFVDGQGPVFRGRIQGAINDQANTGIDGLAGWRVASSQETLNV 102

DB 174 NPSSVSAPPTTSFTPGGSGVPSYNTTQGN-----TTSI-----WNSSNSTIVSNV 223

QY 103 PVTTFGKSTLPAG-----TTFATFYVOOYQ 127

DB 224 TAITGNVTITGDLTITIDPTTSTYLSGFG 256

RESULT 3

A83412

hypothetical protein PA1874 [imported] - Pseudomonas aeruginosa (strain PAO1)

C;Species: Pseudomonas aeruginosa

C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C;Accession: A83412

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho

A;Reference number: A82950; MUID:20437337; PMID:10984043

A;Accession: A83412

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-2468 <STO>

A;Cross-references: UNIPROT:Q912M3; UNIPARC:UPI00000C5483; GB:AE004613; GB:AE004091; NID

A;Experimental source: strain PAO1

C;Genetics:

A;Gene: PA1874

Query Match 13.8%; Score 91.5; DB 2; Length 2468;

Best Local Similarity 26.3%; Pred. No. 10;

Matches 36; Conservative 11; Mismatches 43; Indels 47; Gaps 7;

QY 7 SANWS-----QDP-GFTGPAVAAGQKVGTLISITATGPHNSVSIAGKA 48

DB 1284 SGNSFTPGTFLANGTVVNAVAQDPAGNTGQ-----GSTTVDVAVNTPVVNPNGN 1336

QY 49 SVSGGV---ATVPFVDGQGPVFRGRIQGAINDQANTGIDGLAGWRVASSQETLNV---V 102

DB 1337 LLNGTABPGSTVTLTDGNGNFI-----GQTADGSGNWSFTPGSQLENGTVV 1383

QY 103 PVT---TFGKSTLPAGT 116

DB 1384 NVTASDAAGNTSLPAT 1400

RESULT 4

GNVSNB

Genome polyprotein - maize dwarf mosaic virus (strain B) (fragment)

N;Contains: carboxyl end of nuclear inclusion protein b; coat protein

C;Species: maize dwarf mosaic virus, MDMV

C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004

C;Accession: PH0208

R;Frenkel, M.J.; Jilka, J.M.; McKern, N.M.; Strike, P.M.; Clark Jr., J.M.; Shukla, D.D.;

J. Gen. Virol. 72, 237-242, 1991

A;Title: Unexpected sequence diversity in the amino-terminal ends of the coat proteins

A;Reference number: PH0207; MUID:91132116; PMID:1993866

A;Accession: PH0208

A;Molecule type: genomic RNA

A;Residues: 1-380 <FRE>

A;Cross-references: UNIPROT:P32652; UNIPARC:UPI0000131E4F; GB:D00949; NID:g222059; P1D

C;Species: tobacco etch virus genome polyprotein

C;Keywords: coat protein; inclusion protein

F;1-52/Product: nuclear inclusion protein b (fragment) #status predicted <NIP>

F;53-380/Product: coat protein #status predicted <COA>

Query Match 13.2%; Score 87.5; DB 1; Length 380;

Best Local Similarity 30.1%; Pred. No. 2.9;

Matches 31; Conservative 9; Mismatches 54; Indels 9; Gaps 2;

QY 11 SQDPGFTGPAVAAGQKVGTLISITATGPHNSVSIAGKASVSGGVATVPFVDGQGPVFRG 70

DB 64 SGSQGTTPATGSGAK-----PATSGAGSGGTGAGTGTGQARTSGTGTGSGATGG 117

QY 71 RIQGANINDQANTGIDGLAGWRVASSQETLNVPTTFGKSTLP 113

DB 118 QSGSGSGTEQVNT---GSAGTNATGQDRDQDVGSTGKISVP 157

RESULT 5

Ti6509

hypothetical protein F59A6.3 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C;Accession: Ti6509

R;Nhan, M.

submitted to the EMBL Data Library, December 1995

A;Description: The sequence of C. elegans cosmid F59A6.

A;Reference number: Z18526

A;Accession: Ti6509

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-786 <NHA>

A;Cross-references: UNIPROT:Q21027; UNIPARC:UPI000007A7BF; EMBL:U41994; NID:gi123047;

C;Genetics:

A;Gene: CESP:F59A6.3

A;Introns: 106/1; 620/1; 634/3; 675/3; 775/1

Query Match 12.8%; Score 85; DB 2; Length 786;

Best Local Similarity 27.4%; Pred. No. 11;

Matches 34; Conservative 15; Mismatches 63; Indels 12; Gaps 5;

QY 4 NTTS--ANWSQDPGFTGPAVAAGQKVGTLISITATGPHNSVSIAGKASVSGGVATVP--- 58

DB 348 STTSRASSASDDPTTGTGPTTSGSTASTTS---GSLFSTSL-GSSQSPGSSVSTTPGPS 402

QY 59 FVDGQGPVFRGRIQGANINDQANTGIDGLAGWRVASSQETL--NVPVTFGKSTLPAGT 116

DB 403 TTSGISQSTSGTPTTTSBPTTSGTSTSGTSTSGPSTTSGPSTTTLGTTQSTTSGPSTTPGST 462

QY 117 FTAT 120

DB 463 ISTT 466

RESULT 6

AC3528

extracellular serine proteinase (EC 3.4.21.-) [imported] - Brucella melitensis (strain

C;Species: Brucella melitensis

C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

C;Accession: AC3528

R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova

; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Lete

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A;Title: The genome sequence of the facultative intracellular pathogen Brucella melite

A;Reference number: AD3252; PMID:11756688

A;Accession: AC3528

A;Status: preliminary

A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
 A;Reference number: A82950; MUID:20437337; PMID:10984043
 A;Accession: E82954
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-674 <STO>
 A;Cross-references: UNIPROT:Q9HT30; UNIPARC:UPI000000C6066; GB:AE004091; NID:10984043
 A;Experimental source: strain PA01
 C;Genetics:
 A;Gene: PA5544

Query Match 12.3%; Score 81.5; DB 2; Length 674;
 Best Local Similarity 28.3%; Pred. No. 18;
 Matches 32; Conservative 17; Mismatches 51; Indels 13; Gaps 6;
 QY 15 GFTGPAVAAGKQVTLITATGPHNSVSIAGKAS--VSGGVATVPFVDGQ-QPVFRGR 71
 Db 207 GLFGHRVGGPAKVSFSSALWG-----TITSGVANVVTGQFTPLMKRFGYKPAFAGG 261
 QY 72 IQG-ANINDQANTGIDGLAGRWVASSOETLNVPVTFGKSTL-PAGFTATFY 122
 Db 262 VEATASGSQLPPVPMGAVAFIMA---ETINVPYVEIAKAALIPALLYFGSVY 311

RESULT 11

A43291
 collagen alpha 2(I) chain precursor - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C;Accession: A43291; A54328
 R;Phillips, C.L.; Morgan, A.L.; Lever, L.W.; Wenstrup, R.J.
 J. Invest. Dermatol. 97, 980-984, 1991
 A;Title: Sequence analysis of a full-length cDNA for the murine pro alpha 2(I) collagen
 A;Reference number: A43291; MUID:92372043; PMID:1505972
 A;Accession: A43291
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-1373 <PHI>
 A;Cross-references: UNIPROT:Q01149; UNIPARC:UPI0000044DC6; GB:X58251; NID:950488; PIDN:Q01149
 A;Note: sequence extracted from NCBI backbone (NCBI:112027)
 R;Phillips, C.L.; Lever, L.W.; Pinnell, S.R.; Quarles, L.D.; Wenstrup, R.J.
 J. Invest. Dermatol. 97, 980-984, 1991
 A;Title: Construction of a full-length murine Proalpha2(I) collagen cDNA by the polymerase chain reaction
 A;Reference number: A54328; MUID:92084969; PMID:1748823
 A;Accession: A54328
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-110 <PH2>
 A;Cross-references: UNIPARC:UPI00000173BA1
 C;Genetics:
 A;Gene: COL1A2
 C;Superfamily: collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal homology
 C;Keywords: coiled coil; extracellular matrix; glycoprotein; trimer; triple helix
 F;1145-1373/Domain: fibrillar collagen carboxyl-terminal homology <FCC>

Query Match 12.3%; Score 81.5; DB 1; Length 1373;
 Best Local Similarity 34.1%; Pred. No. 40;
 Matches 29; Conservative 9; Mismatches 30; Indels 17; Gaps 4;
 QY 14 PGFTGPAVAAGKQVTLITATGPHNSVSIAGKAS-----VSGGVATVPFVDGQ-QPVF 68
 Db 957 PGSIGPTGAAG-----APGPHGSVGPAGKHNRGEPGPAAGVGPVAVGPRGSPG 1007
 QY 69 RGRIOG--ANINDQANTGIDGLAGW 91
 Db 1008 QG-IRGDKGEPGDKHGRGLPLKGY 1031

RESULT 12

A70524
 probable PPE protein - *Mycobacterium tuberculosis* (strain H37RV)
 C;Species: *Mycobacterium tuberculosis*
 C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C;Accession: A70524
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
 A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A;Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome sequence
 A;Reference number: A70500; MUID:98295987; PMID:9634230
 A;Accession: A70524
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-2204 <COL>
 A;Cross-references: UNIPARC:UPI000000C155E; GB:Z96800; GB:AL123456; NID:93261800; PIDN:UPI000000C155E
 A;Experimental source: strain H37RV
 C;Genetics:
 A;Gene: PPE

Query Match 12.3%; Score 81.5; DB 2; Length 2204;
 Best Local Similarity 24.8%; Pred. No. 67;
 Matches 33; Conservative 18; Mismatches 51; Indels 31; Gaps 7;
 QY 17 TGPV---AAGK-----VGTLSITATGPHNSVSIAGKASVS---GGVATVPFVDGQ 65
 Db 367 TGDIVLSSIAQRAHFGPITIPNITVVGFTTVAIGPNTAITITGGGAIRIPLISIPAA 426
 QY 66 PVFRGRIQGANINDOA---NTGIDGLAG-----WRVASSOETLN--VPVTFGK 109
 Db 427 PGF---GNSTNPSSGPFNTGAGAGSGFGNGFGANGSFWNLASATSGASGLLNVALGS 482
 QY 110 STLPAGTFTATFY 122
 Db 483 GLANVTTVSGFY 495

RESULT 13

S28634
 adhesin AIDA-I precursor - *Escherichia coli* plasmid pIB6
 C;Species: *Escherichia coli*
 C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
 C;Accession: S28634; S22680; S28881; S72657
 R;Benz, I.
 submitted to the EMBL Data Library, March 1992
 A;Reference number: S28634
 A;Accession: S28634
 A;Molecule type: DNA
 A;Residues: 1-1286 <BEN>
 A;Cross-references: UNIPROT:Q03155; UNIPARC:UPI0000125732; EMBL:X65022; NID:942254; PIDN:UPI0000125732
 R;Benz, I.; Schmidt, M.A.
 Mol. Microbiol. 6, 1539-1546, 1992
 A;Title: AIDA-I, the adhesin involved in diffuse adherence of the diarrhoeagenic *Escherichia coli* serotype O157:H7
 A;Reference number: S22680; MUID:92326638; PMID:1625582
 A;Accession: S22680
 A;Molecule type: DNA
 A;Residues: 839-1286 <BEN>
 A;Cross-references: UNIPARC:UPI000017AA2E; EMBL:X65022
 A;Experimental source: strain 2787
 A;Accession: S28881
 A;Molecule type: protein
 A;Residues: 50-56 <BEN>
 A;Cross-references: UNIPARC:UPI000017AA2F
 A;Experimental source: strain 2787
 R;Suhr, M.; Benz, I.; Schmidt, M.A.
 Mol. Microbiol. 22, 31-42, 1996
 A;Title: Processing of the AIDA-I precursor: removal of AIDA and evidence for the outer membrane localization of AIDA-I
 A;Reference number: S72657; MUID:97055419; PMID:8899706
 A;Accession: S72657
 A;Molecule type: protein
 A;Residues: 847-856 <SUH>
 A;Cross-references: UNIPARC:UPI000017AA30
 A;Experimental source: DAEC strain 2787
 C;Genetics:
 A;Genome: plasmid pIB6

C;Keywords: membrane protein

F;1-49/Domain: signal sequence #status predicted <SIG>
F;50-1286/Product: adhesin AIDA-I #status predicted <MAT>

Query Match 12.0%; Score 79.5; DB 2; Length 1286;
Best Local Similarity 24.6%; Pred. No. 55;
Matches 41; Conservative 19; Mismatches 54; Indels 53; Gaps 7;
QY 4 NTSANWQDPQFTGPA-----VAAGQKVGTL-----SITATGPHNS- 40
DB 493 NFLTAVSMFCTAGSANNVLSGRINAFAGNVVGTILNQEGRYVYSGATATSTVGNNEG 552
QY 41 -----VSIAGKASVSGGVATVPFV-DGQGQVPV-RRIGQANINDQANTG 84
DB 553 REYVLSGGITDGTVLNLSGGLQAVSSGKASATVINEGGAQFVYDGGQVGTGNIKNGGTI- 611
QY 85 IDGLAGWRVASSQETLNVPTTFGK-----STLPAGTFTATFYVQQ 125
DB 612 -----RVDGASALNTALSSGGNLTFTGTATLPELTMAALSVSQ 651

RESULT 14

B99985

Hypothetical protein SA1766 [imported] - Staphylococcus aureus (strain N315)

C;Species: Staphylococcus aureus

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C;Accession: B99985

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A;Reference number: B99758; MUID:21311952; PMID:11418146

A;Accession: B99985

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1509 <KUR>

A;Cross-references: UNIPROT:Q998T6; UNIPARC:UPI00000C7F8E; GB:BA0000018; PID:g13701750; E

A;Experimental source: strain N315

C;Genetics:

A;Gene: SA1766

Query Match 12.0%; Score 79.5; DB 2; Length 1509;
Best Local Similarity 28.6%; Pred. No. 65;
Matches 28; Conservative 9; Mismatches 34; Indels 27; Gaps 3;

QY 9 NWSQDPGFTGPAVAGQKVGTLST--ATGPH-----NSVS 42
DB 1194 NFSKSP-SGTWKPGDVVGLTGTFTGPHLFEMERNGRHFDPPEYLRNKKKGRLS 1252

QY 43 IAGKASVSGGVATVPFVDGQGPVFRGRIQGANINDQ 80

DB 1253 IGGGATSGGATYASRVIRQAQSILGGRYKGIHDQ 1290

RESULT 15

G97016

comE-like protein, Metallo beta-lactamase superfamily hydrolase, secreted [imported] - C

C;Species: Clostridium acetobutylicum

C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004

C;Accession: G97016

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo

A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: G97016

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-320 <KUR>

A;Cross-references: UNIPROT:Q9YKH3; UNIPARC:UPI00000D46B5; GB:AE001437; PIDN:AAK78922.1;

A;Experimental source: Clostridium acetobutylicum ATCC824

C;Genetics:

A;Gene: CAC0946

C;Superfamily: Bacillus halodurans late competence protein homolog

Query Match 11.9%; Score 78.5; DB 2; Length 320;
Best Local Similarity 28.0%; Pred. No. 14;
Matches 26; Conservative 13; Mismatches 41; Indels 13; Gaps 2;
QY 17 TGPVAAAGQKVGTLSTATGPHNSVSIAGKASVSGGVATVPFVDGQGPVFRGRIQGAN 76
DB 142 TNPVVGSTFKVGSANCIVVGPINTNS-----ENLNTYSIVIKLTYGNNKFMFTGDAQSSN 196
QY 77 INDQANTGID-----GLAGWRVASSQETLN 101
DB 197 EPDMINAGFDLSADVLKVGHHGSHSTSSQDFLN 229

Search completed: April 26, 2006, 17:04:59

Job time : 17 secs